PAH-MODULATING COMPOSITIONS AND METHODS

SEQUENCE LISTING

The instant application contains a Sequence Listing which has been submitted electronically in XML format compliant with WIPO Standard ST.26 and is hereby incorporated by reference in its entirety. Said XLM copy, created on November 7, 2022, is named V2065-7025WO_SL.xml and is 51,647,776 bytes in size.

CROSS REFERENCE TO RELATED APPLICATIONS

This application claims the benefit of U.S. Provisional Application No. 63/241,897, filed September 8, 2021, U.S. Provisional Application No. 63/303,927, filed January 27, 2022, and U.S. Provisional Application No. 63/367,025, filed June 24, 2022. The contents of the aforementioned applications are hereby incorporated by reference in their entirety.

BACKGROUND

Integration of a nucleic acid of interest into a genome occurs at low frequency and with little site specificity, in the absence of a specialized protein to promote the insertion event. Some existing approaches, like CRISPR/Cas9, are more suited for small edits that rely on host repair pathways, and are less effective at integrating longer sequences. Other existing approaches, like Cre/loxP, require a first step of inserting a loxP site into the genome and then a second step of inserting a sequence of interest into the loxP site. There is a need in the art for improved compositions (e.g., proteins and nucleic acids) and methods for inserting, altering, or deleting sequences of interest in a genome.

PKU is an inherited disorder involving an autosomal recessive inborn error of metabolism caused by a deficiency in the hepatic enzyme PAH. PAH catalyzes the hydroxylation of phenylalanine to tyrosine, the rate-limiting step in phenylalanine metabolism. The reaction is dependent on tetrahydrobiopterin (BH4), as a cofactor, molecular oxygen, and iron. Loss-of-function mutations in one, or both, copies of the PAH gene lead to a non-functional, or less efficient enzyme. This ultimately results in phenotypically severe forms of PKU where phenylalanine in the blood can accumulate to toxic concentrations, with impaired levels of plasma tyrosine.

Additionally, the deficiency prevents normal synthesis of downstream products, including dopamine, norepinephrine, and melanin.

The *PAH* genomic sequence and its flanking regions span about 171 kb, containing 13 exons. Study of pathogenic allelic variants have identified more than 500 different disease-causing mutations in the *PAH* gene (Mitchell, *et al. Genet Med*. 2011; 13:697-707). Of these mutations, approximately 62% have been characterized as missense, 13% deletions, 11% splice, 6% silent, 5% nonsense, 2% insertion, and < 1% deletion or duplication of exons. The identification of several PAH mutations have been described for their effects on enzymatic activity using enzyme kinetics and crystallographic studies. Mutations affecting the catalytic binding mode, including Y138F, S23A, and Y377F, were observed with reduced propensity for tetramer formation (Flydal, *et al*. *PNAS*. 2019; 116(23):11229-34). Other residues that interact with BH_4 in the precatalytic conformation (amino acids 245–255, 286, 322, and 325) also interact with BH_4 in the catalytic conformation, and, in addition, these sites are actually associated with severe destabilization of PAH.

Naturally occurring N-terminal PAH mutations have been determined to be distributed in a nonrandom pattern, clustering within residues 46-48 (GAL motif) and 65-69 (IESRP motif (SEQ ID NO: 37634)), both motifs highly conserved in pyruvate dehydrogenase (PDH) (Gjetting, *et al*. *Am./ J. Hum. Genet.* 2001; 68:1353-60). Structure-function studies demonstrated that mutations in these regions drastically reduced phenylalanine binding. Most missense mutations identified in PKU to date result in phenotypic outcomes associated with misfolding of the PAH enzyme, increased protein turnover, and loss of enzymatic function. Residues in exons 7-9 and in interdomain regions within the subunit appear to play an important structural role and constitute hotspots for destabilization. Additionally, using recombinant forms of hPAH, mutations in BH_4 responsive domains, including R408W and Y414C showed residual activity, but had perturbed allostery suggesting altered protein conformation (Gersting, *et al*. *Hum. Genet*. 2008; 83:5-17). Mutation analyses and structure-function analyses have identified a robust genotype-phenotype mapping for PAH's role in PKU; however, outside of lifetime symptom management strategies, there has not been a successful cure.

Dietary therapy of phenylalanine (Phe) remains to be the mainstay treatment for PKU since its introduction in 1953. In the 1970s, tetrahydrobiopterin (BH_4) and neurotransmitter precursor (L-dopa/carbidopa and 5-hydroxytryptophan) combination therapy showed promise in modulating

PKU. Since its institution as a therapy, synthetics such as sapropterin have been formulated for as small molecule isomers of BH_4. Although, this form of therapy is generally only useful in patients with mild subsets of PAH-deficient PKU. It is thought that the therapy responsiveness is associated with mutations in the PAH gene resulting in some residual enzyme activity. At high blood concentrations, Phe in the blood will compete with other large neutral amino acids (LNAAs) for transport across the blood-brain barrier. LNAA supplementation has been shown to reduce cerebral Phe concentrations despite the observed increase in plasma Phe levels. Likewise, dietary supplementation with glycomacropeptides (GMP) has been observed to significantly reduce ureagenesis, improved protein retention, and Phe utilization. Although, these strategies do little to address the increased blood levels of Phe or the genotypic drivers.

Modern non-dietary approaches include the development of PAH-based fusion proteins and enzyme substitution therapies. Enzyme substitution therapies can include administration of phenylalanine ammonia-lyase (PAL) to a patient. PAL is an enzyme which catalyzes the conversion of Phe to transcinnamic acid and insignificant amounts of ammonia. Early studies using PAL administered in enteric-coated gelatin capsules to PKU patients, showed reductions in Phe levels; however, repeated dosing *in vivo* resulted in mounting of immune responses. Although, these approaches are not practical from a clinical perspective as several intravenous injections would be required due to the limited half-life of circulating enzymes. Gene therapy has shown some promise, for example using viral vectors, in rescuing PAH functionality. However, the efficacy of this strategy is hampered by the very low gene transfer rate and transient transgene expression. Accordingly, there is a need for new and more effective treatments for targeting *PAH* in PKU.

SUMMARY OF THE INVENTION

This disclosure relates to novel compositions, systems, and methods for altering a genome at one or more locations in a host cell, tissue, or subject, *in vivo* or *in vitro*. The disclosure provides gene modifying systems that are capable of modulating (e.g., inserting, altering, or deleting sequences of interest) phenylalanine hydroxylase (PAH) activity and methods of treating phenylketonuria (PKU) by administering one or more such systems to alter a genomic sequence, such as to correct mutations, within the *PAH* gene on the human chromosome 12q23.2 involved as a genetic driver in PKU.

In one aspect, the disclosure relates to a system for modifying DNA to correct a human PAH gene mutation causing PKU comprising (a) a nucleic acid encoding a gene modifying polypeptide capable of target primed reverse transcription, the polypeptide comprising (i) a reverse transcriptase domain and (ii) a Cas9 nickase that binds DNA and has endonuclease activity, and (b) a template RNA comprising (i) a gRNA spacer that is complementary to a first portion of the human PAH gene, (ii) a gRNA scaffold that binds the polypeptide, (iii) a heterologous object sequence comprising a mutation region to correct the mutation, and (iv) a primer binding site (PBS) sequence comprising at least 3, 4, 5, 6, 7, or 8 bases of 100% homology to a target DNA strand at the 3´ end of the template RNA. In some embodiments, the PAH gene may comprise a R408W mutation. In some embodiments, the PAH gene may comprise a R261Q mutation. In some embodiments, the PAH gene may comprise a R243Q mutation. In some embodiments, the PAH gene may comprise a IVS10-11G>A mutation. The template RNA sequence may comprise a sequence described herein, e.g., in Table 1A, 1B, 1C, 1D, 3A, 3B, 3C, 3D, 4A, 4B, 4C, 4D, 5A-5F, 8A-8D, E3, E3A, BB, E5, E5A, E6, or E6A.

The gRNA spacer may comprise at least 15 bases of 100% homology to the target DNA at the 5´ end of the template RNA. The template RNA may further comprise a PBS sequence comprising at least 5 bases of at least 80% homology to the target DNA strand. The template RNA may comprise one or more chemical modifications.

The domains of the gene modifying polypeptide may be joined by a peptide linker. The polypeptide may comprise one or more peptide linkers. The gene modifying polypeptide may further comprise a nuclear localization signal. The polypeptide may comprise more than one nuclear localization signal, e.g., multiple adjacent nuclear localization signals or one or more nuclear localization signals in different regions of the polypeptide, e.g., one or more nuclear localization signals in the N-terminus of the polypeptide and one or more nuclear localization signals in the C-terminus of the polypeptide. The nucleic acid encoding the gene modifying polypeptide may encode one or more intein domains.

Introduction of the system into a target cell may result in insertion of at least 1, 2, 3, 4, 5, 10, 15, 20, 25, 30, 35, 40, 45, 50, 60, 70, 80, 90, 100, 150, 200, 250, 300, 350, 400, 500, or 1000 base pairs of exogenous DNA. Introduction of the system into a target cell may result in deletion, wherein the deletion is less than 2, 3, 4, 5, 10, 50, or 100 base pairs of genomic DNA

upstream or downstream of the insertion. Introduction of the system into a target cell may result in substitution, e.g., substitution of 1, 2, or 3 nucleotides, e.g., consecutive nucleotides.

The heterologous object sequence may be at least 5, 10, 25, 50, 100, 150, 200, 250, 300, 400, 500, 600, or 700 base pairs.

In one aspect, the disclosure relates to a pharmaceutical composition comprising the system described above and a pharmaceutically acceptable excipient or carrier, wherein the pharmaceutically acceptable excipient or carrier is selected from the group consisting of a plasmid vector, a viral vector, a vesicle, and a lipid nanoparticle. In one aspect, the disclosure relates to a pharmaceutical composition comprising the system described above and multiple pharmaceutically acceptable excipients or carriers, wherein the pharmaceutically acceptable excipients or carriers are selected from the group consisting of a plasmid vector, a viral vector, a vesicle, and a lipid nanoparticle, e.g., where the system described above is delivered by two distinct excipients or carriers, e.g., two lipid nanoparticles, two viral vectors, or one lipid nanoparticle and one viral vector. The viral vector may be an adeno-associated virus (AAV).

In one aspect, the disclosure relates to a host cell (e.g., a mammalian cell, e.g., a human cell) comprising the system described above.

In one aspect, the disclosure relates to a method of correcting a mutation in the human PAH gene in a cell, tissue or subject, the method comprising administering the system described above to the cell, tissue or subject, wherein optionally the correction of the mutant PAH gene comprises an amino acid substitution of W408R, Q261R, and/or Q243R (reversing the pathogenic substitution which is R408W, R261Q, or R243Q). In another aspect, the correction of the mutant PAH gene comprises a nucleic acid substitution of IVS10-11A>G (reversing the pathogenic substitution which is IVS10-11G>A). The system may be introduced *in vivo*, *in vitro*, *ex vivo*, or *in situ*. The nucleic acid of (a) may be integrated into the genome of the host cell. In some embodiments, the nucleic acid of (a) is not integrated into the genome of the host cell. In some embodiments, the heterologous object sequence is inserted at only one target site in the host cell genome. The heterologous object sequence may be inserted at two or more target sites in the host cell genome, e.g., at the same corresponding site in two homologous chromosomes or at two different sites on the same or different chromosomes. The heterologous object sequence may encode a mammalian polypeptide, or a fragment or a variant thereof. The components of the system may be delivered on 1, 2, 3, 4, or more distinct nucleic acid molecules.

The system may be introduced into a host cell by electroporation or by using at least one vehicle selected from a plasmid vector, a viral vector, a vesicle, and a lipid nanoparticle.

Features of the compositions or methods can include one or more of the following enumerated embodiments.

Enumerated Embodiments

1. A template RNA comprising, e.g., from 5’ to 3’:

(i) a gRNA spacer that is complementary to a first portion of the human PAH gene, wherein the gRNA spacer has a sequence comprising the core nucleotides of a gRNA spacer sequence of Table 1A, Table 1B, Table 1C, or Table 1D, or a sequence having 1, 2, or 3 substitutions thereto, and optionally comprises one or more consecutive nucleotides starting with the 3’ end of the flanking nucleotides of the gRNA spacer (e.g., comprises one or more flanking nucleotides that are adjacent to the core nucleotides), or wherein the gRNA spacer has a sequence of a spacer chosen from Tables 5A-5F, 8A-8D, E3, E3A, BB, E5, E5A, E6, or E6A;

(ii) a gRNA scaffold that binds a gene modifying polypeptide (e.g., binds the Cas domain of the gene modifying polypeptide),

(iii) a heterologous object sequence comprising a mutation region to introduce a mutation into (e.g., to correct a mutation in) a second portion of the human PAH gene (wherein optionally the heterologous object sequence comprises, from 5’ to 3’, a post-edit homology region, a mutation region, and a pre-edit homology region), and

(iv) a primer binding site (PBS) sequence comprising at least 3, 4, 5, 6, 7, or 8 bases with 100% identity to a third portion of the human PAH gene.

2. The template RNA of embodiment 1, wherein the heterologous object sequence comprises the core nucleotides of an RT template sequence from Table 3A, Table 3B, Table 3C, or Table 3D, or a sequence having 1, 2, or 3 substitutions thereto, and optionally comprises one or more consecutive nucleotides starting with the 3’ end of the flanking nucleotides of the RT template sequence, or wherein the heterologous object sequence comprises a sequence of an RT template sequence from Tables 5A-5F, 8A-8D, E3, E3A, BB, E5, E5A, E6, or E6A.

3. The template RNA of embodiment 1, wherein the heterologous object sequence comprises the core nucleotides of the RT template sequence of Table 3A, Table 3B, Table 3C, or Table 3D that corresponds to the gRNA spacer sequence, or a sequence having 1, 2, or 3 substitutions thereto, and optionally comprises one or more consecutive nucleotides starting with the 3' end of the flanking nucleotides of the RT template sequence (e.g., comprises one or more flanking nucleotides that are adjacent to the core nucleotides), or wherein the heterologous object sequence comprises a sequence of an RT template sequence from Tables 5A-5F, 8A-8D, E3, E3A, BB, E5, E5A, E6, or E6A.

4. The template RNA according to any one of embodiments 1-3 wherein the PBS sequence has a sequence comprising the core nucleotides of the PBS sequence from the same row of Table 3A, Table 3B, Table 3C, or Table 3D as the RT template sequence, or a sequence having 1, 2, or 3 substitutions thereto, and optionally comprises one or more consecutive nucleotides starting with the 5' end of the flanking nucleotides of the PBS sequence (e.g., comprises one or more flanking nucleotides that are adjacent to the core nucleotides).

5. The template RNA according to any one of embodiments 1-3, wherein the PBS sequence has a sequence comprising the core nucleotides of a PBS sequence of Table 3A, Table 3B, Table 3C, or Table 3D that corresponds to the RT template sequence, or a sequence having 1, 2, or 3 substitutions thereto, the gRNA spacer sequence, or both, and optionally comprises one or more consecutive nucleotides starting with the 5' end of the flanking nucleotides of the PBS sequence, or wherein the PBS sequence comprises a PBS sequence from Tables 5A-5F, 8A-8D, E3, E3A, BB, E5, E5A, E6, or E6A that corresponds to the RT template sequence, or a sequence having 1, 2, or 3 substitutions thereto, the gRNA spacer sequence, or both.

6. The template RNA according to any of embodiments 1-5, wherein the gRNA scaffold comprises a sequence of a gRNA scaffold of Table 12, or a sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, or 99% identity thereto.

7. The template RNA according to any of embodiments 1-5, wherein the gRNA scaffold comprises a sequence of a gRNA scaffold of Table 12 that corresponds to the RT template sequence, the gRNA spacer sequence, or both, or a sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, or 99% identity thereto.

8. A template RNA comprising, e.g., from 5' to 3':

(i) a gRNA spacer that is complementary to a first portion of the human PAH gene,

(ii) a gRNA scaffold that binds a gene modifying polypeptide (e.g., binds the Cas domain of the gene modifying polypeptide),

(iii) a heterologous object sequence comprising a mutation region to introduce a mutation into a second portion of the human PAH gene, wherein the heterologous object sequence comprises the core nucleotides of an RT template sequence of Table 3A, Table 3B, Table 3C, or Table 3D, or a sequence having 1, 2, or 3 substitutions thereto, and optionally comprises one or more consecutive nucleotides starting with the 3' end of the flanking nucleotides of the RT template sequence, or wherein the heterologous object sequence comprises an RT template sequence of Tables 5A-5F, 8A-8D, E3, E3A, BB, E5, E5A, E6, or E6A; and

(iv) a PBS sequence comprising at least 3, 4, 5, 6, 7, or 8 bases of 100% identity to a third portion of the human PAH gene.

9. The template RNA of embodiment 8, wherein the gRNA spacer comprises the core nucleotides of a gRNA spacer sequence of Table 1A, Table 1B, Table 1C, or Table 1D, or a sequence having 1, 2, or 3 substitutions thereto, and optionally comprises one or more consecutive nucleotides starting with the 3' end of the flanking nucleotides of the gRNA spacer sequence, or wherein the gRNA spacer comprises a gRNA spacer sequence of Tables 5A-5F, 8A-8D, E3, E3A, BB, E5, E5A, E6, or E6A.

10. The template RNA of any one of embodiments 1-9, wherein the gRNA spacer comprises ACCTCAATCCTTTGGGTGTA (SEQ ID NO: 16355), or a sequence having 1, 2, or 3 substitutions thereto.

11. The template RNA of any one of embodiments 1-9, wherein the gRNA spacer comprises CCTCAATCCTTTGGGTGTAT (SEQ ID NO: 16332) , or a sequence having 1, 2, or 3 substitutions thereto.

12. The template RNA of any one of embodiments 1-9, wherein the gRNA spacer comprises TGGGTCGTAGCGAACTGAGA (SEQ ID NO: 16102), or a sequence having 1, 2, or 3 substitutions thereto.

13. The template RNA of any one of embodiments 1-9, wherein the gRNA spacer comprises GGGTCGTAGCGAACTGAGAA (SEQ ID NO: 16084), or a sequence having 1, 2, or 3 substitutions thereto.

14. The template RNA of any one of embodiments 1-9, wherein the gRNA spacer comprises TAGCGAACTGAGAAGGGCCA (SEQ ID NO: 16011), or a sequence having 1, 2, or 3 substitutions thereto.

15. The template RNA of any one of embodiments 1-9, wherein the gRNA spacer comprises ACTTTGCTGCCACAATACCT (SEQ ID NO: 16032), or a sequence having 1, 2, or 3 substitutions thereto.

16. The template RNA of embodiment 8, wherein the heterologous object sequence comprises the core nucleotides of the gRNA spacer sequence of Table 1A, Table 1B, Table 1C, or Table 1D that corresponds to the RT template sequence, or a sequence having 1, 2, or 3 substitutions thereto, and optionally comprises one or more consecutive nucleotides starting with the 3’ end of the flanking nucleotides of the gRNA spacer sequence, or wherein the heterologous object sequence comprises the nucleotides of the gRNA spacer sequence of Tables 5A-5F, 8A-8D, E3, E3A, BB, E5, E5A, E6, or E6A that corresponds to the RT template sequence, or a sequence having 1, 2, or 3 substitutions thereto.

17. The template RNA according to any one of embodiments 8-16, wherein the PBS sequence has a sequence comprising the core nucleotides of the PBS sequence from the same

row of Table 3A, Table 3B, Table 3C, or Table 3D as the RT template sequence, or a sequence having 1, 2, or 3 substitutions thereto, and optionally comprises one or more consecutive nucleotides starting with the 5' end of the flanking nucleotides of the PBS sequence.

18. The template RNA according to any one of embodiments 8-16, wherein the PBS sequence has a sequence comprising the core nucleotides of a PBS sequence of Table 3A, Table 3B, Table 3C, or Table 3D that corresponds to the RT template sequence, or a sequence having 1, 2, or 3 substitutions thereto, the gRNA spacer sequence, or both, and optionally comprises one or more consecutive nucleotides starting with the 5' end of the flanking nucleotides of the PBS sequence, or wherein the PBS sequence has a sequence comprising the a PBS sequence of Tables 5A-5F, 8A-8D, E3, E3A, BB, E5, E5A, E6, or E6A that corresponds to the RT template sequence, the gRNA spacer sequence, or both.

19. The template RNA according to any of embodiments 8-18, wherein the gRNA scaffold comprises a sequence of a gRNA scaffold of Table 12, or a sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, or 99% identity thereto.

20. The template RNA according to any of embodiments 8-18, wherein the gRNA scaffold comprises a sequence of a gRNA scaffold of Table 12 that corresponds to the RT template sequence, the gRNA spacer sequence, or both, or a sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, or 99% identity thereto.

21. A gene modifying system for modifying DNA, comprising:

(a) a first RNA comprising, from 5' to 3, (i) a guide RNA sequence that is complementary to a first portion of the human PAH gene, wherein the guide RNA sequence has a sequence comprising the core nucleotides of a spacer sequence of Table 1A, Table 1B, Table 1C, or Table 1D, or a sequence having 1, 2, or 3 substitutions thereto, and optionally comprises one or more consecutive nucleotides starting with the 3' end of the flanking nucleotides of the guide RNA sequence, or wherein the guide RNA sequence has a sequence of a spacer chosen from Tables 5A-5F, 8A-8D, E3, E3A, BB, E5, E5A, E6, or E6A; and (ii) a sequence (e.g., a

scaffold region) that binds a gene modifying polypeptide (e.g., binds the Cas domain of the gene modifying polypeptide), and

(b) a second RNA comprising (iii) a heterologous object sequence comprising a nucleotide substitution to introduce a mutation into a second portion of the human PAH gene (wherein optionally the heterologous object sequence comprises, from 5' to 3', a post-edit homology region, a mutation region, and a pre-edit homology region), (iv) a primer region comprising at least 5, 6, 7, or 8 bases of 100% identity to a third portion of the human PAH gene, and (v) an RRS (RNA binding protein recognition sequence) that binds a gene modifying protein.

22. The gene modifying system of embodiment 21, wherein the heterologous object sequence comprises the core nucleotides of an RT template sequence from Table 3A, Table 3B, Table 3C, or Table 3D, or a sequence having 1, 2, or 3 substitutions thereto, and optionally comprises one or more consecutive nucleotides starting with the 3' end of the flanking nucleotides of the RT template sequence, or wherein the heterologous object sequence comprises a sequence of an RT template sequence from Tables 5A-5F, 8A-8D, E3, E3A, BB, E5, E5A, E6, or E6A, or a sequence having 1, 2, or 3 substitutions thereto.

23. The gene modifying system of embodiment 21, wherein the heterologous object sequence comprises the core nucleotides of the RT template sequence of Table 3A, Table 3B, Table 3C, or Table 3D that corresponds to the gRNA spacer sequence, or a sequence having 1, 2, or 3 substitutions thereto, and optionally comprises one or more consecutive nucleotides starting with the 3' end of the flanking nucleotides of the RT template sequence, or wherein the heterologous object sequence comprises a sequence of an RT template sequence from Tables 5A-5F, 8A-8D, E3, E3A, BB, E5, E5A, E6, or E6A that corresponds to the gRNA spacer sequence, or a sequence having 1, 2, or 3 substitutions thereto.

24. The gene modifying system of any one of embodiments 21-23, wherein the PBS sequence has a sequence comprising the core nucleotides of the PBS sequence from the same row of Table 3A, Table 3B, Table 3C, or Table 3D as the RT template sequence, or a sequence having 1, 2, or 3 substitutions thereto, and optionally comprises one or more consecutive

nucleotides starting with the 5’ end of the flanking nucleotides of the PBS sequence, or wherein the PBS sequence has a sequence of a PBS sequence from Tables 5A-5F, 8A-8D, E3, E3A, BB, E5, E5A, E6, or E6A, or a sequence having 1, 2, or 3 substitutions thereto.

25. The gene modifying system of one of embodiments 21-23, wherein the PBS sequence has a sequence comprising the core nucleotides of a PBS sequence of Table 3A, Table 3B, Table 3C, or Table 3D that corresponds to the RT template sequence, or a sequence having 1, 2, or 3 substitutions thereto, the gRNA spacer sequence, or both, and optionally comprises one or more consecutive nucleotides starting with the 5’ end of the flanking nucleotides of the PBS sequence, or wherein the PBS sequence has a sequence of a PBS sequence from Tables 5A-5F, 8A-8D, E3, E3A, BB, E5, E5A, E6, or E6A that corresponds to the RT template sequence, or a sequence having 1, 2, or 3 substitutions thereto.

26. The gene modifying system of any one of embodiments 21-25, wherein the gRNA scaffold comprises a sequence of a gRNA scaffold of Table 12, or a sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, or 99% identity thereto.

27. The gene modifying system of any one of embodiments 21-25, wherein the gRNA scaffold comprises a sequence of a gRNA scaffold of Table 12 that corresponds to the RT template sequence, the gRNA spacer sequence, or both, or a sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, or 99% identity thereto.

28. A gene modifying system for modifying DNA, comprising:

(a) a first RNA comprising, from 5’ to 3, (i) a guide RNA sequence that is complementary to a first portion of the human PAH gene, and (ii) a sequence (e.g., a scaffold region) that binds a gene modifying polypeptide (e.g., binds the Cas domain of the gene modifying polypeptide), and

(b) a second RNA comprising (iii) a heterologous object sequence comprising a nucleotide substitution to introduce a mutation into a second portion of the human PAH gene, wherein the heterologous object sequence comprises the core nucleotides of an RT template sequence of Table 3A, Table 3B, Table 3C, or Table 3D, or a sequence having 1, 2, or 3

substitutions thereto, and optionally comprises one or more consecutive nucleotides starting with the 3' end of the flanking nucleotides of the RT template sequence, or wherein the heterologous object sequence comprises an RT sequence from Tables 5A-5F, 8A-8D, E3, E3A, BB, E5, E5A, E6, or E6A, or a sequence having 1, 2, or 3 substitutions thereto, and (iv) a primer region comprising at least 5, 6, 7, or 8 bases of 100% homology to a third portion of the human PAH gene, and (v) an RRS (RNA binding protein recognition sequence) that binds a gene modifying protein.

29. The gene modifying system of embodiment 28, wherein the gRNA spacer comprises the core nucleotides of a gRNA spacer sequence of Table 1A, Table 1B, Table 1C, or Table 1D, or a sequence having 1, 2, or 3 substitutions thereto, and optionally comprises one or more consecutive nucleotides starting with the 3' end of the flanking nucleotides of the gRNA spacer sequence, or wherein the gRNA spacer comprises a gRNA spacer sequence from Tables 5A-5F, 8A-8D, E3, E3A, BB, E5, E5A, E6, or E6A, or a sequence having 1, 2, or 3 substitutions thereto.

30. The gene modifying system of embodiment 28, wherein the heterologous object sequence comprises the core nucleotides of the gRNA spacer sequence of Table 1A, Table 1B, Table 1C, or Table 1D that corresponds to the RT template sequence, or a sequence having 1, 2, or 3 substitutions thereto, and optionally comprises one or more consecutive nucleotides starting with the 3' end of the flanking nucleotides of the gRNA spacer sequence, or wherein the heterologous object sequence comprises a gRNA spacer sequence from Tables 5A-5F, 8A-8D, E3, E3A, BB, E5, E5A, E6, or E6A that corresponds to the RT template sequence, or a sequence having 1, 2, or 3 substitutions thereto.

31. The gene modifying system of any one of embodiments 28-30, wherein the PBS sequence has a sequence comprising the core nucleotides of the PBS sequence from the same row of Table 3A, Table 3B, Table 3C, or Table 3D as the RT template sequence, or a sequence having 1, 2, or 3 substitutions thereto, and optionally comprises one or more consecutive nucleotides starting with the 5' end of the flanking nucleotides of the PBS sequence, or wherein the PBS sequence has a sequence comprising a PBS sequence from Tables 5A-5F, 8A-8D, E3, E3A, BB, E5, E5A, E6, or E6A, or a sequence having 1, 2, or 3 substitutions thereto.

32. The gene modifying system of any one of embodiments 28-30, wherein the PBS sequence has a sequence comprising the core nucleotides of a PBS sequence of Table 3A, Table 3B, Table 3C, or Table 3D that corresponds to the RT template sequence, the gRNA spacer sequence, or both, or a sequence having 1, 2, or 3 substitutions thereto, and optionally comprises one or more consecutive nucleotides starting with the 5' end of the flanking nucleotides of the PBS sequence, or wherein the PBS sequence has a sequence comprising a PBS sequence from Tables 5A-5F, 8A-8D, E3, E3A, BB, E5, E5A, E6, or E6A that corresponds to the RT template sequence, the gRNA spacer sequence, or both, or a sequence having 1, 2, or 3 substitutions thereto.

33. The gene modifying system of any one of embodiments 28-32, wherein the gRNA scaffold comprises a sequence of a gRNA scaffold of Table 12, or a sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, or 99% identity thereto.

34. The gene modifying system of any one of embodiments 28-32, wherein the gRNA scaffold comprises a sequence of a gRNA scaffold of Table 12 that corresponds to the RT template sequence, the gRNA spacer sequence, or both, or a sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, or 99% identity thereto.

35. A gRNA comprising (i) a gRNA spacer sequence that is complementary to a first portion of the human PAH gene, wherein the gRNA spacer has a sequence comprising the core nucleotides of a gRNA spacer sequence of Table 1A, Table 1B, Table 1C, or Table 1D, Table 2A, Table 2B, Table 2C, or Table 2D, or Table 4A, Table 4B, Table 4C, or Table 4D, or a sequence having 1, 2, or 3 substitutions thereto and optionally comprises one or more consecutive nucleotides starting with the 3' end of the flanking nucleotides of the gRNA spacer sequence, or wherein the gRNA spacer has a sequence comprising a gRNA spacer sequence from Tables 5A-5F, 8A-8D, E3, E3A, BB, E5, E5A, E6, or E6A or a sequence having 1, 2, or 3 substitutions thereto; and (ii) a gRNA scaffold.

36. The gRNA of embodiment 35, wherein the gRNA scaffold comprises a sequence of a gRNA scaffold of Table 12, or a sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, or 99% identity thereto.

37. The gRNA of embodiment 35, wherein the gRNA scaffold comprises a sequence of a gRNA scaffold of Table 12 that corresponds to the gRNA spacer sequence, or a sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, or 99% identity thereto.

38. A template RNA comprising: (iii) a heterologous object sequence comprising a mutation region to introduce a mutation into a second portion of the human PAH gene, wherein the heterologous object sequence comprises the core nucleotides of an RT template sequence of Table 3A, Table 3B, Table 3C, or Table 3D, or a sequence having 1, 2, or 3 substitutions thereto, and optionally comprises one or more consecutive nucleotides starting with the 3' end of the flanking nucleotides of the RT template sequence, or wherein the heterologous object sequence comprises an RT template sequence from Tables 5A-5F, 8A-8D, E3, E3A, BB, E5, E5A, E6, or E6A or a sequence having 1, 2, or 3 substitutions thereto, and (iv) a PBS sequence comprising at least 5, 6, 7, or 8 bases of 100% homology to a third portion of the human PAH gene.

39. The template RNA according to embodiment 38, wherein the PBS sequence has a sequence comprising the core nucleotides of the PBS sequence from the same row of Table 3A, Table 3B, Table 3C, or Table 3D as the RT template sequence, or a sequence having 1, 2, or 3 substitutions thereto, and optionally comprises one or more consecutive nucleotides starting with the 5' end of the flanking nucleotides of the PBS sequence.

40. The template RNA according to embodiment 38, wherein the PBS sequence has a sequence comprising the core nucleotides of a PBS sequence of Table 3A, Table 3B, Table 3C, or Table 3D that corresponds to the RT template sequence, or a sequence having 1, 2, or 3 substitutions thereto, and optionally comprises one or more consecutive nucleotides starting with the 5' end of the flanking nucleotides of the PBS sequence, or wherein the PBS sequence comprises a PBS sequence from Tables 5A-5F, 8A-8D, E3, E3A, BB, E5, E5A, E6, or E6A that corresponds to the RT template sequence, or a sequence having 1, 2, or 3 substitutions thereto.

41. The template RNA according to any one of embodiments 1-20 or 38-40, the gene modifying system of any one of embodiments 21-35, or the gRNA of any one of embodiments 35-37, wherein the mutation introduced by the system is a W408R, Q261R, Q243R, and/or IVS10-11A>G mutation (e.g., to correct a pathogenic R408W, R261Q, R243Q, and/or IVS10-11G>A mutation) of the PAH gene.

42. The template RNA according to any one of embodiments 1-20 or 38-41 or the gene modifying system of any one of embodiments 35-37 or 41, wherein the pre-edit sequence comprises between about 1 nucleotide to about 35 nucleotides (e.g., comprises about 1-5, 5-10, 10-15, 15-20, 20-25, 25-30, or 30-35 nucleotides) in length.

43. The template RNA according to any one of embodiments 1-20 or 38-42 or the gene modifying system of any one of embodiments 35-37, 41, or 42, wherein the mutation region comprises a single nucleotide.

44. The template RNA according to any one of embodiments 1-20 or 38-42 or the gene modifying system of any one of embodiments35-37, 41, or 42, wherein the mutation region is at least two nucleotides in length.

45. The template RNA according to any one of embodiments 1-20, 38-42, or 44 or the gene modifying system of any one of embodiments 35-37, 41, 42, or 44, wherein the mutation region is up to 32 (e.g., up to 5, 10, 15, 20, 25, 30, or 32) nucleotides in length and comprises one, two, or three sequence differences relative to a second portion of the human PAH gene.

46. The template RNA according to any one of embodiments 1-20, 38-42, 44, or 45 or the gene modifying system of any one of embodiments 35-37, 41, 42, 44, or 45, wherein the mutation region comprises two sequences differences relative to a second portion of the human PAH gene.

47. The template RNA according to any one of embodiments 1-20, 38-42, or 44-46 or the gene modifying system of any one of embodiments 35-37, 41, 42, or 44-46, wherein the

mutation region comprises a first region (e.g., a first nucleotide) designed to correct a pathogenic mutation in the PAH gene and a second region (e.g., a second nucleotide) designed to inactivate a PAM sequence (e.g., a "PAM-kill" mutation as described herein).

48. The template RNA according to any one of embodiments 1-20 or 38-46 or the gene modifying system of any one of embodiments 35-37 or 41-46, wherein the mutation region comprises less than 80%, 70%, 60%, 50%, 40%, or 30% identity to corresponding portion of the human PAH gene.

49. The template RNA of any one of the preceding embodiments, wherein the template RNA comprises one or more silent mutations (e.g., silent substitutions), e.g., as exemplified in Tables 7A-7C, 8A-8D, E6, or E6A.

50. The template RNA of any of the preceding embodiments, wherein the mutation region comprises a first region designed to correct a pathogenic mutation in the PAH gene and a second region designed to introduce a silent substitution.

51. The template RNA of any one of the preceding embodiments, which comprises one or more chemically modified nucleotides.

52. A gene modifying system comprising:

a template RNA of any of embodiments 1-20, 38-46, or a system of any of embodiments 35-37 or 41-46, and

a gene modifying polypeptide, or a nucleic acid (e.g., RNA) encoding the gene modifying polypeptide.

53. The gene modifying system of embodiment 52, wherein the gene modifying polypeptide comprises:

a reverse transcriptase (RT) domain (e.g., an RT domain from a retrovirus, or a polypeptide domain having at least 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, or 99% amino acids sequence identity thereto); and

a Cas domain that binds to the target DNA molecule and is heterologous to the RT domain (e.g., a Cas9 domain); and

optionally, a linker disposed between the RT domain and the Cas domain.

54. The gene modifying system of embodiment 53, wherein the RT domain comprises:

(a) an RT domain of Table 6; or

(b) an RT domain from a murine leukemia virus (MMLV), a porcine endogenous retrovirus (PERV); Avian reticuloendotheliosis virus (AVIRE), a feline leukemia virus (FLV), simian foamy virus (SFV) (e.g., SFV3L), bovine leukemia virus (BLV), Mason-Pfizer monkey virus (MPMV), human foamy virus (HFV), or bovine foamy/syncytial virus (BFV/BSV).

55. The gene modifying system of embodiment 53 or 54, wherein the Cas domain comprises a Cas domain of Table 7 or Table 8.

56. The gene modifying system of any one of embodiments 53-55, wherein the Cas domain:

(a) is a Cas9 domain;

(b) is a SpCas9 domain, a BlatCas9 domain, a Nme2Cas9 domain, a PnpCas9 domain, a SauCas9 domain, a SauCas9-KKH domain, a SauriCas9 domain, a SauriCas9-KKH domain, a ScaCas9-Sc++ domain, a SpyCas9 domain, a SpyCas9-NG domain, a SpyCas9-SpRY domain, or a St1Cas9 domain; and/or

(c) is a Cas9 domain comprising an N670A mutation, an N611A mutation, an N605A mutation, an N580A mutation, an N588A mutation, an N872A mutation, an N863 mutation, an N622A mutation, or an H840A mutation.

57. The gene modifying system of embodiment 56, wherein the Cas9 domain binds a PAM sequence listed in Table 7 or Table 12.

58. The gene modifying system of embodiment 57, wherein a second portion of the human PAH gene overlaps with a PAM recognized by the Cas domain, e.g., wherein the second portion of the human PAH gene is within the PAM or wherein the PAM is within the second portion of the human PAH gene).

59. The gene modifying system any one of embodiments 52-58, wherein the gRNA spacer is a gRNA spacer according to Table 1A, Table 1B, Table 1C, or Table 1D, and the Cas domain comprises a Cas domain listed in the same row of Table 1A, Table 1B, Table 1C, or Table 1D, or a sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, or 99% identity thereto.

60. The gene modifying system of any one of embodiments 52-58, wherein the template RNA comprises a sequence of a template RNA sequence of Table 5A-5F, 8A-8D, E3, E3A, BB, E5, E5A, E6, or E6A or a sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, or 99% identity thereto.

61. The gene modifying system of any one of embodiments 52-60, wherein:

(a) the template RNA comprises a sequence of a template RNA sequence of Tables 3A-3D, 5A-5F, 8A-8D, E3, E3A, BB, E5, E5A, E6, or E6A;

(b) the Cas domain comprises a Cas domain of Table 7 or Table 8;

(c) the linker comprises a linker sequence of Table 10 (e.g., of any of SEQ ID NOs: 5217, 5106, 5190, and 5218); and

(d) the gene modifying polypeptide comprises one or two NLS sequences from Table 11 (e.g., of any of SEQ ID NOs: 5245, 5290, 5323, 5330, 5349, 5350, 5351, and 4001).

62. The gene modifying system of any of embodiments 52-61, which produces a first nick in a first strand of the human PAH gene.

63. The gene modifying system of embodiment 62, which further comprises a second strand-targeting gRNA that directs a second nick to the second strand of the human PAH gene.

64. The gene modifying system of embodiment 63, wherein the second strand-targeting gRNA comprises:

(i) a sequence comprising the core nucleotides of a left gRNA spacer sequence or a right gRNA spacer sequence from Table 2A, Table 2B, Table 2C, or Table 2D, and optionally

comprises one or more consecutive nucleotides starting with the 3’ end of the flanking nucleotides of the left gRNA spacer sequence or right gRNA spacer sequence; or

(ii) a second -strand-targeting gRNA comprising a spacer sequence of Table 6A, or a spacer sequence having 1, 2, or 3 substitutions thereto.

65. The gene modifying system of embodiment 63, wherein the second strand-targeting gRNA comprises a sequence comprising the core nucleotides of a left gRNA spacer sequence or a right gRNA spacer sequence from Table 2A, Table 2B, Table 2C, or Table 2D that corresponds to the gRNA spacer sequence of (i), and optionally comprises one or more consecutive nucleotides starting with the 3’ end of the flanking nucleotides of the left gRNA spacer sequence or right gRNA spacer sequence.

66. The gene modifying system of embodiment 63, wherein the second strand-targeting gRNA comprises:

(i) a sequence comprising the core nucleotides of a second nick gRNA sequence from Table 4A, Table 4B, Table 4C, Table 4D, or a sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, or 99% identity thereto, and optionally comprises one or more consecutive nucleotides starting with the 3’ end of the flanking nucleotides of the second nick gRNA sequence; or

(ii) a second -strand-targeting gRNA comprising a spacer sequence from Table 6A or a sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, or 99% identity thereto.

67. The gene modifying system of embodiment 63, wherein the second strand-targeting gRNA comprises a sequence comprising the core nucleotides of the second nick gRNA sequence from Table 4A, Table 4B, Table 4C, or Table 4D that corresponds to the gRNA spacer sequence of (i), or a sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, or 99% identity thereto, and optionally comprises one or more consecutive nucleotides starting with the 3’ end of the flanking nucleotides of the second nick gRNA sequence.

68. The gene modifying system of any one of embodiments 52-67, wherein the second strand-targeting gRNA has a "PAM-in orientation" with the template RNA of the gene modifying system, e.g., as exemplified in Tables 2A-2D, 4A-4D, or 6A.

69. The gene modifying system of any one of embodiments 52-68, the second strand-targeting gRNA targets a sequence overlapping the target mutation of the template RNA.

70. The gene modifying system of embodiment 69, wherein second strand-targeting gRNA comprises:

(i) a sequence (e.g., a spacer sequence) complementary to the PAH mutation;

(ii) a sequence (e.g., a spacer sequence) complementary to the wild-type sequence at the target locus;

(iii) a sequence (e.g., a spacer sequence) complementary to a SNP proximal to the target locus, e.g., a SNP contained in the genomic DNA of a subject (e.g., a patient);

(iv) a sequence (e.g., spacer sequence) complementary to or comprising one or more silent substitutions proximal to the target locus.

71. The template RNA, gene modifying system, or gRNA, of any one of the preceding embodiments, wherein the gRNA spacer comprises about 1, 2, 3, or more flanking nucleotides of the gRNA spacer.

72. The template RNA or gene modifying system of any one of the preceding embodiments, wherein the heterologous object sequence comprises about 2, 3, 4, 5, 10, 20, 30, 40, or more flanking nucleotides of the RT template sequence.

73. The template RNA or gene modifying system, of any one of the preceding embodiments, wherein the heterologous object sequence comprises between about 8-30, 9-25, 10-20, 11-16, or 12-15 (e.g., about 11-16) nucleotides.

74. The template RNA or gene modifying system, of any one of the preceding embodiments, wherein the mutation region comprises 1, 2, or 3 nucleotide positions of sequence differences relative to the corresponding portion of the human PAH gene.

75. The template RNA or gene modifying system of any one of the preceding embodiments, wherein the mutation region comprises at least 2 nucleotide positions of sequence difference relative to the corresponding portion of the human PAH gene.

76. The template RNA or gene modifying system, of any one of the preceding embodiments, wherein the post-edit homology region and/or pre-edit homology region comprises 100% identity to the PAH gene.

77. The template RNA or gene modifying system of any one of the preceding embodiments, wherein the PBS sequence additionally comprises about 1, 2, 3, 4, 5, 6, 7, or more flanking nucleotides.

78. The template RNA or gene modifying system of any one of the preceding embodiments, wherein the PBS sequence comprises about 5-20, 8-16, 8-14, 8-13, 9-13, 9-12, or 10-12 (e.g., about 9-12) nucleotides.

79. The template RNA or gene modifying system of any one of the preceding embodiments, wherein the PBS sequence binds within 1, 2, 3, 4, 5, 6, 7, 8, 9, or 10 nucleotides of a nick site in the PAH gene.

80. The gene modifying system of any one of the preceding embodiments, wherein the domains of the gene modifying polypeptide are joined by a peptide linker.

81. The gene modifying system of embodiment 80, wherein the linker comprises a sequence of a linker of Table 10 (e.g., of any of SEQ ID NOs: 5217, 5106, 5190, and 5218).

82. The gene modifying system of any one of the preceding embodiments, wherein the gene modifying polypeptide further comprise one or more nuclear localization sequences (NLS).

83. The gene modifying system of embodiment 82, wherein the gene modifying polypeptide comprises a first NLS and a second NLS.

84. The gene modifying system of embodiment 82 or 83, wherein the NLS comprises a sequence of a NLS of Table 11 (e.g., of any of SEQ ID NOs: 5245, 5290, 5323, 5330, 5349, 5350, 5351, and 4001).

85. A template RNA comprising a sequence of a template RNA of Table 4A-4D, 5A-5F, 8A-8D, E3, E3A, BB, E5, E5A, E6, or E6A, or a sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, or 99% identity thereto.

86. A template RNA comprising a sequence of a template RNA of Tables 4A-4D, 5A-5F, 8A-8D, E3, E3A, BB, E5, E5A, E6, or E6A.

87. A gene modifying system comprising:

(i) a template RNA comprising a sequence of a template RNA of Table 4A, Table 4B, Table 4C, or Table 4D, or a sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, or 99% identity thereto; and

(ii) a second-nick gRNA sequence from the same row of Table 4A, Table 4B, Table 4C, or Table 4D as (i), a sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, or 99% identity thereto.

88. A gene modifying system comprising:

(i) a template RNA comprising a sequence of a template RNA of Table 4A, Table 4B, Table 4C, or Table 4D; and

(ii) a second-nick gRNA sequence from the same row of Table 4A, Table 4B, Table 4C, or Table 4D as (i).

89. A DNA encoding the template RNA of any one of embodiments 1-20, 38-48, 71-79, 85, or 86, or the gRNA of any one of embodiments 34-37.

90. A pharmaceutical composition, comprising the system of any one of embodiments 49-84, 87, or 88, or one or more nucleic acids encoding the same, and a pharmaceutically acceptable excipient or carrier.

91. The pharmaceutical composition of embodiment 90, wherein the pharmaceutically acceptable excipient or carrier is selected from the group consisting of a plasmid vector, a viral vector, a vesicle, and a lipid nanoparticle.

92. The pharmaceutical composition of embodiment 91, wherein the viral vector is an adeno-associated virus.

93. A host cell (e.g., a mammalian cell, e.g., a human cell) comprising the template RNA or gene modifying system of any one of the preceding embodiments.

94. A method of making the template RNA of any one of embodiments 1-20, 38-48, 71-79, 85, or 86, the method comprising synthesizing the template RNA by *in vitro* transcription (e.g., solid state synthesis) or by introducing a DNA encoding the template RNA into a host cell under conditions that allow for production of the template RNA.

95. A method for modifying a target site in the human PAH gene in a cell, the method comprising contacting the cell with the gene modifying system of any one of embodiments 49-84, 87, or 88, or DNA encoding the same, thereby modifying the target site in the human PAH gene in a cell.

96. A method for modifying a target site in the human PAH gene in a cell, the method comprising contacting the cell with: (i) the template RNA of any one of embodiments 49-84, 87, or 88, or DNA encoding the same; and (ii) a gene modifying polypeptide or a nucleic acid

encoding a gene modifying polypeptide, thereby modifying the target site in the human PAH gene in a cell.

97. A method for treating a subject having a disease or condition associated with a mutation in the human PAH gene, the method comprising administering to the subject the gene modifying system of any one of embodiments 49-84, 87, or 88, or DNA encoding the same, thereby treating the subject having a disease or condition associated with a mutation in the human PAH gene.

98. A method for treating a subject having a disease or condition associated with a mutation in the human PAH gene, the method comprising administering to the subject the template RNA of any one of embodiments 49-84, 87, or 88, or DNA encoding the same; and (ii) a gene modifying polypeptide or a nucleic acid encoding a gene modifying polypeptide, thereby treating the subject having a disease or condition associated with a mutation in the human PAH gene.

99. The method of embodiment 97 or 98, wherein the disease or condition is phenylketonuria (PKU).

100. The method of any one of embodiments 97-99, wherein the subject has a R408W, R261Q, R243Q, and/or IVS10-11G>A mutation.

101. A method for treating a subject having PKU the method comprising administering to the subject the gene modifying system of any one of embodiments 49-84, 87, or 88, or DNA encoding the same, thereby treating the subject having PKU.

102. A method for treating a subject having PKU the method comprising administering to the subject (i) the template RNA of any one of embodiments 49-84, 87, or 88, or DNA encoding the same, and (ii) a gene modifying polypeptide or a nucleic acid encoding a gene modifying polypeptide, thereby treating the subject having PKU.

103. The gene modifying system or method of any one of the preceding embodiments, wherein introduction of the system into a target cell results in a correction of a pathogenic mutation in the PAH gene.

104. The gene modifying system or method of any one of the preceding embodiments, wherein the pathogenic mutation is a W408R, Q261R, Q243R, and/or IVS10-11A>G mutation, and wherein the correction comprises an amino acid substitution of R408W, R261Q, or R243Q, or a nucleic acid substitution of IVS10-11G>A.

105. The gene modifying system or method of any of the preceding embodiments, wherein correction of the mutation occurs in at least 30% (e.g., 30%, 40%, 50%, 60%, 70%, or more) of target nucleic acids.

106. The gene modifying system or method of any of the preceding embodiments, wherein correction of the mutation occurs in at least 30% (e.g., 30%, 40%, 50%, 60%, 70%, or more) of target cells.

107. The gene modifying system or method of any of the preceding embodiments, wherein the gene modifying system comprises a second strand-targeting gRNA, and wherein correction of the mutation in a population of target cells is increased relative to a population of target cells treated with a gene modifying system comprising a template RNA without a second strand-targeting gRNA.

108. The gene modifying system or method of any of the preceding embodiments, wherein the template RNA comprises one or more silent substitutions (e.g., as exemplified in Tables 7A, X4, and X4A), and wherein correction of the mutation in a population of target cells is increased relative to a population of target cells treated with a gene modifying system comprising a template RNA that does not comprise one or more silent substitutions.

109. The method of any of the preceding embodiments, wherein the cell is a mammalian cell, such as a human cell.

110. The method of any one of the preceding embodiments, wherein the subject is a human.

111. The method of any of the preceding embodiments, wherein the contacting occurs *ex vivo*, e.g., wherein the cell's or subject's DNA is modified *ex vivo*.

112. The method of any of the preceding embodiments, wherein the contacting occurs *in vivo*, e.g., wherein the cell's or subject's DNA is modified *in vivo*.

113. The method of any of the preceding embodiments, wherein contacting the cell or the subject with the system comprises contacting the cell or a cell within the subject with a nucleic acid (e.g., DNA or RNA) encoding the gene modifying polypeptide under conditions that allow for production of the gene modifying polypeptide.

Additional Enumerated Embodiments

A1. A template RNA comprising, from 5' to 3':

(i) a gRNA spacer that is complementary to a first portion of the human PAH gene, wherein the gRNA spacer has a nucleotide sequence comprising ACCTCAATCCTTTGGGTGTA (SEQ ID NO: 16355), or a nucleotide sequence having 1, 2, or 3 substitution thereto;

(ii) a gRNA scaffold that binds a Cas domain of a gene modifying polypeptide,

(iii) a heterologous object sequence comprising a mutation region to correct a mutation in a second portion of the human PAH gene, and

(iv) a primer binding site (PBS) sequence comprising at least 5 bases with 100% identity to a third portion of the human PAH gene.

A2. The template RNA of embodiment A1, wherein the gRNA spacer has a nucleotide sequence comprising ACCTCAATCCTTTGGGTGTA (SEQ ID NO: 16355).

A3. The template RNA of any of the preceding embodiments, wherein the heterologous object sequence comprises a sequence of at least 30 nucleotides from the 3' end of a sequence

according to tcactcaagcctgtggttttggtcttaggaactttgctgccacaatacctCggcccttctcagttcgctacgacccatac (SEQ ID NO: 24984), or a sequence having 1, 2, 3, or 4 substitutions thereto.

A4. The template RNA of any of the preceding embodiments, wherein the heterologous object sequence comprises a sequence of tcactcaagcctgtggttttggtcttaggaactttgctgccacaatacctCggcccttctcagttcgctacgacccatac (SEQ ID NO: 24984), or comprises at least 40, 50, 60, or 70 nucleotides from the 3' end of said sequence, or a sequence having 1, 2, 3, or 4 substitutions thereto.

A5. The template RNA of any of the preceding embodiments, wherein the heterologous object sequence comprises a sequence of at least 30 nucleotides from the 3' end of a sequence according to tcactcaagcctgtggttttggtcttaggaactttgctgccacaatacctCggcccttctcagttcgctacgacccatac (SEQ ID NO: 24984).

A6. The template RNA of any of the preceding embodiments, wherein the heterologous object sequence comprises a sequence of tcactcaagcctgtggttttggtcttaggaactttgctgccacaatacctCggcccttctcagttcgctacgacccatac (SEQ ID NO: 24984), or comprises at least 40, 50, 60, or 70 nucleotides from the 3' end of said sequence.

A7. The template RNA of any of the preceding embodiments, wherein the PBS comprises a sequence of at least 5, 6, 7, or 8 nucleotides from the 5' end of a sequence according to acccaaagg, or a sequence having 1 substitution thereto.

A8. The template RNA of any of the preceding embodiments, wherein the PBS comprises a sequence of acccaaagg

A9. A template RNA comprising, from 5' to 3':

(i) a gRNA spacer that is complementary to a first portion of the human PAH gene, wherein the gRNA spacer has a nucleotide sequence comprising CCTCAATCCTTTGGGTGTAT (SEQ ID NO: 16332), or a nucleotide sequence having 1, 2, or 3 substitution thereto;

(ii) a gRNA scaffold that binds a Cas domain of a gene modifying polypeptide,

(iii) a heterologous object sequence comprising a mutation region to correct a mutation in a second portion of the human PAH gene, and

(iv) a primer binding site (PBS) sequence comprising at least 5 bases with 100% identity to a third portion of the human PAH gene.

A10. The template RNA of embodiment A9, wherein the gRNA spacer has a nucleotide sequence comprising CCTCAATCCTTTGGGTGTAT (SEQ ID NO: 16332).

A11. The template RNA of any of the preceding embodiments, wherein the heterologous object sequence comprises a sequence of at least 50 nucleotides from the 3' end of a sequence according to tcactcaagcctgtggttttggtcttaggaactttgctgccacaatacctCggcccttctcagttcgctacgacccata (SEQ ID NO: 24975), or a sequence having 1, 2, 3, or 4 substitutions thereto.

A12. The template RNA of any of the preceding embodiments, wherein the heterologous object sequence comprises a sequence of tcactcaagcctgtggttttggtcttaggaactttgctgccacaatacctCggcccttctcagttcgctacgacccata (SEQ ID NO: 24975), or comprises at least 60 or 70 nucleotides from the 3' end of said sequence, or a sequence having 1, 2, 3, or 4 substitutions thereto.

A13. The template RNA of any of the preceding embodiments, wherein the heterologous object sequence comprises a sequence of at least 50 nucleotides from the 3' end of a sequence according to tcactcaagcctgtggttttggtcttaggaactttgctgccacaatacctCggcccttctcagttcgctacgacccata (SEQ ID NO: 24975).

A14. The template RNA of any of the preceding embodiments, wherein the heterologous object sequence comprises a sequence of tcactcaagcctgtggttttggtcttaggaactttgctgccacaatacctCggcccttctcagttcgctacgacccata (SEQ ID NO: 24975), or comprises at least 60 or 70 nucleotides from the 3' end of said sequence.

A15. The template RNA of any of the preceding embodiments, wherein the PBS comprises a sequence of at least 5, 6, 7, or 8 nucleotides from the 5' end of a sequence according to cacccaaag, or a sequence having 1 substitution thereto.

A16. The template RNA of any of the preceding embodiments, wherein the PBS comprises a sequence of cacccaaag.

A17. A template RNA comprising, from 5' to 3':

(i) a gRNA spacer that is complementary to a first portion of the human PAH gene, wherein the gRNA spacer has a nucleotide sequence comprising TGGGTCGTAGCGAACTGAGA (SEQ ID NO: 16102), or a nucleotide sequence having 1, 2, or 3 substitution thereto;

(ii) a gRNA scaffold that binds a Cas domain of a gene modifying polypeptide,

(iii) a heterologous object sequence comprising a mutation region to correct a mutation in a second portion of the human PAH gene, and

(iv) a primer binding site (PBS) sequence comprising at least 5 bases with 100% identity to a third portion of the human PAH gene.

A18. The template RNA of embodiment A17, wherein the gRNA spacer has a nucleotide sequence comprising TGGGTCGTAGCGAACTGAGA (SEQ ID NO: 16102).

A19. The template RNA of any of the preceding embodiments, wherein the heterologous object sequence comprises a sequence of at least 10 nucleotides from the 3' end of a sequence according to tcactcaagcctgtggttttggtcttaggaactttgctgccacaatacctCggcccttct (SEQ ID NO: 24863), or a sequence having 1, 2, 3, or 4 substitutions thereto.

A20. The template RNA of any of the preceding embodiments, wherein the heterologous object sequence comprises a sequence of tcactcaagcctgtggttttggtcttaggaactttgctgccacaatacctCggcccttct (SEQ ID NO: 24863), or comprises at least 20, 30, 40, of 50 nucleotides from the 3' end of said sequence, or a sequence having 1, 2, 3, or 4 substitutions thereto.

A21. The template RNA of any of the preceding embodiments, wherein the heterologous object sequence comprises a sequence of at least 10 nucleotides from the 3' end of a sequence according to tcactcaagcctgtggttttggtcttaggaactttgctgccacaatacctCggcccttct (SEQ ID NO: 24863).

A22. The template RNA of any of the preceding embodiments, wherein the heterologous object sequence comprises a sequence of tcactcaagcctgtggttttggtcttaggaactttgctgccacaatacctCggcccttct (SEQ ID NO: 24863), or comprises at least 20, 30, 40, of 50 nucleotides from the 3' end of said sequence.

A23. The template RNA of any of the preceding embodiments, wherein the PBS comprises a sequence of at least 5, 6, 7, or 8 nucleotides from the 5' end of a sequence according to cagttcgct, or a sequence having 1 substitution thereto.

A24. The template RNA of any of the preceding embodiments, wherein the PBS comprises a sequence of cagttcgct.

A25. A template RNA comprising, from 5' to 3':

(i) a gRNA spacer that is complementary to a first portion of the human PAH gene, wherein the gRNA spacer has a nucleotide sequence comprising GGGTCGTAGCGAACTGAGAA (SEQ ID NO: 16084), or a nucleotide sequence having 1, 2, or 3 substitution thereto;

(ii) a gRNA scaffold that binds a Cas domain of a gene modifying polypeptide,

(iii) a heterologous object sequence comprising a mutation region to correct a mutation in a second portion of the human PAH gene, and

(iv) a primer binding site (PBS) sequence comprising at least 5 bases with 100% identity to a third portion of the human PAH gene.

A26. The template RNA of embodiment A25, wherein the gRNA spacer has a nucleotide sequence comprising GGGTCGTAGCGAACTGAGAA (SEQ ID NO: 16084).

A27. The template RNA of any of the preceding embodiments, wherein the heterologous object sequence comprises a sequence of at least 9 nucleotides from the 3’ end of a sequence according to tcactcaagcctgtggttttggtcttaggaactttgctgccacaatacctCggcccttc (SEQ ID NO: 24856), or a sequence having 1, 2, 3, or 4 substitutions thereto.

A28. The template RNA of any of the preceding embodiments, wherein the heterologous object sequence comprises a sequence of tcactcaagcctgtggttttggtcttaggaactttgctgccacaatacctCggcccttc (SEQ ID NO: 24856), or comprises at least 10, 20, 30, 40, or 50 nucleotides from the 3’ end of said sequence, or a sequence having 1, 2, 3, or 4 substitutions thereto.

A29. The template RNA of any of the preceding embodiments, wherein the heterologous object sequence comprises a sequence of at least 9 nucleotides from the 3’ end of a sequence according to tcactcaagcctgtggttttggtcttaggaactttgctgccacaatacctCggcccttc (SEQ ID NO: 24856).

A30. The template RNA of any of the preceding embodiments, wherein the heterologous object sequence comprises a sequence of tcactcaagcctgtggttttggtcttaggaactttgctgccacaatacctCggcccttc (SEQ ID NO: 24856), or comprises at least 10, 20, 30, 40, or 50 nucleotides from the 3’ end of said sequence.

A31. The template RNA of any of the preceding embodiments, wherein the PBS comprises a sequence of at least 5, 6, 7, or 8 nucleotides from the 5’ end of a sequence according to tcagttcgc, or a sequence having 1 substitution thereto.

A32. The template RNA of any of the preceding embodiments, wherein the PBS comprises a sequence of tcagttcgc

A33. A template RNA comprising, from 5’ to 3’:

(i) a gRNA spacer that is complementary to a first portion of the human PAH gene, wherein the gRNA spacer has a nucleotide sequence comprising

TAGCGAACTGAGAAGGGCCA (SEQ ID NO: 16011), or a nucleotide sequence having 1, 2, or 3 substitution thereto;

(ii) a gRNA scaffold that binds a Cas domain of a gene modifying polypeptide,

(iii) a heterologous object sequence comprising a mutation region to correct a mutation in a second portion of the human PAH gene, and

(iv) a primer binding site (PBS) sequence comprising at least 5 bases with 100% identity to a third portion of the human PAH gene.

A34. The template RNA of embodiment A33, wherein the gRNA spacer has a nucleotide sequence comprising TAGCGAACTGAGAAGGGCCA (SEQ ID NO: 16011).

A35. The template RNA of any of the preceding embodiments, wherein the heterologous object sequence comprises a sequence of at least 3 nucleotides from the 3’ end of a sequence according to tcactcaagcctgtggttttggtcttaggaactttgctgccacaatacctCgg (SEQ I DNO: 24817), or a sequence having 1, 2, 3, or 4 substitutions thereto.

A36. The template RNA of any of the preceding embodiments, wherein the heterologous object sequence comprises a sequence of tcactcaagcctgtggttttggtcttaggaactttgctgccacaatacctCgg (SEQ I DNO: 24817), or comprises at least 5, 10, 20, 30, 40, or 50 nucleotides from the 3’ end of said sequence, or a sequence having 1, 2, 3, or 4 substitutions thereto.

A37. The template RNA of any of the preceding embodiments, wherein the heterologous object sequence comprises a sequence of at least 3 nucleotides from the 3’ end of a sequence according to tcactcaagcctgtggttttggtcttaggaactttgctgccacaatacctCgg (SEQ I DNO: 24817).

A38. The template RNA of any of the preceding embodiments, wherein the heterologous object sequence comprises a sequence of tcactcaagcctgtggttttggtcttaggaactttgctgccacaatacctCgg (SEQ ID NO: 24817), or comprises at least 5, 10, 20, 30, 40, or 50 nucleotides from the 3’ end of said sequence.

A39. The template RNA of any of the preceding embodiments, wherein the PBS comprises a sequence of at least 5, 6, 7, or 8 nucleotides from the 5’ end of a sequence according to cccttctca, or a sequence having 1 substitution thereto.

A40. The template RNA of any of the preceding embodiments, wherein the PBS comprises a sequence of cccttctca.

A41. A template RNA comprising, from 5’ to 3’:

(i) a gRNA spacer that is complementary to a first portion of the human PAH gene, wherein the gRNA spacer has a nucleotide sequence comprising ACTTTGCTGCCACAATACCT (SEQ ID NO: 16032), or a nucleotide sequence having 1, 2, or 3 substitution thereto;

(ii) a gRNA scaffold that binds a Cas domain of a gene modifying polypeptide,

(iii) a heterologous object sequence comprising a mutation region to correct a mutation in a second portion of the human PAH gene, and

(iv) a primer binding site (PBS) sequence comprising at least 5 bases with 100% identity to a third portion of the human PAH gene.

A42. The template RNA of embodiment A41, wherein the gRNA spacer has a nucleotide sequence comprising ACTTTGCTGCCACAATACCT (SEQ ID NO: 16032).

A43. The template RNA of any of the preceding embodiments, wherein the heterologous object sequence comprises a sequence of at least 4 nucleotides from the 3’ end of a sequence according to caagacctcaatcctttgggtgtatgggtcgtagcgaactgagaagggccGagg (SEQ ID NO: 24825), or a sequence having 1, 2, 3, or 4 substitutions thereto.

A44. The template RNA of any of the preceding embodiments, wherein the heterologous object sequence comprises a sequence of caagacctcaatcctttgggtgtatgggtcgtagcgaactgagaagggccGagg (SEQ ID NO: 24825), or comprises at least 5, 10, 20, 30, 40, or 50 nucleotides from the 3’ end of said sequence, or a sequence having 1, 2, 3, or 4 substitutions thereto.

A45. The template RNA of any of the preceding embodiments, wherein the heterologous object sequence comprises a sequence of at least 4 nucleotides from the 3’ end of a sequence according to caagacctcaatcctttgggtgtatgggtcgtagcgaactgagaagggccGagg (SEQ ID NO: 24825).

A46. The template RNA of any of the preceding embodiments, wherein the heterologous object sequence comprises a sequence of caagacctcaatcctttgggtgtatgggtcgtagcgaactgagaagggccGagg (SEQ ID NO: 24825), or comprises at least 5, 10, 20, 30, 40, or 50 nucleotides from the 3’ end of said sequence.

A47. The template RNA of any of the preceding embodiments, wherein the PBS comprises a sequence of at least 5, 6, 7, 8, 9, 10, or 15 nucleotides from the 5’ end of a sequence according to tattgtggcagcaaagt (SEQ ID NO: 37633), or a sequence having 1 substitution thereto.

A48. The template RNA of any of the preceding embodiments, wherein the PBS comprises a sequence of tattgtggcagcaaagt (SEQ ID NO: 37633).

A49. The template RNA of any of the preceding embodiments, wherein the gRNA scaffold has a sequence according to GTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAA AGTGGCACCGAGTCGGTGC (SEQ ID NO: 37627), or a sequence having at least 90% identity thereto.

A50. The template RNA of any of the preceding embodiments, wherein the gRNA scaffold has a sequence according to GTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAA AGTGGCACCGAGTCGGTGC (SEQ ID NO: 37627).

A51. The template RNA of any of the preceding embodiments, wherein the mutation region comprises a single nucleotide.

A52. The template RNA of any of embodiments A1-51, wherein the mutation region is at least two nucleotides in length.

A53. The template RNA of any of the preceding embodiments, wherein the mutation region is up to 20 nucleotides in length and comprises one, two, or three sequence differences relative to the second portion of the human PAH gene.

A54. The template RNA of any of embodiments A1-53, wherein the mutation region comprises a first region designed to correct a pathogenic mutation in the PAH gene and a second region designed to inactivate a PAM sequence.

A55. The template RNA of any of embodiments A1-54, wherein the mutation region comprises a first region designed to correct a pathogenic mutation in the PAH gene and a second region designed to introduce a silent substitution.

A56. The template RNA of any of the preceding embodiments, which is configured to edit a pathogenic R408W mutation in the human PAH gene.

A57. The template RNA of embodiment A56, which is configured to convert an R408W mutation to arginine.

A58. The template RNA of any of the preceding embodiments, which comprises one or more chemically modified nucleotides.

A59. A gene modifying system comprising:
a template RNA of any of the preceding embodiments, and
a gene modifying polypeptide, or a nucleic acid encoding the gene modifying polypeptide.

A60. The gene modifying system of embodiment A59, wherein the gene modifying polypeptide comprises an RT domain having a sequence according to SEQ ID NO: 8,003, or a sequence having at least 70%, 80%, 85%, 90%, 95%, 98%, or 99% identity thereto.

A61. The gene modifying system of embodiment A59, wherein the gene modifying polypeptide comprises an RT domain having a sequence according to SEQ ID NO: 8,020, or a sequence having at least 70%, 80%, 85%, 90%, 95%, 98%, or 99% identity thereto.

A62. The gene modifying system of embodiment 5A9, wherein the gene modifying polypeptide comprises an RT domain having a sequence according to SEQ ID NO: 8,074, or a sequence having at least 70%, 80%, 85%, 90%, 95%, 98%, or 99% identity thereto.

A63. The gene modifying system of embodiment A59, wherein the gene modifying polypeptide comprises an RT domain having a sequence according to SEQ ID NO: 8,113, or a sequence having at least 70%, 80%, 85%, 90%, 95%, 98%, or 99% identity thereto.

A64. The gene modifying system of embodiment A59, wherein the gene modifying polypeptide comprises DNA binding domain having a sequence of a Cas9 nickase comprising an N863A mutation, e.g., a sequence according to SEQ ID NO: 11,096, or a sequence having at least 70%, 80%, 85%, 90%, 95%, 98%, or 99% identity thereto.

A65. The gene modifying system of embodiment A59, which produces a first nick in a first strand of the human PAH gene.

A66. The gene modifying system of embodiment A65, which further comprises a second strand-targeting gRNA that directs a second nick to the second strand of the human PAH gene.

A67. The gene modifying system of embodiment A66, wherein the first nick and the second nick are 80-120 nucleotides apart.

A68. The gene modifying system of embodiment A66, wherein the template RNA and the second strand-targeting gRNA are configured to produce an outward nick orientation.

A69. The gene modifying system of embodiment A66, wherein the second strand-targeting gRNA comprises a spacer sequence that is complementary to a human PAH gene having a disease mutation or a wild-type sequence.

A70. A method for modifying a target site in the human PAH gene in a cell, the method comprising contacting the cell with the gene modifying system of embodiment 59, thereby modifying the target site in the human PAH gene in a cell.

A71. The method of embodiment A70, wherein correction of the mutation occurs in at least 30% of target nucleic acids.

A72. A method for treating a subject having a disease or condition associated with a mutation in the human PAH gene, wherein the disease or condition is phenylketonuria (PKU) or hyperphenylalaninemia (e.g., mild or severe hyperphenylalaninemia), the method comprising administering to the subject the gene modifying system of embodiment 59, thereby treating the subject having a disease or condition associated with a mutation in the human PAH gene.

BRIEF DESCRIPTION OF THE DRAWINGS

The patent or application file contains at least one drawing executed in color. Copies of this patent or patent application publication with color drawing(s) will be provided by the Office upon request and payment of the necessary fee.

FIG. 1 depicts a gene modifying system as described herein. The left hand diagram shows the gene modifying polypeptide, which comprises a Cas nickase domain (e.g., spCas9 N863A) and a reverse transcriptase domain (RT domain) which are linked by a linker. The right hand diagram shows the template RNA which comprises, from 5' to 3', a gRNA spacer, a gRNA scaffold, a heterologous object sequence, and a primer binding site sequence (PBS sequence). The heterologous object sequence can comprise a mutation region that comprises one or more sequence differences relative to the target site. The heterologous object sequence can also comprise a pre-edit homology region and a post-edit homology region, which flank the mutation region. Without wishing to be bound by theory, it is thought that the gRNA spacer of the template RNA binds to the second strand of a target site in the genome, and the gRNA

scaffold of the template RNA binds to the gene modifying polypeptide, e.g., localizing the gene modifying polypeptide to the target site in the genome. It is thought that the Cas domain of the gene modifying polypeptide nicks the target site (e.g., the first strand of the target site), e.g., allowing the PBS sequence to bind to a sequence adjacent to the site to be altered on the first strand of the target site. It is thought that the RT domain of the gene modifying polypeptide uses the first strand of the target site that is bound to the complementary sequence comprising the PBS sequence of the template RNA as a primer and the heterologous object sequence of the template RNA as a template to, e.g., polymerize a sequence complementary to the heterologous object sequence. Without wishing to be bound by theory, it is thought that reverse transcription can then proceed through the pre-edit homology region, then through the mutation region, and then through the post-edit homology region, thereby producing a DNA strand comprising a mutation specified by the heterologous object sequence.

FIG. 2 is a graph showing the percent rewriting achieved using the RNAV209-013 or RNAV214-040 gene modifying polypeptides with the indicated template RNAs.

FIG. 3 is a graph showing the amount of *Fah* mRNA relative to wild type when template RNAs are used with the RNAV209-013 or RNAV214-040 gene modifying polypeptides.

FIG.4 is a graph showing the percentage of Cas9-positive hepatocytes 6 hours following dosing with LNPs containing various gene modifying polypeptides and template RNAs.

FIG. 5 is a graph showing the rewrite levels in liver samples 6 days following dosing with LNPs containing various gene modifying polypeptides and template RNAs.

FIG. 6 is a graph showing wild type *Fah* mRNA restoration compared to littermate heterozygous mice in liver samples following dosing with LNPs containing various gene modifying polypeptides and template RNAs.

FIG. 7 is a graph showing Fah protein distribution in liver samples following dosing with LNPs containing various gene modifying polypeptides and template RNAs.

FIG. 8 is a series of western blots showing Cas9-RT Expression 6 hours after infusion of Cas9-RT mRNA + TTR guide LNP. Each lane represents an individual animal where 20 µg of tissue homogenate was added per lane. Positive control was from an *in vitro* cell experiment where Cas9-RT was expressed (described previously). GAPDH was used as a loading control for each sample. n=4 per group, vehicle or treated.

FIG. 9 is a graph showing gene editing of TTR locus after treatment with Cas9-RT mRNA + TTR guide LNP. Level of indels detected at the TTR locus measured by TIDE analysis of Sanger sequencing of the TTR locus where the protospacer targets.

FIG. 10 is a graph showing that TTR Serum levels decrease after treatment with Cas9-RT mRNA + TTR guide LNP. Measurement of circulating TTR levels 5 days after mice were treated with LNPs encapsulating Cas9-RT + TTR guide RNA.

FIG. 11 is a graph showing Cas9-RT Expression after infusion of Cas9-RT mRNA + TTR guide LNP. Relative expression quantified by ProteinSimple Jess capillary electrophoresis Western blot. Numbers in the symbols are animal number in group. Vehicle n=2, Cas9-RT + TTR guide n=3.

FIG. 12 is a graph showing gene editing of TTR locus after infusion of Cas9-RT mRNA + TTR guide LNP. Level of indels detected at the TTR locus were measured by amplicon sequencing of the TTR locus where the protospacer targets. Each animal had 8 different biopsies taken across the liver where amplicon sequencing measured the percentage of reads showing an indel.

FIG. 13 is a graph showing percent rewriting in primary mouse hepatocytes nucleofected with various gene modifying systems.

FIG. 14 is a graph showing percent editing in primary mouse hepatocytes nucleofected with various gene modifying systems containing second-nick gRNAs.

FIG. 15 is a heat map showing rewriting efficiency of various gene modifying systems with or without second-nick gRNAs.

FIG. 16 is a graph showing the percent of mouse hepatocytes expressing Cas9 six hours post-dosing with various gene modifying systems.

FIG. 17 is a pair of western blots showing expression of Cas9 in mouse liver samples six hours post-dosing with various gene modifying systems.

FIG. 18 is a graph showing the level of phenylalanine (Phe) present in plasma samples 7 days post-dosing with various gene modifying systems.

FIGs. 19A-19B are graphs showing percent rewriting (**FIG. 19A**) and percent indel (**FIG. 19B**) in mouse liver 7 days post-dosing with various gene modifying systems.

FIGs. 20A-20C are graphs showing percent rewriting in liver samples (**FIG. 20A**),levels of Phe in plasma (**FIG. 20B**), and percent indels in mouse liver (**FIG. 20C)** 7 days post-dosing with various gene modifying systems.

FIGs. 21A-21B are a pair of graphs showing percent rewriting and percent indel in liver samples (**FIG. 21A**) and levels of Phe in plasma (**FIG. 21B**) 7 days post-dosing with various gene modifying systems with or without second-nick gRNAs.

FIG. 22 is a graph showing the level of phenylalanine (Phe) in the plasma versus percent rewriting in samples obtained from mice treated with various gene modifying systems.

FIG. 23 is a graph showing percent rewriting in HEK293T cells containing the ***M fascicularis*** PAH gene for four different mutation types using template RNAs containing four different spacer sequences.

FIGs. 24A-24C are graphs showing percent rewriting (FIG. 24A) and percent indels (FIG. 24B) in mouse liver cells, or concentration of Phe in plasma (FIG. 24C) days post-dosing with LNPs comprising various gene modifying systems.

FIGs. 25A-25C are heat maps showing percent rewriting for each combination of template RNA and second strand-targeting RNA in primary human hepatocytes (**FIG. 25A**) and primary mouse hepatocytes (**FIG. 25C**) following transfection with (**FIGs. 25A** and **25B**) or LNP delivery of (**FIG. 25C**) various gene modifying systems.

FIGs. 26A-26B are graphs showing percent rewriting (FIG. 26A) and percent indels (FIG. 26B) in 7- and 28-day liver samples following LNP delivery of gene modifying systems to mice.

FIG. 27 is a graph showing the concentration of Phe in 7- and 28-day plasma samples following LNP delivery of gene modifying systems to mice.

FIG. 28 is a graph showing the concentration of Phe in 7- and 28-day brain samples following LNP delivery of gene modifying systems to mice.

FIG. 29 is a graph showing the concentration of Phe in the brain versus concentration of Phe in the plasma from samples used to generate **FIGs. 27** and **28**.

FIGs. 30A-30H are heat maps showing percent rewriting for each combination of template RNA and second strand-targeting RNA following mRNA delivery of gene modifying systems to primary cyno hepatocytes.

FIGs. 31A-31B are a graph stratified by silent substitution (**FIG. 31A**) showing percent total rewriting following mRNA delivery of various gene modifying systems utilizing the hPKU3

template RNAs comprising various silent substitutions into human iPSC-derived hepatoblasts and a chart (**FIG. 31B**) showing the particular silent substitutions utilized in **FIG. 31A**. FIG. 31B discloses SEQ ID NOS 37642-37649, respectively, in order of appearance.

FIGs. 32A-32B are a graph stratified by silent substitution (**FIG. 32A**) showing percent total rewriting following mRNA delivery of various gene modifying systems utilizing the hPKU4 template RNAs comprising various silent substitutions into human iPSC-derived hepatoblasts and a chart (**FIG. 32B**) showing the particular silent substitutions utilized in **FIG. 32A**. FIG. 32B discloses SEQ ID NOS 37650-37657, respectively, in order of appearance.

FIGs. 33A-33B are a graph (33A) and a chart (33B) showing are a graph stratified by silent substitution (**FIG. 33A**) showing percent total rewriting following mRNA delivery of various gene modifying systems utilizing the hPKU5 template RNAs comprising various silent substitutions into human iPSC-derived hepatoblasts and a chart (**FIG. 33B**) showing the particular silent substitutions utilized in **FIG. 33A**. FIG. 33B discloses SEQ ID NOS 37658-37665, respectively, in order of appearance.

FIGs. 34A-34B are a graph stratified by silent substitution (**FIG. 34A**) showing percent total rewriting following mRNA delivery of various gene modifying systems utilizing the hPKU6 template RNAs comprising various silent substitutions into human iPSC-derived hepatoblasts and a chart (**FIG. 34B**) showing the particular silent substitutions utilized in **FIG. 34A**.

FIG. 35 is a graph showing serum levels of Phe in mice following treatment with LNPs comprising various gene modifying systems.

FIGs. 36A-36B are graphs showing percent rewriting (**FIG. 36A**) and percent indels (**FIG. 36B**) in mouse liver following treatment with LNPs comprising various gene modifying systems.

DETAILED DESCRIPTION

Definitions

The term “expression cassette,” as used herein, refers to a nucleic acid construct comprising nucleic acid elements sufficient for the expression of the nucleic acid molecule of the instant invention.

A “gRNA spacer”, as used herein, refers to a portion of a nucleic acid that has complementarity to a target nucleic acid and can, together with a gRNA scaffold, target a Cas protein to the target nucleic acid.

A “gRNA scaffold”, as used herein, refers to a portion of a nucleic acid that can bind a Cas protein and can, together with a gRNA spacer, target the Cas protein to the target nucleic acid. In some embodiments, the gRNA scaffold comprises a crRNA sequence, tetraloop, and tracrRNA sequence.

A “gene modifying polypeptide”, as used herein, refers to a polypeptide comprising a retroviral reverse transcriptase, or a polypeptide comprising an amino acid sequence having at least 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, or 99% amino acid sequence identity to a retroviral reverse transcriptase, which is capable of integrating a nucleic acid sequence (e.g., a sequence provided on a template nucleic acid) into a target DNA molecule (e.g., in a mammalian host cell, such as a genomic DNA molecule in the host cell). In some embodiments, the gene modifying polypeptide is capable of integrating the sequence substantially without relying on host machinery. In some embodiments, the gene modifying polypeptide integrates a sequence into a random position in a genome, and in some embodiments, the gene modifying polypeptide integrates a sequence into a specific target site. In some embodiments, a gene modifying polypeptide includes one or more domains that, collectively, facilitate 1) binding the template nucleic acid, 2) binding the target DNA molecule, and 3) facilitate integration of the at least a portion of the template nucleic acid into the target DNA. Gene modifying polypeptides include both naturally occurring polypeptides as well as engineered variants of the foregoing, e.g., having one or more amino acid substitutions to the naturally occurring sequence. Gene modifying polypeptides also include heterologous constructs, e.g., where one or more of the domains recited above are heterologous to each other, whether through a heterologous fusion (or other conjugate) of otherwise wild-type domains, as well as fusions of modified domains, e.g., by way of replacement or fusion of a heterologous sub-domain or other substituted domain. Exemplary gene modifying polypeptides, and systems comprising them and methods of using them, that can be used in the methods provided herein are described, e.g., in PCT/US2021/020948, which is incorporated herein by reference with respect to gene modifying polypeptides that comprise a retroviral reverse transcriptase domain. In some embodiments, a gene modifying polypeptide integrates a sequence into a gene. In some embodiments, a gene modifying polypeptide integrates a sequence into a sequence outside of a gene. A “gene modifying system,” as used herein, refers to a system comprising a gene modifying polypeptide and a template nucleic acid.

The term “domain” as used herein refers to a structure of a biomolecule that contributes to a specified function of the biomolecule. A domain may comprise a contiguous region (e.g., a contiguous sequence) or distinct, non-contiguous regions (e.g., non-contiguous sequences) of a biomolecule. Examples of protein domains include, but are not limited to, an endonuclease domain, a DNA binding domain, a reverse transcription domain; an example of a domain of a nucleic acid is a regulatory domain, such as a transcription factor binding domain. In some embodiments, a domain (e.g., a Cas domain) can comprise two or more smaller domains (e.g., a DNA binding domain and an endonuclease domain).

As used herein, the term “exogenous”, when used with reference to a biomolecule (such as a nucleic acid sequence or polypeptide) means that the biomolecule was introduced into a host genome, cell or organism by the hand of man. For example, a nucleic acid that is as added into an existing genome, cell, tissue or subject using recombinant DNA techniques or other methods is exogenous to the existing nucleic acid sequence, cell, tissue or subject.

As used herein, “first strand” and “second strand”, as used to describe the individual DNA strands of target DNA, distinguish the two DNA strands based upon which strand the reverse transcriptase domain initiates polymerization, e.g., based upon where target primed synthesis initiates. The first strand refers to the strand of the target DNA upon which the reverse transcriptase domain initiates polymerization, e.g., where target primed synthesis initiates. The second strand refers to the other strand of the target DNA. First and second strand designations do not describe the target site DNA strands in other respects; for example, in some embodiments the first and second strands are nicked by a polypeptide described herein, but the designations ‘first’ and ‘second’ strand have no bearing on the order in which such nicks occur.

The term “heterologous,” as used herein to describe a first element in reference to a second element means that the first element and second element do not exist in nature disposed as described. For example, a heterologous polypeptide, nucleic acid molecule, construct or sequence refers to (a) a polypeptide, nucleic acid molecule or portion of a polypeptide or nucleic acid molecule sequence that is not native to a cell in which it is expressed, (b) a polypeptide or nucleic acid molecule or portion of a polypeptide or nucleic acid molecule that has been altered or mutated relative to its native state, or (c) a polypeptide or nucleic acid molecule with an altered expression as compared to the native expression levels under similar conditions. For example, a heterologous regulatory sequence (e.g., promoter, enhancer) may be used to regulate

expression of a gene or a nucleic acid molecule in a way that is different than the gene or a nucleic acid molecule is normally expressed in nature. In another example, a heterologous domain of a polypeptide or nucleic acid sequence (e.g., a DNA binding domain of a polypeptide or nucleic acid encoding a DNA binding domain of a polypeptide) may be disposed relative to other domains or may be a different sequence or from a different source, relative to other domains or portions of a polypeptide or its encoding nucleic acid. In certain embodiments, a heterologous nucleic acid molecule may exist in a native host cell genome, but may have an altered expression level or have a different sequence or both. In other embodiments, heterologous nucleic acid molecules may not be endogenous to a host cell or host genome but instead may have been introduced into a host cell by transformation (e.g., transfection, electroporation), wherein the added molecule may integrate into the host genome or can exist as extra-chromosomal genetic material either transiently (e.g., mRNA) or semi-stably for more than one generation (e.g., episomal viral vector, plasmid or other self-replicating vector).

As used herein, “insertion” of a sequence into a target site refers to the net addition of DNA sequence at the target site, e.g., where there are new nucleotides in the heterologous object sequence with no cognate positions in the unedited target site. In some embodiments, a nucleotide alignment of the PBS sequence and heterologous object sequence to the target nucleic acid sequence would result in an alignment gap in the target nucleic acid sequence.

As used herein, a “deletion” generated by a heterologous object sequence in a target site refers to the net deletion of DNA sequence at the target site, e.g., where there are nucleotides in the unedited target site with no cognate positions in the heterologous object sequence. In some embodiments, a nucleotide alignment of the PBS sequence and heterologous object sequence to the target nucleic acid sequence would result in an alignment gap in the molecule comprising the PBS sequence and heterologous object sequence.

The term “inverted terminal repeats” or “ITRs” as used herein refers to AAV viral cis-elements named so because of their symmetry. These elements promote efficient multiplication of an AAV genome. It is hypothesized that the minimal elements for ITR function are a Rep-binding site (RBS; 5´-GCGCGCTCGCTCGCTC-3´ for AAV2; SEQ ID NO: 4601) and a terminal resolution site (TRS; 5´-AGTTGG-3´ for AAV2) plus a variable palindromic sequence allowing for hairpin formation. According to the present invention, an ITR comprises at least these three elements (RBS, TRS, and sequences allowing the formation of an hairpin). In

addition, in the present invention, the term "ITR" refers to ITRs of known natural AAV serotypes (e.g. ITR of a serotype 1, 2, 3, 4, 5, 6, 7, 8, 9, 10 or 11 AAV), to chimeric ITRs formed by the fusion of ITR elements derived from different serotypes, and to functional variants thereof. "Functional variant" refers to a sequence presenting a sequence identity of at least 80%, 85%, 90%, preferably of at least 95% with a known ITR and allowing multiplication of the sequence that includes said ITR in the presence of Rep proteins.

The term "mutation region," as used herein, refers to a region in a template RNA having one or more sequence difference relative to the corresponding sequence in a target nucleic acid. The sequence difference may comprise, for example, a substitution, insertion, frameshift, or deletion.

The term "mutated" when applied to nucleic acid sequences means that nucleotides in a nucleic acid sequence are inserted, deleted, or changed compared to a reference (e.g., native) nucleic acid sequence. A single alteration may be made at a locus (a point mutation), or multiple nucleotides may be inserted, deleted, or changed at a single locus. In addition, one or more alterations may be made at any number of loci within a nucleic acid sequence. A nucleic acid sequence may be mutated by any method known in the art.

"Nucleic acid molecule" refers to both RNA and DNA molecules including, without limitation, complementary DNA ("cDNA"), genomic DNA ("gDNA"), and messenger RNA ("mRNA"), and also includes synthetic nucleic acid molecules, such as those that are chemically synthesized or recombinantly produced, such as RNA templates, as described herein. The nucleic acid molecule can be double-stranded or single-stranded, circular, or linear. If single-stranded, the nucleic acid molecule can be the sense strand or the antisense strand. Unless otherwise indicated, and as an example for all sequences described herein under the general format "SEQ ID NO:," or "nucleic acid comprising SEQ ID NO:1" refers to a nucleic acid, at least a portion which has either (i) the sequence of SEQ ID NO:1, or (ii) a sequence complimentary to SEQ ID NO:1. The choice between the two is dictated by the context in which SEQ ID NO:1 is used. For instance, if the nucleic acid is used as a probe, the choice between the two is dictated by the requirement that the probe be complementary to the desired target. Nucleic acid sequences of the present disclosure may be modified chemically or biochemically or may contain non-natural or derivatized nucleotide bases, as will be readily appreciated by those of skill in the art. Such modifications include, for example, labels, methylation,

substitution of one or more naturally occurring nucleotides with an analog, inter-nucleotide modifications such as uncharged linkages (for example, methyl phosphonates, phosphotriesters, phosphoramidates, carbamates, etc.), charged linkages (for example, phosphorothioates, phosphorodithioates, etc.), pendant moieties, (for example, polypeptides), intercalators (for example, acridine, psoralen, etc.), chelators, alkylators, and modified linkages (for example, alpha anomeric nucleic acids, etc.). Also included are chemically modified bases (see, for example, Table 13), backbones (see, for example, Table 14), and modified caps (see, for example, Table 15). Also included are synthetic molecules that mimic polynucleotides in their ability to bind to a designated sequence via hydrogen bonding and other chemical interactions. Such molecules are known in the art and include, for example, those in which peptide linkages substitute for phosphate linkages in the backbone of a molecule, e.g., peptide nucleic acids (PNAs). Other modifications can include, for example, analogs in which the ribose ring contains a bridging moiety or other structure such as modifications found in "locked" nucleic acids (LNAs). In various embodiments, the nucleic acids are in operative association with additional genetic elements, such as tissue-specific expression-control sequence(s) (e.g., tissue-specific promoters and tissue-specific microRNA recognition sequences), as well as additional elements, such as inverted repeats (e.g., inverted terminal repeats, such as elements from or derived from viruses, e.g., AAV ITRs) and tandem repeats, inverted repeats/direct repeats, homology regions (segments with various degrees of homology to a target DNA), untranslated regions (UTRs) (5′, 3′, or both 5′ and 3′ UTRs), and various combinations of the foregoing. The nucleic acid elements of the systems provided by the invention can be provided in a variety of topologies, including single-stranded, double-stranded, circular, linear, linear with open ends, linear with closed ends, and particular versions of these, such as doggybone DNA (dbDNA), closed-ended DNA (ceDNA).

As used herein, a "gene expression unit" is a nucleic acid sequence comprising at least one regulatory nucleic acid sequence operably linked to at least one effector sequence. A first nucleic acid sequence is operably linked with a second nucleic acid sequence when the first nucleic acid sequence is placed in a functional relationship with the second nucleic acid sequence. For instance, a promoter or enhancer is operably linked to a coding sequence if the promoter or enhancer affects the transcription or expression of the coding sequence. Operably

linked DNA sequences may be contiguous or non-contiguous. Where necessary to join two protein-coding regions, operably linked sequences may be in the same reading frame.

The terms "host genome" or "host cell", as used herein, refer to a cell and/or its genome into which protein and/or genetic material has been introduced. It should be understood that such terms are intended to refer not only to the particular subject cell and/or genome, but to the progeny of such a cell and/or the genome of the progeny of such a cell. Because certain modifications may occur in succeeding generations due to either mutation or environmental influences, such progeny may not, in fact, be identical to the parent cell, but are still included within the scope of the term "host cell" as used herein. A host genome or host cell may be an isolated cell or cell line grown in culture, or genomic material isolated from such a cell or cell line, or may be a host cell or host genome which composing living tissue or an organism. In some instances, a host cell may be an animal cell or a plant cell, e.g., as described herein. In certain instances, a host cell may be a mammalian cell, a human cell, avian cell, reptilian cell, bovine cell, horse cell, pig cell, goat cell, sheep cell, chicken cell, or turkey cell. In certain instances, a host cell may be a corn cell, soy cell, wheat cell, or rice cell.

As used herein, "operative association" describes a functional relationship between two nucleic acid sequences, such as a 1) promoter and 2) a heterologous object sequence, and means, in such example, the promoter and heterologous object sequence (e.g., a gene of interest) are oriented such that, under suitable conditions, the promoter drives expression of the heterologous object sequence. For instance, a template nucleic acid carrying a promoter and a heterologous object sequence may be single-stranded, e.g., either the (+) or (-) orientation. An "operative association" between the promoter and the heterologous object sequence in this template means that, regardless of whether the template nucleic acid will be transcribed in a particular state, when it is in the suitable state (e.g., is in the (+) orientation, in the presence of required catalytic factors, and NTPs, etc.), it is accurately transcribed. Operative association applies analogously to other pairs of nucleic acids, including other tissue-specific expression control sequences (such as enhancers, repressors and microRNA recognition sequences), IR/DR, ITRs, UTRs, or homology regions and heterologous object sequences or sequences encoding a retroviral RT domain.

The term "primer binding site sequence" or "PBS sequence," as used herein, refers to a portion of a template RNA capable of binding to a region comprised in a target nucleic acid

sequence. In some instances, a PBS sequence is a nucleic acid sequence comprising at least 3, 4, 5, 6, 7, or 8 bases with 100% identity to the region comprised in the target nucleic acid sequence. In some embodiments the primer region comprises at least 5, 6, 7, 8 bases with 100% identity to the region comprised in the target nucleic acid sequence. Without wishing to be bound by theory, in some embodiments when a template RNA comprises a PBS sequence and a heterologous object sequence, the PBS sequence binds to a region comprised in a target nucleic acid sequence, allowing a reverse transcriptase domain to use that region as a primer for reverse transcription, and to use the heterologous object sequence as a template for reverse transcription.

As used herein, a "stem-loop sequence" refers to a nucleic acid sequence (e.g., RNA sequence) with sufficient self-complementarity to form a stem-loop, e.g., having a stem comprising at least two (e.g., 3, 4, 5, 6, 7, 8, 9, or 10) base pairs, and a loop with at least three (e.g., four) base pairs. The stem may comprise mismatches or bulges.

As used herein, a "tissue-specific expression-control sequence" means nucleic acid elements that increase or decrease the level of a transcript comprising the heterologous object sequence in a target tissue in a tissue-specific manner, e.g., preferentially in on-target tissue(s), relative to off-target tissue(s). In some embodiments, a tissue-specific expression-control sequence preferentially drives or represses transcription, activity, or the half-life of a transcript comprising the heterologous object sequence in the target tissue in a tissue-specific manner, e.g., preferentially in an on-target tissue(s), relative to an off-target tissue(s). Exemplary tissue-specific expression-control sequences include tissue-specific promoters, repressors, enhancers, or combinations thereof, as well as tissue-specific microRNA recognition sequences. Tissue specificity refers to on-target (tissue(s) where expression or activity of the template nucleic acid is desired or tolerable) and off-target (tissue(s) where expression or activity of the template nucleic acid is not desired or is not tolerable). For example, a tissue-specific promoter drives expression preferentially in on-target tissues, relative to off-target tissues. In contrast, a microRNA that binds the tissue-specific microRNA recognition sequences is preferentially expressed in off-target tissues, relative to on-target tissues, thereby reducing expression of a template nucleic acid in off-target tissues. Accordingly, a promoter and a microRNA recognition sequence that are specific for the same tissue, such as the target tissue, have contrasting functions (promote and repress, respectively, with concordant expression levels, i.e., high levels of the microRNA in off-target tissues and low levels in on-target tissues, while promoters drive high

expression in on-target tissues and low expression in off-target tissues) with regard to the transcription, activity, or half-life of an associated sequence in that tissue.

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Introduction

This disclosure relates to methods for treating phenylketonuria (PKU) and compositions for targeting, editing, modifying or manipulating a DNA sequence (e.g., inserting a heterologous object sequence into a target site of a mammalian genome) at one or more locations in a DNA sequence in a cell, tissue or subject, e.g., *in vivo* or *in vitro*. The heterologous object DNA sequence may include, e.g., a substitution.

More specifically, the disclosure provides methods for treating PKU using reverse transcriptase-based systems for altering a genomic DNA sequence of interest, e.g., by inserting, deleting, or substituting one or more nucleotides into/from the sequence of interest.

The disclosure provides, in part, methods for treating PKU using a gene modifying system comprising a gene modifying polypeptide component and a template nucleic acid (e.g., template RNA) component. In some embodiments, a gene modifying system can be used to introduce an alteration into a target site in a genome. In some embodiments, the gene modifying polypeptide component comprises a writing domain (e.g., a reverse transcriptase domain), a DNA-binding domain, and an endonuclease domain (e.g., nickase domain). In some embodiments, the template nucleic acid (e.g., template RNA) comprises a sequence (e.g., a gRNA spacer) that binds a target site in the genome (e.g., that binds to a second strand of the target site), a sequence (e.g., a gRNA scaffold) that binds the gene modifying polypeptide component, a heterologous object sequence, and a PBS sequence. Without wishing to be bound by theory, it is thought that the template nucleic acid (e.g., template RNA) binds to the second strand of a target site in the genome, and binds to the gene modifying polypeptide component (e.g., localizing the polypeptide component to the target site in the genome). It is thought that the endonuclease (e.g., nickase) of the gene modifying polypeptide component cuts the target site (e.g., the first strand of the target site), e.g., allowing the PBS sequence to bind to a sequence adjacent to the site to be altered on the first strand of the target site. It is thought that the writing domain (e.g., reverse transcriptase domain) of the polypeptide component uses the first strand of

the target site that is bound to the complementary sequence comprising the PBS sequence of the template nucleic acid as a primer and the heterologous object sequence of the template nucleic acid as a template to, e.g., polymerize a sequence complementary to the heterologous object sequence. Without wishing to be bound by theory, it is thought that selection of an appropriate heterologous object sequence can result in substitution, deletion, and/or insertion of one or more nucleotides at the target site.

Gene modifying systems

In some embodiments, a gene modifying system described herein comprises: (A) a gene modifying polypeptide or a nucleic acid encoding the gene modifying polypeptide, wherein the gene modifying polypeptide comprises (i) a reverse transcriptase domain, and either (x) an endonuclease domain that contains DNA binding functionality or (y) an endonuclease domain and separate DNA binding domain; and (B) a template RNA. A gene modifying polypeptide, in some embodiments, acts as a substantially autonomous protein machine capable of integrating a template nucleic acid sequence into a target DNA molecule (e.g., in a mammalian host cell, such as a genomic DNA molecule in the host cell), substantially without relying on host machinery. For example, the gene modifying protein may comprise a DNA-binding domain, a reverse transcriptase domain, and an endonuclease domain. In some embodiments, the DNA-binding function may involve an RNA component that directs the protein to a DNA sequence, e.g., a gRNA spacer. In other embodiments, the gene modifying polypeptide may comprise a reverse transcriptase domain and an endonuclease domain. The RNA template element of a gene modifying system is typically heterologous to the gene modifying polypeptide element and provides an object sequence to be inserted (reverse transcribed) into the host genome. In some embodiments, the gene modifying polypeptide is capable of target primed reverse transcription. In some embodiments, the gene modifying polypeptide is capable of second-strand synthesis.

In some embodiments the gene modifying system is combined with a second polypeptide. In some embodiments, the second polypeptide may comprise an endonuclease domain. In some embodiments, the second polypeptide may comprise a polymerase domain, e.g., a reverse transcriptase domain. In some embodiments, the second polypeptide may comprise a DNA-dependent DNA polymerase domain. In some embodiments, the second polypeptide aids in

completion of the genome edit, e.g., by contributing to second-strand synthesis or DNA repair resolution.

A functional gene modifying polypeptide can be made up of unrelated DNA binding, reverse transcription, and endonuclease domains. This modular structure allows combining of functional domains, e.g., dCas9 (DNA binding), MMLV reverse transcriptase (reverse transcription), FokI (endonuclease). In some embodiments, multiple functional domains may arise from a single protein, e.g., Cas9 or Cas9 nickase (DNA binding, endonuclease).

In some embodiments, a gene modifying polypeptide includes one or more domains that, collectively, facilitate 1) binding the template nucleic acid, 2) binding the target DNA molecule, and 3) facilitate integration of the at least a portion of the template nucleic acid into the target DNA. In some embodiments, the gene modifying polypeptide is an engineered polypeptide that comprises one or more amino acid substitutions to a corresponding naturally occurring sequence. In some embodiments, the gene modifying polypeptide comprises two or more domains that are heterologous relative to each other, e.g., through a heterologous fusion (or other conjugate) of otherwise wild-type domains, or well as fusions of modified domains, e.g., by way of replacement or fusion of a heterologous sub-domain or other substituted domain. For instance, in some embodiments, one or more of: the RT domain is heterologous to the DBD; the DBD is heterologous to the endonuclease domain; or the RT domain is heterologous to the endonuclease domain.

In some embodiments, a template RNA molecule for use in the system comprises, from 5′ to 3′ (1) a gRNA spacer; (2) a gRNA scaffold; (3) heterologous object sequence (4) a primer binding site (PBS) sequence. In some embodiments:

(1) Is a gRNA spacer of ~18-22 nt, e.g., is 20 nt

(2) Is a gRNA scaffold comprising one or more hairpin loops, e.g., 1, 2, of 3 loops for associating the template with a Cas domain, e.g., a nickase Cas9 domain. In some embodiments, the gRNA scaffold comprises the sequence, from 5′ to 3′, GTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGGACCGAGTCGGTCC (SEQ ID NO: 5008).

(3) In some embodiments, the heterologous object sequence is, e.g., 7-74, e.g., 10-20, 20-30, 30-40, 40-50, 50-60, 60-70, or 70-80 nt or, 80-90 nt in length. In some embodiments, the first (most 5′) base of the sequence is not C.

(4) In some embodiments, the PBS sequence that binds the target priming sequence after nicking occurs is e.g., 3-20 nt, e.g., 7-15 nt, e.g., 12-14 nt. In some embodiments, the PBS sequence has 40-60% GC content.

In some embodiments, a second gRNA associated with the system may help drive complete integration. In some embodiments, the second gRNA may target a location that is 0-200 nt away from the first-strand nick, e.g., 0-50, 50-100, 100-200 nt away from the first-strand nick. In some embodiments, the second gRNA can only bind its target sequence after the edit is made, e.g., the gRNA binds a sequence present in the heterologous object sequence, but not in the initial target sequence.

In some embodiments, a gene modifying system described herein is used to make an edit in HEK293, K562, U2OS, or HeLa cells. In some embodiment, a gene modifying system is used to make an edit in primary cells, e.g., primary cortical neurons from E18.5 mice.

In some embodiments, a gene modifying polypeptide as described herein comprises a reverse transcriptase or RT domain (e.g., as described herein) that comprises a MoMLV RT sequence or variant thereof. In embodiments, the MoMLV RT sequence comprises one or more mutations selected from D200N, L603W, T330P, T306K, W313F, D524G, E562Q, D583N, P51L, S67R, E67K, T197A, H204R, E302K, F309N, L435G, N454K, H594Q, D653N, R110S, and K103L. In embodiments, the MoMLV RT sequence comprises a combination of mutations, such as D200N, L603W, and T330P, optionally further including T306K and/or W313F.

In some embodiments, an endonuclease domain (e.g., as described herein) nCas9, e.g., comprising an N863A mutation (e.g., in spCas9) or a H840A mutation.

In some embodiments, the heterologous object sequence (e.g., of a system as described herein) is about 1-50, 50-100, 100-200, 200-300, 300-400, 400-500, 500-600, 600-700, 700-800, 800-900, 900-1000, or more, nucleotides in length.

In some embodiments, the RT and endonuclease domains are joined by a flexible linker, e.g., comprising the amino acid sequence SGGSSGGSSGSETPGTSESATPESSGGSSGGSS (SEQ ID NO: 5006).

In some embodiments, the endonuclease domain is N-terminal relative to the RT domain. In some embodiments, the endonuclease domain is C-terminal relative to the RT domain.

In some embodiments, the system incorporates a heterologous object sequence into a target site by TPRT, e.g., as described herein.

In some embodiments, a gene modifying polypeptide comprises a DNA binding domain. In some embodiments, a gene modifying polypeptide comprises an RNA binding domain. In some embodiments, the RNA binding domain comprises an RNA binding domain of B-box protein, MS2 coat protein, dCas, or an element of a sequence of a table herein. In some embodiments, the RNA binding domain is capable of binding to a template RNA with greater affinity than a reference RNA binding domain.

In some embodiments, a gene modifying system is capable of producing an insertion into the target site of at least 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, or 100 nucleotides (and optionally no more than 500, 400, 300, 200, or 100 nucleotides). In some embodiments, a gene modifying system is capable of producing an insertion into the target site of at least 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, or 100 nucleotides (and optionally no more than 500, 400, 300, 200, or 100 nucleotides). In some embodiments, a gene modifying system is capable of producing an insertion into the target site of at least 0.2, 0.3, 0.4, 0.5, 0.6, 0.7, 0.8, 0.9, 1, 1.5, 2, 2.5, 3, 3.5, 4, 4.5, 5, 5.5, 6, 6.5, 7, 7.5, 8, 8.5, 9, 9.5 or 10 kilobases (and optionally no more than 1, 5, 10, or 20 kilobases). In some embodiments, a gene modifying system is capable of producing a deletion of at least 81, 85, 90, 95, 100, 110, 120, 130, 140, 150, 160, 170, 180, 190, or 200 nucleotides (and optionally no more than 500, 400, 300, or 200 nucleotides). In some embodiments, a gene modifying system is capable of producing a deletion of at least 81, 85, 90, 95, 100, 110, 120, 130, 140, 150, 160, 170, 180, 190, or 200 nucleotides (and optionally no more than 500, 400, 300, or 200 nucleotides). In some embodiments, a gene modifying system is capable of producing a deletion of at least 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, 100, 110, 120, 130, 140, 150, 160, 170, 180, 190, or 200 nucleotides (and optionally no more than 500, 400, 300, or 200 nucleotides). In some embodiments, a gene modifying system is capable of producing a deletion of at least 0.2, 0.3, 0.4, 0.5, 0.6, 0.7, 0.8, 0.9, 1, 1.5, 2, 2.5, 3, 3.5, 4, 4.5, 5, 5.5, 6, 6.5, 7, 7.5, 8, 8.5, 9, 9.5 or 10 kilobases (and optionally no more than 1, 5, 10, or 20 kilobases). In some embodiments, a gene modifying system is capable of producing a substitution into the target site of at least 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25, 30, 35, 40, 45, 50, 60, 70, 80, 90, or 100 or more

nucleotides. In some embodiments, a gene modifying system is capable of producing a substitution in the target site of 1-2, 2-3, 3-4, 4-5, 5-10, 10-15, 15-20, 20-30, 30-40, 40-50, 50-60, 60-70, 70-80, 80-90, or 90-100 nucleotides.

In some embodiments, the substitution is a transition mutation. In some embodiments, the substitution is a transversion mutation. In some embodiments, the substitution converts an adenine to a thymine, an adenine to a guanine, an adenine to a cytosine, a guanine to a thymine, a guanine to a cytosine, a guanine to an adenine, a thymine to a cytosine, a thymine to an adenine, a thymine to a guanine, a cytosine to an adenine, a cytosine to a guanine, or a cytosine to a thymine.

In some embodiments, an insertion, deletion, substitution, or combination thereof, increases or decreases expression (e.g. transcription or translation) of a gene. In some embodiments, an insertion, deletion, substitution, or combination thereof, increases or decreases expression (e.g. transcription or translation) of a gene by altering, adding, or deleting sequences in a promoter or enhancer, e.g. sequences that bind transcription factors. In some embodiments, an insertion, deletion, substitution, or combination thereof alters translation of a gene (e.g. alters an amino acid sequence), inserts or deletes a start or stop codon, alters or fixes the translation frame of a gene. In some embodiments, an insertion, deletion, substitution, or combination thereof alters splicing of a gene, e.g. by inserting, deleting, or altering a splice acceptor or donor site. In some embodiments, an insertion, deletion, substitution, or combination thereof alters transcript or protein half-life. In some embodiments, an insertion, deletion, substitution, or combination thereof alters protein localization in the cell (e.g. from the cytoplasm to a mitochondria, from the cytoplasm into the extracellular space (e.g. adds a secretion tag)). In some embodiments, an insertion, deletion, substitution, or combination thereof alters (e.g. improves) protein folding (e.g. to prevent accumulation of misfolded proteins). In some embodiments, an insertion, deletion, substitution, or combination thereof, alters, increases, decreases the activity of a gene, e.g. a protein encoded by the gene.

Exemplary gene modifying polypeptides, and systems comprising them and methods of using them are described, e.g., in PCT/US2021/020948, which is incorporated herein by reference with respect to retroviral RT domains, including the amino acid and nucleic acid sequences therein.

Exemplary gene modifying polypeptides and retroviral RT domain sequences are also described, e.g., in International Application No. PCT/US21/20948 filed March 4, 2021, e.g., at Table 30, Table 31, and Table 44 therein; the entire application is incorporated by reference herein with respect to retroviral RTs, e.g., in said sequences and tables. Accordingly, a gene modifying polypeptide described herein may comprise an amino acid sequence according to any of the Tables mentioned in this paragraph, or a domain thereof (e.g., a retroviral RT domain), or a functional fragment or variant of any of the foregoing, or an amino acid sequence having at least 70%, 80%, 85%, 90%, 95%, or 99% identity thereto.

In some embodiments, a polypeptide for use in any of the systems described herein can be a molecular reconstruction or ancestral reconstruction based upon the aligned polypeptide sequence of multiple homologous proteins. In some embodiments, a reverse transcriptase domain for use in any of the systems described herein can be a molecular reconstruction or an ancestral reconstruction, or can be modified at particular residues, based upon alignments of reverse transcriptase domains from the same or different sources. A skilled artisan can, based on the Accession numbers provided herein, align polypeptides or nucleic acid sequences, e.g., by using routine sequence analysis tools as Basic Local Alignment Search Tool (BLAST) or CD-Search for conserved domain analysis. Molecular reconstructions can be created based upon sequence consensus, e.g. using approaches described in Ivics et al., Cell 1997, 501 – 510 ; Wagstaff et al., Molecular Biology and Evolution 2013, 88-99.

Polypeptide components of gene modifying systems

In some embodiments, the gene modifying polypeptide possesses the functions of DNA target site binding, template nucleic acid (e.g., RNA) binding, DNA target site cleavage, and template nucleic acid (e.g., RNA) writing, e.g., reverse transcription. In some embodiments, each functions is contained within a distinct domain. In some embodiments, a function may be attributed to two or more domains (e.g., two or more domains, together, exhibit the functionality). In some embodiments, two or more domains may have the same or similar function (e.g., two or more domains each independently have DNA-binding functionality, e.g., for two different DNA sequences). In other embodiments, one or more domains may be capable of enabling one or more functions, e.g., a Cas9 domain enabling both DNA binding and target site cleavage. In some embodiments, the domains are all located within a single polypeptide. In

some embodiments, a first domain is in one polypeptide and a second domain is in a second polypeptide. For example, in some embodiments, the sequences may be split between a first polypeptide and a second polypeptide, e.g., wherein the first polypeptide comprises a reverse transcriptase (RT) domain and wherein the second polypeptide comprises a DNA-binding domain and an endonuclease domain, e.g., a nickase domain. As a further example, in some embodiments, the first polypeptide and the second polypeptide each comprise a DNA binding domain (e.g., a first DNA binding domain and a second DNA binding domain). In some embodiments, the first and second polypeptide may be brought together post-translationally via a split-intein to form a single gene modifying polypeptide.

In some aspects, a gene modifying polypeptide described herein comprises (e.g., a system described herein comprises a gene modifying polypeptide that comprises): 1) a Cas domain (e.g., a Cas nickase domain, e.g., a Cas9 nickase domain); 2) a reverse transcriptase (RT) domain of Table D, or a sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, or 99% identity thereto, wherein the RT domain is C-terminal of the Cas domain; and a linker disposed between the RT domain and the Cas domain, wherein the linker has a sequence from the same row of Table D as the RT domain, or a sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, or 99% identity thereto.

In some embodiments, the RT domain has a sequence with 100% identity to the RT domain of Table D and the linker has a sequence with 100% identity to the linker sequence from the same row of Table D as the RT domain. In some embodiments, the Cas domain comprises a sequence of Table 8, or a sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, 98%, or 99% identity thereto. In some embodiments, the gene modifying polypeptide comprises an amino acid sequence according to any of SEQ ID NOs: 1-3332 in the sequence listing, or a sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, or 99% identity thereto.

In some embodiments, the gene modifying polypeptide comprises a GG amino acid sequence between the Cas domain and the linker, an AG amino acid sequence between the RT domain and the second NLS, and/or a GG amino acid sequence between the linker and the RT domain. In some embodiments, the gene modifying polypeptide comprises a sequence of SEQ ID NO: 4000 which comprises the first NLS and the Cas domain, or a sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, 98%, or 99% identity thereto. In some embodiments, the gene modifying polypeptide comprises a sequence of SEQ ID NO: 4001 which comprises the

second NLS, or a sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, 98%, or 99% identity thereto.

Exemplary N-terminal NLS-Cas9 domain

MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLF
DSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRLEESFLVEEDKKHERHP
IFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDV
DKLFIQLVQTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALS
LGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVN
TEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFY
KFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR
EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKN
LPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLK
EDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDR
EMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNF
MQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPE
NIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRD
MYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ
LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKL
IREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIKKYPKLESEFVYGDY
KVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKG
RDFATVRKVLSMPQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAY
SVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFE
LENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEI
IEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR
KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGG (SEQ ID NO: 4000)

Exemplary C-terminal sequence comprising an NLS

AGKRTADGSEFEKRTADGSEFESPKKKAKVE (SEQ ID NO: 4001)

<u>Writing domain (RT Domain)</u>

In certain aspects of the present invention, the writing domain of the gene modifying system possesses reverse transcriptase activity and is also referred to as a reverse transcriptase domain (a RT domain). In some embodiments, the RT domain comprises an RT catalytic portion and RNA-binding region (e.g., a region that binds the template RNA).

In some embodiments, a nucleic acid encoding the reverse transcriptase is altered from its natural sequence to have altered codon usage, e.g. improved for human cells. In some

embodiments the reverse transcriptase domain is a heterologous reverse transcriptase from a retrovirus. In some embodiments, the RT domain comprising a gene modifying polypeptide has been mutated from its original amino acid sequence, e.g., has at least 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 20, 30, 40, 50, 60, 70, 80, 90, or 100 substitutions. In some embodiments, the RT domain is derived from the RT of a retrovirus, e.g., HIV-1 RT, Moloney Murine Leukemia Virus (MMLV) RT, avian myeloblastosis virus (AMV) RT, or Rous Sarcoma Virus (RSV) RT.

In some embodiments, the retroviral reverse transcriptase (RT) domain exhibits enhanced stringency of target-primed reverse transcription (TPRT) initiation, e.g., relative to an endogenous RT domain. In some embodiments, the RT domain initiates TPRT when the 3 nt in the target site immediately upstream of the first strand nick, e.g., the genomic DNA priming the RNA template, have at least 66% or 100% complementarity to the 3 nt of homology in the RNA template. In some embodiments, the RT domain initiates TPRT when there are less than 5 nt mismatched (e.g., less than 1, 2, 3, 4, or 5 nt mismatched) between the template RNA homology and the target DNA priming reverse transcription. In some embodiments, the RT domain is modified such that the stringency for mismatches in priming the TPRT reaction is increased, e.g., wherein the RT domain does not tolerate any mismatches or tolerates fewer mismatches in the priming region relative to a wild-type (e.g., unmodified) RT domain. In some embodiments, the RT domain comprises a HIV-1 RT domain. In embodiments, the HIV-1 RT domain initiates lower levels of synthesis even with three nucleotide mismatches relative to an alternative RT domain (e.g., as described by Jamburuthugoda and Eickbush J Mol Biol 407(5):661-672 (2011); incorporated herein by reference in its entirety). In some embodiments, the RT domain forms a dimer (e.g., a heterodimer or homodimer). In some embodiments, the RT domain is monomeric. In some embodiments, an RT domain, naturally functions as a monomer or as a dimer (e.g., heterodimer or homodimer). In some embodiments, an RT domain naturally functions as a monomer, e.g., is derived from a virus wherein it functions as a monomer. In embodiments, the RT domain is selected from an RT domain from murine leukemia virus (MLV; sometimes referred to as MoMLV) (e.g., P03355), porcine endogenous retrovirus (PERV) (e.g., UniProt Q4VFZ2), mouse mammary tumor virus (MMTV) (e.g., UniProt P03365), Avian reticuloendotheliosis virus (AVIRE) (e.g., UniProtKB accession: P03360); Feline leukemia virus (FLV or FeLV) (e.g., e.g., UniProtKB accession: P10273); Mason-Pfizer monkey virus (MPMV) (e.g., UniProt P07572), bovine leukemia virus (BLV) (e.g., UniProt P03361), human T-cell

leukemia virus-1 (HTLV-1) (e.g., UniProt P03362), human foamy virus (HFV) (e.g., UniProt P14350), simian foamy virus (SFV) (e.g., SFV3L) (e.g., UniProt P23074 or P27401), or bovine foamy/syncytial virus (BFV/BSV) (e.g., UniProt O41894), or a functional fragment or variant thereof (e.g., an amino acid sequence having at least 70%, 80%, 90%, 95%, or 99% identity thereto). In some embodiments, an RT domain is dimeric in its natural functioning. In some embodiments, the RT domain is derived from a virus wherein it functions as a dimer. In embodiments, the RT domain is selected from an RT domain from avian sarcoma/leukemia virus (ASLV) (e.g., UniProt A0A142BKH1), Rous sarcoma virus (RSV) (e.g., UniProt P03354), avian myeloblastosis virus (AMV) (e.g., UniProt Q83133), human immunodeficiency virus type I (HIV-1) (e.g., UniProt P03369), human immunodeficiency virus type II (HIV-2) (e.g., UniProt P15833), simian immunodeficiency virus (SIV) (e.g., UniProt P05896), bovine immunodeficiency virus (BIV) (e.g., UniProt P19560), equine infectious anemia virus (EIAV) (e.g., UniProt P03371), or feline immunodeficiency virus (FIV) (e.g., UniProt P16088) (Herschhorn and Hizi *Cell Mol Life Sci* 67(16):2717-2747 (2010)), or a functional fragment or variant thereof (e.g., an amino acid sequence having at least 70%, 80%, 90%, 95%, or 99% identity thereto). Naturally heterodimeric RT domains may, in some embodiments, also be functional as homodimers. In some embodiments, dimeric RT domains are expressed as fusion proteins, e.g., as homodimeric fusion proteins or heterodimeric fusion proteins. In some embodiments, the RT function of the system is fulfilled by multiple RT domains (e.g., as described herein). In further embodiments, the multiple RT domains are fused or separate, e.g., may be on the same polypeptide or on different polypeptides.

In some embodiments, a gene modifying system described herein comprises an integrase domain, e.g., wherein the integrase domain may be part of the RT domain. In some embodiments, an RT domain (e.g., as described herein) comprises an integrase domain. In some embodiments, an RT domain (e.g., as described herein) lacks an integrase domain, or comprises an integrase domain that has been inactivated by mutation or deleted. In some embodiment, a gene modifying system described herein comprises an RNase H domain, e.g., wherein the RNase H domain may be part of the RT domain. In some embodiments, the RNase H domain is not part of the RT domain and is covalently linked via a flexible linker. In some embodiments, an RT domain (e.g., as described herein) comprises an RNase H domain, e.g., an endogenous RNAse H domain or a heterologous RNase H domain. In some embodiments, an RT domain (e.g., as

described herein) lacks an RNase H domain. In some embodiments, an RT domain (e.g., as described herein) comprises an RNase H domain that has been added, deleted, mutated, or swapped for a heterologous RNase H domain. In some embodiments, the polypeptide comprises an inactivated endogenous RNase H domain. In some embodiments, an endogenous RNase H domain from one of the other domains of the polypeptide is genetically removed such that it is not included in the polypeptide, e.g., the endogenous RNase H domain is partially or completely truncated from the comprising domain. In some embodiments, mutation of an RNase H domain yields a polypeptide exhibiting lower RNase activity, e.g., as determined by the methods described in Kotewicz et al. *Nucleic Acids Res* 16(1):265-277 (1988) (incorporated herein by reference in its entirety), e.g., lower by at least 10%, 20%, 30%, 40%, 50%, 60%, 70%, 80%, or 90% compared to an otherwise similar domain without the mutation. In some embodiments, RNase H activity is abolished.

In some embodiments, an RT domain is mutated to increase fidelity compared to an otherwise similar domain without the mutation. For instance, in some embodiments, a YADD (SEQ ID NO: 37635) or YMDD motif (SEQ ID NO: 37636) in an RT domain (e.g., in a reverse transcriptase) is replaced with YVDD (SEQ ID NO: 37637). In embodiments, replacement of the YADD (SEQ ID NO: 37635) or YMDD (SEQ ID NO: 37636) or YVDD (SEQ ID NO: 37637) results in higher fidelity in retroviral reverse transcriptase activity (e.g., as described in Jamburuthugoda and Eickbush J Mol Biol 2011; incorporated herein by reference in its entirety).

In some embodiments, a gene modifying polypeptide described herein comprises an RT domain having an amino acid sequence according to Table 6, or a sequence having at least 70%, 80%, 85%, 90%, 95%, 97%, 98%, or 99% identity thereto. In some embodiments, a nucleic acid described herein encodes an RT domain having an amino acid sequence according to Table 6, or a sequence having at least 70%, 80%, 85%, 90%, 95%, 97%, 98%, or 99% identity thereto.

Table 6: Exemplary reverse transcriptase domains from retroviruses

RT Name	SEQ ID NO:	RT amino acid sequence
AVIRE_P03360	8,001	TAPLEEEYRLFLEAPIQNVTLLEQWKREIPKVWAEINPPGLASTQAPIHVQLLSTALPVRVRQYPITLEAKRSLRETIRKFRAAGILRPVHSPWNTPLLPV RKSGTSEYRMVQDLREVNKRVETIHPTVPNPYTLLSLLPPDRIWYSVLDLKDAFFCIPLAPESQLIFAFEWADAEEGESGQLTWTRLPQGFKNSPTLFD EALNRDLQGFRLDHPSVSLLQYVDDLLIAADTQAACLSATRDLLMTLAELGYRVSGKKAQLCQEEVTYLGFKIHKGSRSLSNSRTQAILQIPVPKTKRQV REFLGTIGYCRLWIPGFAELAQPLYAATRGGNDPLVWGEKEEEAFQSLKLALTQPPALALPSLDKPFQLFVEETSGAAKGVLTQALGPWKRPVAYLSK RLDPVAAGWPRCLRAIAAAALLTREASKLTFGQDIEITSSHNLESLLRSPPDKWLTNARITQYQVLLLDPPRVRFKQTAALNPATLLPETDDTLPIHHCLD TLDSLTSTRPDLTDQPLAQAEATLFTDGSSYIRDGKRYAGAAVVTLDSVIWAEPLPIGTSAQKAELIALTKALEWSKDKSVNIYTDSRYAFATLHVHGMIY RERGLLTAGGKAIKNAPEILALLTAVWLPKRVAVMHCKGHQKDDAPTSTGNRRADEVAREVAIRPLSTQATIS
AVIRE_P03360_3mut	8,002	TAPLEEEYRLFLEAPIQNVTLLEQWKREIPKVWAEINPPGLASTQAPIHVQLLSTALPVRVRQYPITLEAKRSLRETIRKFRAAGILRPVHSPWNTPLLPV RKSGTSEYRMVQDLREVNKRVETIHPTVPNPYTLLSLLPPDRIWYSVLDLKDAFFCIPLAPESQLIFAFEWADAEEGESGQLTWTRLPQGFKNSPTLFN EALNRDLQGFRLDHPSVSLLQYVDDLLIAADTQAACLSATRDLLMTLAELGYRVSGKKAQLCQEEVTYLGFKIHKGSRSLSNSRTQAILQIPVPKTKRQV

RT Name	SEQ ID NO:	RT amino acid sequence
		REFLGTIGYCRLWIPGFAELAQPLYAATRPGNDPLVWGEKEEEAFQSLKLALTQPPALALPSLDKPFQLFVEETSGAAKGVLTQALGPWKRPVAYLSK RLDPVAAGWPRCLRAIAAAALLTREASKLTFGQDIEITSSHNLESLLRSPPDKWLTNARITQYQVLLLDPPRVRFKQTAALNPATLLPETDDTLPIHHCLD TLDSLTSTRPDLTDQPLAQAEATLFTDGSSYIRDGKRYAGAAVVTLDSVIWAEPLPIGTSAQKAELIALTKALEWSKDKSVNIYTDSRYAFATLHVHGMIY RERGWLTAGGKAIKNAPEILALLTAVWLPKRVAVMHCKGHQKDDAPTSTGNRRADEVAREVAIRPLSTQATIS
AVIRE_P03360_3mutA 8,003		TAPLEEEYRLFLEAPIQNVTLLEQWKREIPKVWAEINPPGLASTQAPIHVQLLSTALPVRVRQYPITLEAKRSLRETIRKFRAAGILRPVHSPWNTPLLPV RKSGTSEYRMVQDLREVNKRVETIHPTVPNPYTLLSLLPPDRIWYSVLDLKDAFFCIPLAPESQLIFAFEWADAEEGESGQLTWTRLPQGFKNSPTLFN EALNRDLQGFRLDHPSVSLLQYVDDLLIAADTQAACLSATRDLLMTLAELGYRVSGKKAQLCQEEVTYLGFKIHKGSRSLSNSRTQAILQIPVPKTKRQV REFLGKIGYCRLFIPGFAELAQPLYAATRPGNDPLVWGEKEEEAFQSLKLALTQPPALALPSLDKPFQLFVEETSGAAKGVLTQALGPWKRPVAYLSKR LDPVAAGWPRCLRAIAAAALLTREASKLTFGQDIEITSSHNLESLLRSPPDKWLTNARITQYQVLLLDPPRVRFKQTAALNPATLLPETDDTLPIHHCLDT LDSLTSTRPDLTDQPLAQAEATLFTDGSSYIRDGKRYAGAAVVTLDSVIWAEPLPIGTSAQKAELIALTKALEWSKDKSVNIYTDSRYAFATLHVHGMIY RERGWLTAGGKAIKNAPEILALLTAVWLPKRVAVMHCKGHQKDDAPTSTGNRRADEVAREVAIRPLSTQATIS
BAEVM_P10272 8,004		TVSLQDEHRLFDIPVTTSLPDVWLQDFPQAWAETGGLGRAKCQAPIIIDLKPTAVPVSIKQYPMSLEAHMGIRQHIIKFLELGVLRPCRSPWNTPLLPVK KPGTQDYRPVQDLREINKRTVDIHPTVPNPYNLLSTLKPDYSWYTVLDLKDAFFCLPLAPQSQELFAFEWKDPERGISGQLTWTRLPQGFKNSPTLFD EALHRDLTDFRTQHPEVTLLQYVDDLLLAAPTKKACTQGTRHLLQELGEKGYRASAKKAQICQTKVTYLGYILSEGKRWLTPGRIETVARIPPPRNPRE VREFLGTAGFCRLWIPGFAELAAPLYALTKESTPFTWQTEHQLAFEALKKALLSAPALGLPDTSKPFTLFLDERQGIAKGVLTQKLGPWKRPVAYLSKK LDPVAAGWPPCLRIMAATAMLVKDSAKLTLGQPLTVITPHTLEAIVRQPPDRWITNARLTHYQALLLDTDRVQFGPPVTLNPATLLPVPENQPSPHDCR QVLAETHGTREDLKDQELPDADHTWYTDGSSYLDSGTRRAGAAVVDGHNTIWAQSLPPGTSAQKAELIALTKALELSKGKKANIYTDSRYAFATAHTH GSIYERRGLLTSEGKEIKNKAEIIALLKALFLPQEVAIIHCPGHQKGQDPVAVGNRQADRVARQAAMAEVLTLATEPDNTSHIT
BAEVM_P10272_3mut 8,005		TVSLQDEHRLFDIPVTTSLPDVWLQDFPQAWAETGGLGRAKCQAPIIIDLKPTAVPVSIKQYPMSLEAHMGIRQHIIKFLELGVLRPCRSPWNTPLLPVK KPGTQDYRPVQDLREINKRTVDIHPTVPNPYNLLSTLKPDYSWYTVLDLKDAFFCLPLAPQSQELFAFEWKDPERGISGQLTWTRLPQGFKNSPTLFN EALHRDLTDFRTQHPEVTLLQYVDDLLLAAPTKKACTQGTRHLLQELGEKGYRASAKKAQICQTKVTYLGYILSEGKRWLTPGRIETVARIPPPRNPRE VREFLGTAGFCRLWIPGFAELAAPLYALTKPSTPFTWQTEHQLAFEALKKALLSAPALGLPDTSKPFTLFLDERQGIAKGVLTQKLGPWKRPVAYLSKK LDPVAAGWPPCLRIMAATAMLVKDSAKLTLGQPLTVITPHTLEAIVRQPPDRWITNARLTHYQALLLDTDRVQFGPPVTLNPATLLPVPENQPSPHDCR QVLAETHGTREDLKDQELPDADHTWYTDGSSYLDSGTRRAGAAVVDGHNTIWAQSLPPGTSAQKAELIALTKALELSKGKKANIYTDSRYAFATAHTH GSIYERRGWLTSEGKEIKNKAEIIALLKALFLPQEVAIIHCPGHQKGQDPVAVGNRQADRVARQAAMAEVLTLATEPDNTSHIT
BAEVM_P10272_3mutA 8,006		TVSLQDEHRLFDIPVTTSLPDVWLQDFPQAWAETGGLGRAKCQAPIIIDLKPTAVPVSIKQYPMSLEAHMGIRQHIIKFLELGVLRPCRSPWNTPLLPVK KPGTQDYRPVQDLREINKRTVDIHPTVPNPYNLLSTLKPDYSWYTVLDLKDAFFCLPLAPQSQELFAFEWKDPERGISGQLTWTRLPQGFKNSPTLFN EALHRDLTDFRTQHPEVTLLQYVDDLLLAAPTKKACTQGTRHLLQELGEKGYRASAKKAQICQTKVTYLGYILSEGKRWLTPGRIETVARIPPPRNPRE VREFLGKAGFCRLFIPGFAELAAPLYALTKPSTPFTWQTEHQLAFEALKKALLSAPALGLPDTSKPFTLFLDERQGIAKGVLTQKLGPWKRPVAYLSKKL DPVAAGWPPCLRIMAATAMLVKDSAKLTLGQPLTVITPHTLEAIVRQPPDRWITNARLTHYQALLLDTDRVQFGPPVTLNPATLLPVPENQPSPHDCRQ VLAETHGTREDLKDQELPDADHTWYTDGSSYLDSGTRRAGAAVVDGHNTIWAQSLPPGTSAQKAELIALTKALELSKGKKANIYTDSRYAFATAHTHG SIYERRGWLTSEGKEIKNKAEIIALLKALFLPQEVAIIHCPGHQKGQDPVAVGNRQADRVARQAAMAEVLTLATEPDNTSHIT
BLVAU_P25059 8,007		GVLDAPPSHIGLEHLPPPPEVPQFPLNLERLQALQDLVHRSLEAGYISPWDGPGNNPVFPVRKPNGAWRFVHDLRVTNALTKPIPALSPGPPDLTAIPT HLPHIICLDLKDAFFQIPVEDRFRSYFAFTLPTPGGLQPHRRFAWRVLPQGFINSPALFERALQEPLRQVSAAFSQSLLVSYMDDILYVSPTEEQRLQCY QTMAAHLRDLGFQVASEKTRQTPSPVPFLGQMVHERMVTYQSLPTLQISSPISLHQLQTVLGDLQWVSRGTPTTRRPLQLLYSSLKGIDDPRAIIHLSP EQQQGIAELRQALSHNARSRYNEQEPLLAYVHLTRAGSTLVLFQKGAQFPLAYFQTPLTDNQASPWGLLLLLGCQYLQAQALSSYAKTILKYYHNLPK TSLDNWIQSSEDPRVQELLQLWPQISSQGIQPPGPWKTLVTRAEVFLTPQFSPEPIPAALCLFSDGAARRGAYCLWKDHLLDFQAVPAPESAQKGELA GLLAGLAAAPPEPLNIWVDSKYLYSLLRTLVLGAWLQPDPVPSYALLYKSLLRHPAIFVGHVRSHSSASHPIASLNNYVDQL
BLVAU_P25059_2mut 8,008		GVLDAPPSHIGLEHLPPPPEVPQFPLNLERLQALQDLVHRSLEAGYISPWDGPGNNPVFPVRKPNGAWRFVHDLRVTNALTKPIPALSPGPPDLTAIPT HLPHIICLDLKDAFFQIPVEDRFRSYFAFTLPTPGGLQPHRRFAWRVLPQGFINSPALFQRALQEPLRQVSAAFSQSLLVSYMDDILYVSPTEEQRLQCY QTMAAHLRDLGFQVASEKTRQTPSPVPFLGQMVHERMVTYQSLPTLQISSPISLHQLQTVLGDLQWVSRGTPTTRRPLQLLYSSLKPIDDPRAIIHLSP EQQQGIAELRQALSHNARSRYNEQEPLLAYVHLTRAGSTLVLFQKGAQFPLAYFQTPLTDNQASPWGLLLLLGCQYLQAQALSSYAKTILKYYHNLPK TSLDNWIQSSEDPRVQELLQLWPQISSQGIQPPGPWKTLVTRAEVFLTPQFSPEPIPAALCLFSDGAARRGAYCLWKDHLLDFQAVPAPESAQKGELA GLLAGLAAAPPEPLNIWVDSKYLYSLLRTLVLGAWLQPDPVPSYALLYKSLLRHPAIFVGHVRSHSSASHPIASLNNYVDQL
BLVJ_P03361 8,009		GVLDTPPSHIGLEHLPPPPEVPQFPLNLERLQALQDLVHRSLEAGYISPWDGPGNNPVFPVRKPNGAWRFVHDLRATNALTKPIPALSPGPPDLTAIPT HPPHIICLDLKDAFFQIPVEDRFRFYLSFTLPSPGGLQPHRRFAWRVLPQGFINSPALFERALQEPLRQVSAAFSQSLLVSYMDDILYASPTEEQRSQCY QALAARLRDLGFQVASEKTSQTPSPVPFLGQMVHEQIVTYQSLPTLQISSPISLHQLQAVLGDLQWVSRGTPTTRRPLQLLYSSLKRHHDPRAIIQLSPE QLQGIAELRQALSHNARSRYNEQEPLLAYVHLTRAGSTLVLFQKGAQFPLAYFQTPLTDNQASPWGLLLLLGCQYLQTQALSSYAKPILKYYHNLPKTS LDNWIQSSEDPRVQELLQLWPQISSQGIQPPGPWKTLITRAEVFLTPQFSPDPIPAALCLFSDGATGRGAYCLWKDHLLDFQAVPAPESAQKGELAGL LAGLAAAPPEPVNIWVDSKYLYSLLRTLVLGAWLQPDPVPSYALLYKSLLRHPAIVVGHVRSHSSASHPIASLNNYVDQL
BLVJ_P03361_2mut 8,010		GVLDTPPSHIGLEHLPPPPEVPQFPLNLERLQALQDLVHRSLEAGYISPWDGPGNNPVFPVRKPNGAWRFVHDLRATNALTKPIPALSPGPPDLTAIPT HPPHIICLDLKDAFFQIPVEDRFRFYLSFTLPSPGGLQPHRRFAWRVLPQGFINSPALFNRALQEPLRQVSAAFSQSLLVSYMDDILYASPTEEQRSQCY QALAARLRDLGFQVASEKTSQTPSPVPFLGQMVHEQIVTYQSLPTLQISSPISLHQLQAVLGDLQWVSRGTPTTRRPLQLLYSSLKRHHDPRAIIQLSPE QLQGIAELRQALSHNARSRYNEQEPLLAYVHLTRAGSTLVLFQKGAQFPLAYFQTPLTDNQASPWGLLLLLGCQYLQTQALSSYAKPILKYYHNLPKTS LDNWIQSSEDPRVQELLQLWPQISSQGIQPPGPWKTLITRAEVFLTPQFSPDPIPAALCLFSDGATGRGAYCLWKDHLLDFQAVPAPESAQKGELAGL LAGLAAAPPEPVNIWVDSKYLYSLLRTWVLGAWLQPDPVPSYALLYKSLLRHPAIVVGHVRSHSSASHPIASLNNYVDQL
BLVJ_P03361_2mutB 8,011		GVLDTPPSHIGLEHLPPPPEVPQFPLNLERLQALQDLVHRSLEAGYISPWDGPGNNPVFPVRKPNGAWRFVHDLRATNALTKPIPALSPGPPDLTAPP THPPHIICLDLKDAFFQIPVEDRFRFYLSFTLPSPGGLQPHRRFAWRVLPQGFINSPALFQRALQEPLRQVSAAFSQSLLVSYMDDILYASPTEEQRSQC YQALAARLRDLGFQVASEKTSQTPSPVPFLGQMVHEQIVTYQSLPTLQISSPISLHQLQAVLGDLQWVSRGTPTTRRPLQLLYSSLKRHHDPRAIIQLSP EQLQGIAELRQALSHNARSRYNEQEPLLAYVHLTRAGSTLVLFQKGAQFPLAYFQTPLTDNQASPWGLLLLLGCQYLQTQALSSYAKPILKYYHNLPKT SLDNWIQSSEDPRVQELLQLWPQISSQGIQPPGPWKTLITRAEVFLTPQFSPDPIPAALCLFSDGATGRGAYCLWKDHLLDFQAVPAPESAQKGELAG LLAGLAAAPPEPVNIWVDSKYLYSLLRTWVLGAWLQPDPVPSYALLYKSLLRHPAIVVGHVRSHSSASHPIASLNNYVDQL
FFV_O93209 8,012		MDLLKPLTVERKGVKIKGYWNSQADITCVPKDLLQGEEPVRQQNVTTIHGTQEGDVYYVNLKIDGRRINTEVIGTTLDYAIITPGDVPWILKKPLELTIKLD LEEQQGTLLNNSILSKKGKEELKQLFEKYSALWQSWENQVGHRRIRPHKIATGTVKPTPQKQYHINPKAKPDIQIVINDLLKQGVLIQKESTMNTPVYPV PKPNGRWRMVLDYRAVNKVTPLIAVQNQHSYGILGSLFKGRYKTTIDLSNGFWAHPIVPEDYWITAFTWQGKQYCWTVLPQGFLNSPGLFTGDVVDL LQGIPNVEVYVDDVYISHDSEKEHLEYLDILFNRLKEAGYIISLKKSNIANSIVDFLGFQITNEGRGLTDTFKEKLENITAPTTLKQLQSILGLLNFARNFIPD FTELIAPLYALIPKSTKNYVPWQIEHSTTLETLITKLNGAEYLQGRKGDKTLIMKVNASYTTGYIRYYNEGEKKPISYVSIVFSKTELKFTELEKLLTTVHKG

RT Name	SEQ ID NO:	RT amino acid sequence
		LLKALDLSMGQNIHVYSPIVSMQNIQKTPQTAKKALASRWLSWLSYLEDPRIRFFYDPQMPALKDLPAVDTGKDNKKHPSNFQHIFYTDGSAITSPTKE GHLNAGMGIVYFINKDGNLQKQQEWSISLGNHTAQFAEIAAFEFALKKCLPLGGNILVVTDSNYVAKAYNEELDVWASNGFVNNRKKPLKHISKWKSV ADLKRLRPDVVVTHEPGHQKLDSSPHAYGNNLADQLATQASFKVH
FFV_O 93209_ 2mut	8,013	MDLLKPLTVERKGVKIKGYWNSQADITCVPKDLLQGEEPVRQQNVTTIHGTQEGDVYYVNLKIDGRRINTEVIGTTLDYAIITPGDVPWILKKPLELTIKLD LEEQQGTLLNNSILSKKGKEELKQLFEKYSALWQSWENQVGHRRIRPHKIATGTVKPTPQKQYHINPKAKPDIQIVINDLLKQGVLIQKESTMNTPVYPV PKPNGRWRMVLDYRAVNKVTPLIAVQNQHSYGILGSLFKGRYKTTIDLSNGFWAHPIVPEDYWITAFTWQGKQYCWTVLPQGFLNSPGLFNGDVVDL LQGIPNVEVYVDDVYISHDSEKEHLEYLDILFNRLKEAGYIISLKKSNIANSIVDFLGFQITNEGRGLTDTFKEKLENITAPTTLKQLQSILGLLNFARNFIPD FTELIAPLYALIPKSPKNYVPWQIEHSTTLETLITKLNGAEYLQGRKGDKTLIMKVNASYTTGYIRYYNEGEKKPISYVSIVFSKTELKFTELEKLLTTVHKG LLKALDLSMGQNIHVYSPIVSMQNIQKTPQTAKKALASRWLSWLSYLEDPRIRFFYDPQMPALKDLPAVDTGKDNKKHPSNFQHIFYTDGSAITSPTKE GHLNAGMGIVYFINKDGNLQKQQEWSISLGNHTAQFAEIAAFEFALKKCLPLGGNILVVTDSNYVAKAYNEELDVWASNGFVNNRKKPLKHISKWKSV ADLKRLRPDVVVTHEPGHQKLDSSPHAYGNNLADQLATQASFKVH
FFV_O 93209_ 2mutA	8,014	MDLLKPLTVERKGVKIKGYWNSQADITCVPKDLLQGEEPVRQQNVTTIHGTQEGDVYYVNLKIDGRRINTEVIGTTLDYAIITPGDVPWILKKPLELTIKLD LEEQQGTLLNNSILSKKGKEELKQLFEKYSALWQSWENQVGHRRIRPHKIATGTVKPTPQKQYHINPKAKPDIQIVINDLLKQGVLIQKESTMNTPVYPV PKPNGRWRMVLDYRAVNKVTPLIAVQNQHSYGILGSLFKGRYKTTIDLSNGFWAHPIVPEDYWITAFTWQGKQYCWTVLPQGFLNSPGLFNGDVVDL LQGIPNVEVYVDDVYISHDSEKEHLEYLDILFNRLKEAGYIISLKKSNIANSIVDFLGFQITNEGRGLTDTFKEKLENITAPTTLKQLQSILGKLNFARNFIPD FTELIAPLYALIPKSPKNYVPWQIEHSTTLETLITKLNGAEYLQGRKGDKTLIMKVNASYTTGYIRYYNEGEKKPISYVSIVFSKTELKFTELEKLLTTVHKG LLKALDLSMGQNIHVYSPIVSMQNIQKTPQTAKKALASRWLSWLSYLEDPRIRFFYDPQMPALKDLPAVDTGKDNKKHPSNFQHIFYTDGSAITSPTKE GHLNAGMGIVYFINKDGNLQKQQEWSISLGNHTAQFAEIAAFEFALKKCLPLGGNILVVTDSNYVAKAYNEELDVWASNGFVNNRKKPLKHISKWKSV ADLKRLRPDVVVTHEPGHQKLDSSPHAYGNNLADQLATQASFKVH
FFV_O 93209-Pro	8,015	VPWILKKPLELTIKLDLEEQQGTLLNNSILSKKGKEELKQLFEKYSALWQSWENQVGHRRIRPHKIATGTVKPTPQKQYHINPKAKPDIQIVINDLLKQGV LIQKESTMNTPVYPVPKPNGRWRMVLDYRAVNKVTPLIAVQNQHSYGILGSLFKGRYKTTIDLSNGFWAHPIVPEDYWITAFTWQGKQYCWTVLPQGF LNSPGLFTGDVVDLLQGIPNVEVYVDDVYISHDSEKEHLEYLDILFNRLKEAGYIISLKKSNIANSIVDFLGFQITNEGRGLTDTFKEKLENITAPTTLKQLQ SILGLLNFARNFIPDFTELIAPLYALIPKSTKNYVPWQIEHSTTLETLITKLNGAEYLQGRKGDKTLIMKVNASYTTGYIRYYNEGEKKPISYVSIVFSKTELK FTELEKLLTTVHKGLLKALDLSMGQNIHVYSPIVSMQNIQKTPQTAKKALASRWLSWLSYLEDPRIRFFYDPQMPALKDLPAVDTGKDNKKHPSNFQHI FYTDGSAITSPTKEGHLNAGMGIVYFINKDGNLQKQQEWSISLGNHTAQFAEIAAFEFALKKCLPLGGNILVVTDSNYVAKAYNEELDVWASNGFVNNR KKPLKHISKWKSVADLKRLRPDVVVTHEPGHQKLDSSPHAYGNNLADQLATQASFKVH
FFV_O 93209-Pro_2mut	8,016	VPWILKKPLELTIKLDLEEQQGTLLNNSILSKKGKEELKQLFEKYSALWQSWENQVGHRRIRPHKIATGTVKPTPQKQYHINPKAKPDIQIVINDLLKQGV LIQKESTMNTPVYPVPKPNGRWRMVLDYRAVNKVTPLIAVQNQHSYGILGSLFKGRYKTTIDLSNGFWAHPIVPEDYWITAFTWQGKQYCWTVLPQGF LNSPGLFNGDVVDLLQGIPNVEVYVDDVYISHDSEKEHLEYLDILFNRLKEAGYIISLKKSNIANSIVDFLGFQITNEGRGLTDTFKEKLENITAPTTLKQLQ SILGLLNFARNFIPDFTELIAPLYALIPKSPKNYVPWQIEHSTTLETLITKLNGAEYLQGRKGDKTLIMKVNASYTTGYIRYYNEGEKKPISYVSIVFSKTELK FTELEKLLTTVHKGLLKALDLSMGQNIHVYSPIVSMQNIQKTPQTAKKALASRWLSWLSYLEDPRIRFFYDPQMPALKDLPAVDTGKDNKKHPSNFQHI FYTDGSAITSPTKEGHLNAGMGIVYFINKDGNLQKQQEWSISLGNHTAQFAEIAAFEFALKKCLPLGGNILVVTDSNYVAKAYNEELDVWASNGFVNNR KKPLKHISKWKSVADLKRLRPDVVVTHEPGHQKLDSSPHAYGNNLADQLATQASFKVH
FFV_O 93209-Pro_2mutA	8,017	VPWILKKPLELTIKLDLEEQQGTLLNNSILSKKGKEELKQLFEKYSALWQSWENQVGHRRIRPHKIATGTVKPTPQKQYHINPKAKPDIQIVINDLLKQGV LIQKESTMNTPVYPVPKPNGRWRMVLDYRAVNKVTPLIAVQNQHSYGILGSLFKGRYKTTIDLSNGFWAHPIVPEDYWITAFTWQGKQYCWTVLPQGF LNSPGLFNGDVVDLLQGIPNVEVYVDDVYISHDSEKEHLEYLDILFNRLKEAGYIISLKKSNIANSIVDFLGFQITNEGRGLTDTFKEKLENITAPTTLKQLQ SILGKLNFARNFIPDFTELIAPLYALIPKSPKNYVPWQIEHSTTLETLITKLNGAEYLQGRKGDKTLIMKVNASYTTGYIRYYNEGEKKPISYVSIVFSKTELK FTELEKLLTTVHKGLLKALDLSMGQNIHVYSPIVSMQNIQKTPQTAKKALASRWLSWLSYLEDPRIRFFYDPQMPALKDLPAVDTGKDNKKHPSNFQHI FYTDGSAITSPTKEGHLNAGMGIVYFINKDGNLQKQQEWSISLGNHTAQFAEIAAFEFALKKCLPLGGNILVVTDSNYVAKAYNEELDVWASNGFVNNR KKPLKHISKWKSVADLKRLRPDVVVTHEPGHQKLDSSPHAYGNNLADQLATQASFKVH
FLV_P 10273	8,018	TLQLEEEYRLFEPESTQKQEMDIWLKNFPQAWAETGGMGTAHCQAPVLIQLKATATPISIRQYPMPHEAYQGIKPHIRRMLDQGILKPCQSPWNTPLLP VKKPGTEDYRPVQDLREVNKRVEDIHPTVPNPYNLLSTLPPSHPWYTVLDLKDAFFCLRLHSESQLLFAFEWRDPEIGLSGQLTWTRLPQGFKNSPTL FDEALHSDLADFRVRYPALVLLQYVDDLLLAAATRTECLEGTKALLETLGNKGYRASAKKAQICLQEVTYLGYSLKDGQRWLTKARKEAILSIPVPKNSR QVREFLGTAGYCRLWIPGFAELAAPLYPLTRPGTLFQWGTEQQLAFEDIKKALLSSPALGLPDITKPFELFIDENSGFAKGVLVQKLGPWKRPVAYLSK KLDTVASGWPPCLRMVAAIAILVKDAGKLTLGQPLTILTSHPVEALVRQPPNKWLSNARMTHYQAMLLDAERVHFGPTVSLNPATLLPLPSGGNHHDC LQILAETHGTRPDLTDQPLPDADLTWYTDGSSFIRNGEREAGAAVTTESEVIWAAPLPPGTSAQRAELIALTQALKMAEGKKLTVYTDSRYAFATTHVH GEIYRRRGLLTSEGKEIKNKNEILALLEALFLPKRLSIIHCPGHQKGDSPQAKGNRLADDTAKKAATETHSSLTVLP
FLV_P 10273_ 3mut	8,019	TLQLEEEYRLFEPESTQKQEMDIWLKNFPQAWAETGGMGTAHCQAPVLIQLKATATPISIRQYPMPHEAYQGIKPHIRRMLDQGILKPCQSPWNTPLLP VKKPGTEDYRPVQDLREVNKRVEDIHPTVPNPYNLLSTLPPSHPWYTVLDLKDAFFCLRLHSESQLLFAFEWRDPEIGLSGQLTWTRLPQGFKNSPTL FNEALHSDLADFRVRYPALVLLQYVDDLLLAAATRTECLEGTKALLETLGNKGYRASAKKAQICLQEVTYLGYSLKDGQRWLTKARKEAILSIPVPKNSR QVREFLGTAGYCRLWIPGFAELAAPLYPLTRPGTLFQWGTEQQLAFEDIKKALLSSPALGLPDITKPFELFIDENSGFAKGVLVQKLGPWKRPVAYLSK KLDTVASGWPPCLRMVAAIAILVKDAGKLTLGQPLTILTSHPVEALVRQPPNKWLSNARMTHYQAMLLDAERVHFGPTVSLNPATLLPLPSGGNHHDC LQILAETHGTRPDLTDQPLPDADLTWYTDGSSFIRNGEREAGAAVTTESEVIWAAPLPPGTSAQRAELIALTQALKMAEGKKLTVYTDSRYAFATTHVH GEIYRRRGWLTSEGKEIKNKNEILALLEALFLPKRLSIIHCPGHQKGDSPQAKGNRLADDTAKKAATETHSSLTVLP
FLV_P 10273_ 3mutA	8,020	TLQLEEEYRLFEPESTQKQEMDIWLKNFPQAWAETGGMGTAHCQAPVLIQLKATATPISIRQYPMPHEAYQGIKPHIRRMLDQGILKPCQSPWNTPLLP VKKPGTEDYRPVQDLREVNKRVEDIHPTVPNPYNLLSTLPPSHPWYTVLDLKDAFFCLRLHSESQLLFAFEWRDPEIGLSGQLTWTRLPQGFKNSPTL FNEALHSDLADFRVRYPALVLLQYVDDLLLAAATRTECLEGTKALLETLGNKGYRASAKKAQICLQEVTYLGYSLKDGQRWLTKARKEAILSIPVPKNSR QVREFLGKAGYCRLFIPGFAELAAPLYPLTRPGTLFQWGTEQQLAFEDIKKALLSSPALGLPDITKPFELFIDENSGFAKGVLVQKLGPWKRPVAYLSKK LDTVASGWPPCLRMVAAIAILVKDAGKLTLGQPLTILTSHPVEALVRQPPNKWLSNARMTHYQAMLLDAERVHFGPTVSLNPATLLPLPSGGNHHDCL QILAETHGTRPDLTDQPLPDADLTWYTDGSSFIRNGEREAGAAVTTESEVIWAAPLPPGTSAQRAELIALTQALKMAEGKKLTVYTDSRYAFATTHVHG EIYRRRGWLTSEGKEIKNKNEILALLEALFLPKRLSIIHCPGHQKGDSPQAKGNRLADDTAKKAATETHSSLTVLP
FOAM V_P14 350	8,021	MNPLQLLQPLPAEIKGTKLLAHWNSGATITCIPESFLEDEQPIKKTLIKTIHGEKQQNVYYVTFKVKGRKVEAEVIASPYEYILLSPTDVPWLTQQPLQLTIL VPLQEYQEKILSKTALPEDQKQQLKTLFVKYDNLWQHWENQVGHRKIRPHNIATGDYPPRPQKQYPINPKAKPSIQIVIDDLLKQGVLTPQNSTMNTPV YPVPKPDGRWRMVLDYREVNKTIPLTAAQNQHSAGILATIVRQKYKTTLDLANGFWAHPITPESYWLTAFTWQGKQYCWTRLPQGFLNSPALFTADV VDLLKEIPNVQVYVDDIYLSHDDPKEHVQQLEKVFQILLQAGYVVSLKKSEIGQKTVEFLGFNITKEGRGLTDTFKTKLLNITPPKDLKQLQSILGLLNFAR NFIPNFAELVQPLYNLIASAKGKYIEWSEENTKQLNMVIEALNTASNLEERLPEQRLVIKVNTSPSAGYVRYYNETGKKPIMYLNYVFSKAELKFSMLEKL LTTMHKALIKAMDLAMGQEILVYSPIVSMTKIQKTPLPERKALPIRWITWMTYLEDPRIQFHYDKTLPELKHIPDVYTSSQSPVKHPSQYEGVFYTDGSAI

RT Name	SEQ ID NO:	RT amino acid sequence
		KSPDPTKSNNAGMGIVHATYKPEYQVLNQWSIPLGNHTAQMAEIAAVEFACKKALKIPGPVLVITDSFYVAESANKELPYWKSNGFVNNKKKPLKHISK WKSIAECLSMKPDITIQHEKGISLQIPVFILKGNALADKLATQGSYVVN
FOAMV_P14350_2mut	8,022	MNPLQLLQPLPAEIKGTKLLAHWNSGATITCIPESFLEDEQPIKKTLIKTIHGEKQQNVYYVTFKVKGRKVEAEVIASPYEYILLSPTDVPWLTQQPLQLTIL VPLQEYQEKILSKTALPEDQKQQLKTLFVKYDNLWQHWENQVGHRKIRPHNIATGDYPPRPQKQYPINPKAKPSIQIVIDDLLKQGVLTPQNSTMNTPV YPVPKPDGRWRMVLDYREVNKTIPLTAAQNQHSAGILATIVRQKYKTTLDLANGFWAHPITPESYWLTAFTWQGKQYCWTRLPQGFLNSPALFNADV VDLLKEIPNVQVYVDDIYLSHDDPKEHVQQLEKVFQILLQAGYVVSLKKSEIGQKTVEFLGFNITKEGRGLTDTFKTKLLNITPPKDLKQLQSILGLLNFAR NFIPNFAELVQPLYNLIAPAKGKYIEWSEENTKQLNMVIEALNTASNLEERLPEQRLVIKVNTSPSAGYVRYYNETGKKPIMYLNYVFSKAELKFSMLEKL LTTMHKALIKAMDLAMGQEILVYSPIVSMTKIQKTPLPERKALPIRWITWMTYLEDPRIQFHYDKTLPELKHIPDVYTSSQSPVKHPSQYEGVFYTDGSAI KSPDPTKSNNAGMGIVHATYKPEYQVLNQWSIPLGNHTAQMAEIAAVEFACKKALKIPGPVLVITDSFYVAESANKELPYWKSNGFVNNKKKPLKHISK WKSIAECLSMKPDITIQHEKGISLQIPVFILKGNALADKLATQGSYVVN
FOAMV_P14350_2mutA	8,023	MNPLQLLQPLPAEIKGTKLLAHWNSGATITCIPESFLEDEQPIKKTLIKTIHGEKQQNVYYVTFKVKGRKVEAEVIASPYEYILLSPTDVPWLTQQPLQLTIL VPLQEYQEKILSKTALPEDQKQQLKTLFVKYDNLWQHWENQVGHRKIRPHNIATGDYPPRPQKQYPINPKAKPSIQIVIDDLLKQGVLTPQNSTMNTPV YPVPKPDGRWRMVLDYREVNKTIPLTAAQNQHSAGILATIVRQKYKTTLDLANGFWAHPITPESYWLTAFTWQGKQYCWTRLPQGFLNSPALFNADV VDLLKEIPNVQVYVDDIYLSHDDPKEHVQQLEKVFQILLQAGYVVSLKKSEIGQKTVEFLGFNITKEGRGLTDTFKTKLLNITPPKDLKQLQSILGKLNFAR NFIPNFAELVQPLYNLIAPAKGKYIEWSEENTKQLNMVIEALNTASNLEERLPEQRLVIKVNTSPSAGYVRYYNETGKKPIMYLNYVFSKAELKFSMLEKL LTTMHKALIKAMDLAMGQEILVYSPIVSMTKIQKTPLPERKALPIRWITWMTYLEDPRIQFHYDKTLPELKHIPDVYTSSQSPVKHPSQYEGVFYTDGSAI KSPDPTKSNNAGMGIVHATYKPEYQVLNQWSIPLGNHTAQMAEIAAVEFACKKALKIPGPVLVITDSFYVAESANKELPYWKSNGFVNNKKKPLKHISK WKSIAECLSMKPDITIQHEKGISLQIPVFILKGNALADKLATQGSYVVN
FOAMV_P14350-Pro	8,024	VPWLTQQPLQLTILVPLQEYQEKILSKTALPEDQKQQLKTLFVKYDNLWQHWENQVGHRKIRPHNIATGDYPPRPQKQYPINPKAKPSIQIVIDDLLKQG VLTPQNSTMNTPVYPVPKPDGRWRMVLDYREVNKTIPLTAAQNQHSAGILATIVRQKYKTTLDLANGFWAHPITPESYWLTAFTWQGKQYCWTRLPQ GFLNSPALFTADVVDLLKEIPNVQVYVDDIYLSHDDPKEHVQQLEKVFQILLQAGYVVSLKKSEIGQKTVEFLGFNITKEGRGLTDTFKTKLLNITPPKDLK QLQSILGLLNFARNFIPNFAELVQPLYNLIASAKGKYIEWSEENTKQLNMVIEALNTASNLEERLPEQRLVIKVNTSPSAGYVRYYNETGKKPIMYLNYVF SKAELKFSMLEKLLTTMHKALIKAMDLAMGQEILVYSPIVSMTKIQKTPLPERKALPIRWITWMTYLEDPRIQFHYDKTLPELKHIPDVYTSSQSPVKHPS QYEGVFYTDGSAIKSPDPTKSNNAGMGIVHATYKPEYQVLNQWSIPLGNHTAQMAEIAAVEFACKKALKIPGPVLVITDSFYVAESANKELPYWKSNGF VNNKKKPLKHISKWKSIAECLSMKPDITIQHEKGISLQIPVFILKGNALADKLATQGSYVVN
FOAMV_P14350-Pro_2mut	8,025	VPWLTQQPLQLTILVPLQEYQEKILSKTALPEDQKQQLKTLFVKYDNLWQHWENQVGHRKIRPHNIATGDYPPRPQKQYPINPKAKPSIQIVIDDLLKQG VLTPQNSTMNTPVYPVPKPDGRWRMVLDYREVNKTIPLTAAQNQHSAGILATIVRQKYKTTLDLANGFWAHPITPESYWLTAFTWQGKQYCWTRLPQ GFLNSPALFNADVVDLLKEIPNVQVYVDDIYLSHDDPKEHVQQLEKVFQILLQAGYVVSLKKSEIGQKTVEFLGFNITKEGRGLTDTFKTKLLNITPPKDL KQLQSILGLLNFARNFIPNFAELVQPLYNLIAPAKGKYIEWSEENTKQLNMVIEALNTASNLEERLPEQRLVIKVNTSPSAGYVRYYNETGKKPIMYLNYV FSKAELKFSMLEKLLTTMHKALIKAMDLAMGQEILVYSPIVSMTKIQKTPLPERKALPIRWITWMTYLEDPRIQFHYDKTLPELKHIPDVYTSSQSPVKHP SQYEGVFYTDGSAIKSPDPTKSNNAGMGIVHATYKPEYQVLNQWSIPLGNHTAQMAEIAAVEFACKKALKIPGPVLVITDSFYVAESANKELPYWKSNG FVNNKKKPLKHISKWKSIAECLSMKPDITIQHEKGISLQIPVFILKGNALADKLATQGSYVVN
FOAMV_P14350-Pro_2mutA	8,026	VPWLTQQPLQLTILVPLQEYQEKILSKTALPEDQKQQLKTLFVKYDNLWQHWENQVGHRKIRPHNIATGDYPPRPQKQYPINPKAKPSIQIVIDDLLKQG VLTPQNSTMNTPVYPVPKPDGRWRMVLDYREVNKTIPLTAAQNQHSAGILATIVRQKYKTTLDLANGFWAHPITPESYWLTAFTWQGKQYCWTRLPQ GFLNSPALFNADVVDLLKEIPNVQVYVDDIYLSHDDPKEHVQQLEKVFQILLQAGYVVSLKKSEIGQKTVEFLGFNITKEGRGLTDTFKTKLLNITPPKDL KQLQSILGKLNFARNFIPNFAELVQPLYNLIAPAKGKYIEWSEENTKQLNMVIEALNTASNLEERLPEQRLVIKVNTSPSAGYVRYYNETGKKPIMYLNYV FSKAELKFSMLEKLLTTMHKALIKAMDLAMGQEILVYSPIVSMTKIQKTPLPERKALPIRWITWMTYLEDPRIQFHYDKTLPELKHIPDVYTSSQSPVKHP SQYEGVFYTDGSAIKSPDPTKSNNAGMGIVHATYKPEYQVLNQWSIPLGNHTAQMAEIAAVEFACKKALKIPGPVLVITDSFYVAESANKELPYWKSNG FVNNKKKPLKHISKWKSIAECLSMKPDITIQHEKGISLQIPVFILKGNALADKLATQGSYVVN
GALV_P21414	8,027	VLNLEEEYRLHEKPVPSSIDPSWLQLFPTVWAERAGMGLANQVPPVVVELRSGASPVAVRQYPMSKEAREGIRPHIQKFLDLGVLVPCRSPWNTPLL PVKKPGTNDYRPVQDLREINKRVQDIHPTVPNPYNLLSSLPPSYTWYSVLDLKDAFFCLRLHPNSQPLFAFEWKDPEKGNTGQLTWTRLPQGFKNSP TLFDEALHRDLAPFRALNPQVVLLQYVDDLLVAAPTYEDCKKGTQKLLQELSKLGYRVSAKKAQLCQREVTYLGYLLKEGKRWLTPARKATVMKIPVP TTPRQVREFLGTAGFCRLWIPGFASLAAPLYPLTKESIPFIWTEEHQQAFDHIKKALLSAPALALPDLTKPFTLYIDERAGVARGVLTQTLGPWRRPVAY LSKKLDPVASGWPTCLKAVAAVALLLKDADKLTLGQNVTVIASHSLESIVRQPPDRWMTNARMTHYQSLLLNERVSFAPPAVLNPATLLPVESEATPVH RCSEILAEETGTRRDLEDQPLPGVPTWYTDGSSFITEGKRRAGAPIVDGKRTVWASSLPEGTSAQKAELVALTQALRLAEGKNINIYTDSRYAFATAHIH GAIYKQRGLLTSAGKDIKNKEEILALLEAIHLPRRVAIIHCPGHQRGSNPVATGNRRADEAAKQAALSTRVLAGTTKP
GALV_P21414_3mut	8,028	VLNLEEEYRLHEKPVPSSIDPSWLQLFPTVWAERAGMGLANQVPPVVVELRSGASPVAVRQYPMSKEAREGIRPHIQKFLDLGVLVPCRSPWNTPLL PVKKPGTNDYRPVQDLREINKRVQDIHPTVPNPYNLLSSLPPSYTWYSVLDLKDAFFCLRLHPNSQPLFAFEWKDPEKGNTGQLTWTRLPQGFKNSP TLFNEALHRDLAPFRALNPQVVLLQYVDDLLVAAPTYEDCKKGTQKLLQELSKLGYRVSAKKAQLCQREVTYLGYLLKEGKRWLTPARKATVMKIPVP TTPRQVREFLGTAGFCRLWIPGFASLAAPLYPLTKPSIPFIWTEEHQQAFDHIKKALLSAPALALPDLTKPFTLYIDERAGVARGVLTQTLGPWRRPVAY LSKKLDPVASGWPTCLKAVAAVALLLKDADKLTLGQNVTVIASHSLESIVRQPPDRWMTNARMTHYQSLLLNERVSFAPPAVLNPATLLPVESEATPVH RCSEILAEETGTRRDLEDQPLPGVPTWYTDGSSFITEGKRRAGAPIVDGKRTVWASSLPEGTSAQKAELVALTQALRLAEGKNINIYTDSRYAFATAHIH GAIYKQRGWLTSAGKDIKNKEEILALLEAIHLPRRVAIIHCPGHQRGSNPVATGNRRADEAAKQAALSTRVLAGTTKP
GALV_P21414_3mutA	8,029	VLNLEEEYRLHEKPVPSSIDPSWLQLFPTVWAERAGMGLANQVPPVVVELRSGASPVAVRQYPMSKEAREGIRPHIQKFLDLGVLVPCRSPWNTPLL PVKKPGTNDYRPVQDLREINKRVQDIHPTVPNPYNLLSSLPPSYTWYSVLDLKDAFFCLRLHPNSQPLFAFEWKDPEKGNTGQLTWTRLPQGFKNSP TLFNEALHRDLAPFRALNPQVVLLQYVDDLLVAAPTYEDCKKGTQKLLQELSKLGYRVSAKKAQLCQREVTYLGYLLKEGKRWLTPARKATVMKIPVP TTPRQVREFLGKAGFCRLFIPGFASLAAPLYPLTKPSIPFIWTEEHQQAFDHIKKALLSAPALALPDLTKPFTLYIDERAGVARGVLTQTLGPWRRPVAYL SKKLDPVASGWPTCLKAVAAVALLLKDADKLTLGQNVTVIASHSLESIVRQPPDRWMTNARMTHYQSLLLNERVSFAPPAVLNPATLLPVESEATPVH RCSEILAEETGTRRDLEDQPLPGVPTWYTDGSSFITEGKRRAGAPIVDGKRTVWASSLPEGTSAQKAELVALTQALRLAEGKNINIYTDSRYAFATAHIH GAIYKQRGWLTSAGKDIKNKEEILALLEAIHLPRRVAIIHCPGHQRGSNPVATGNRRADEAAKQAALSTRVLAGTTKP
HTL1A_P03362	8,030	AVLGLEHLPRPPQISQFPLNPERLQALQHLVRKALEAGHIEPYTGPGNNPVFPVKKANGTWRFIHDLRATNSLTIDLSSSSPGPPDLSSLPTTLAHLQTI DLRDAFFQIPLPKQFQPYFAFTVPQQCNYGPGTRYAWKVLPQGFKNSPTLFEMQLAHILQPIRQAFPQCTILQYMDDILLASPSHEDLLLLSEATMASLI SHGLPVSENKTQQTPGTIKFLGQIISPNHLTYDAVPTVPIRSRWALPELQALLGEIQWVSKGTPTLRQPLHSLYCALQRHTDPRDQIYLNPSQVQSLVQL RQALSQNCRSRLVQTLPLLGAIMLTLTGTTTVVFQSKEQWPLVWLHAPLPHTSQCPWGQLLASAVLLLDKYTLQSYGLLCQTIHHNISTQTFNQFIQTS DHPSVPILLHHSHRFKNLGAQTGELWNTFLKTAAPLAPVKALMPVFTLSPVIINTAPCLFSDGSTSRAAYILWDKQILSQRSFPLPPPHKSAQRAELLGLL HGLSSARSWRCLNIFLDSKYLYHYLRTLALGTFQGRSSQAPFQALLPRLLSRKVVYLHHVRSHTNLPDPISRLNALTDALLITPVLQL

RT Name	SEQ ID NO:	RT amino acid sequence
HTL1A_P03362_2mut	8,031	AVLGLEHLPRPPQISQFPLNPERLQALQHLVRKALEAGHIEPYTGPGNNPVFPVKKANGTWRFIHDLRATNSLTIDLSSSSPGPPDLSSLPTTLAHLQTI DLRDAFFQIPLPKQFQPYFAFTVPQQCNYGPGTRYAWKVLPQGFKNSPTLFQMQLAHILQPIRQAFPQCTILQYMDDILLASPSHEDLLLLSEATMASLI SHGLPVSENKTQQTPGTIKFLGQIISPNHLTYDAVPTVPIRSRWALPELQALLGEIQWVSKGTPTLRQPLHSLYCALQPHTDPRDQIYLNPSQVQSLVQL RQALSQNCRSRLVQTLPLLGAIMLTLTGTTTVVFQSKEQWPLVWLHAPLPHTSQCPWGQLLASAVLLLDKYTLQSYGLLCQTIHHNISTQTFNQFIQTS DHPSVPILLHHSHRFKNLGAQTGELWNTFLKTAAPLAPVKALMPVFTLSPVIINTAPCLFSDGSTSRAAYILWDKQILSQRSFPLPPPHKSAQRAELLGLL HGLSSARSWRCLNIFLDSKYLYHYLRTLALGTFQGRSSQAPFQALLPRLLSRKVVYLHHVRSHTNLPDPISRLNALTDALLITPVLQL
HTL1A_P03362_2mutB	8,032	AVLGLEHLPRPPQISQFPLNPERLQALQHLVRKALEAGHIEPYTGPGNNPVFPVKKANGTWRFIHDLRATNSLTIDLSSSSPGPPDLSSPPTTLAHLQTI DLRDAFFQIPLPKQFQPYFAFTVPQQCNYGPGTRYAWKVLPQGFKNSPTLFQMQLAHILQPIRQAFPQCTILQYMDDILLASPSHEDLLLLSEATMASLI SHGLPVSENKTQQTPGTIKFLGQIISPNHLTYDAVPTVPIRSRWALPELQALLGEIQWVSKGTPTLRQPLHSLYCALQPHTDPRDQIYLNPSQVQSLVQL RQALSQNCRSRLVQTLPLLGAIMLTLTGTTTVVFQSKEQWPLVWLHAPLPHTSQCPWGQLLASAVLLLDKYTLQSYGLLCQTIHHNISTQTFNQFIQTS DHPSVPILLHHSHRFKNLGAQTGELWNTFLKTAAPLAPVKALMPVFTLSPVIINTAPCLFSDGSTSRAAYILWDKQILSQRSFPLPPPHKSAQRAELLGLL HGLSSARSWRCLNIFLDSKYLYHYLRTLALGTFQGRSSQAPFQALLPRLLSRKVVYLHHVRSHTNLPDPISRLNALTDALLITPVLQL
HTL1C_P14078	8,033	AVLGLEHLPRPPEISQFPLNPERLQALQHLVRKALEAGHIEPYTGPGNNPVFPVKKANGTWRFIHDLRATNSLTIDLSSSSPGPPDLSSLPTTLAHLQTI DLKDAFFQIPLPKQFQPYFAFTVPQQCNYGPGTRYAWRVLPQGFKNSPTLFEMQLAHILQPIRQAFPQCTILQYMDDILLASPSHADLQLLSEATMASLI SHGLPVSENKTQQTPGTIKFLGQIISPNHLTYDAVPKVPIRSRWALPELQALLGEIQWVSKGTPTLRQPLHSLYCALQRHTDPRDQIYLNPSQVQSLVQL RQALSQNCRSRLVQTLPLLGAIMLTLTGTTTVVFQSKQQWPLVWLHAPLPHTSQCPWGQLLASAVLLLDKYTLQSYGLLCQTIHHNISTQTFNQFIQTS DHPSVPILLHHSHRFKNLGAQTGELWNTFLKTTAPLAPVKALMPVFTLSPVIINTAPCLFSDGSTSQAAYILWDKHILSQRSFPLPPPHKSAQRAELLGLL HGLSSARSWRCLNIFLDSKYLYHYLRTLALGTFQGRSSQAPFQALLPRLLSRKVVYLHHVRSHTNLPDPISRLNALTDALLITPVLQL
HTL1C_P14078_2mut	8,034	AVLGLEHLPRPPEISQFPLNPERLQALQHLVRKALEAGHIEPYTGPGNNPVFPVKKANGTWRFIHDLRATNSLTIDLSSSSPGPPDLSSLPTTLAHLQTI DLKDAFFQIPLPKQFQPYFAFTVPQQCNYGPGTRYAWRVLPQGFKNSPTLFQMQLAHILQPIRQAFPQCTILQYMDDILLASPSHADLQLLSEATMASLI SHGLPVSENKTQQTPGTIKFLGQIISPNHLTYDAVPKVPIRSRWALPELQALLGEIQWVSKGTPTLRQPLHSLYCALQRHTDPRDQIYLNPSQVQSLVQL RQALSQNCRSRLVQTLPLLGAIMLTLTGTTTVVFQSKQQWPLVWLHAPLPHTSQCPWGQLLASAVLLLDKYTLQSYGLLCQTIHHNISTQTFNQFIQTS DHPSVPILLHHSHRFKNLGAQTGELWNTFLKTTAPLAPVKALMPVFTLSPVIINTAPCLFSDGSTSQAAYILWDKHILSQRSFPLPPPHKSAQRAELLGLL HGLSSARSWRCLNIFLDSKYLYHYLRTLALGTFQGRSSQAPFQALLPRLLSRKVVYLHHVRSHTNLPDPISRLNALTDALLITPVLQL
HTL1L_P0C211	8,035	GLEHLPRPPEISQFPLNPERLQALQHLVRKALEAGHIEPYTGPGNNPVFPVKKANGTWRFIHDLRATNSLTVDLSSSSPGPPDLSSLPTTLAHLQTIDLK DAFFQIPLPKQFQPYFAFTVPQQCNYGPGTRYAWKVLPQGFKNSPTLFEMQLASILQPIRQAFPQCVILQYMDDILLASPSPEDLQQLSEATMASLISH GLPVSQDKTQQTPGTIKFLGQIISPNHITYDAVPTVPIRSRWALPELQALLGEIQWVSKGTPTLRQPLHSLYCALQGHTDPRDQIYLNPSQVQSLMQLQ QALSQNCRSRLAQTLPLLGAIMLTLTGTTTVVFQSKQQWPLVWLHAPLPHTSQCPWGQLLASAVLLLDKYTLQSYGLLCQTIHHNISIQTFNQFIQTSD HPSVPILLHHSHRFKNLGAQTGELWNTFLKTAAPLAPVKALTPVFTLSPIIINTAPCLFSDGSTSQAAYILWDKHILSQRSFPLPPPHKSAQQAELLGLLH GLSSARSWHCLNIFLDSKYLYHYLRTLALGTFQGKSSQAPFQALLPRLLAHKVIYLHHVRSHTNLPDPISKLNALTDALLITPIL
HTL1L_P0C211_2mut	8,036	GLEHLPRPPEISQFPLNPERLQALQHLVRKALEAGHIEPYTGPGNNPVFPVKKANGTWRFIHDLRATNSLTVDLSSSSPGPPDLSSLPTTLAHLQTIDLK DAFFQIPLPKQFQPYFAFTVPQQCNYGPGTRYAWKVLPQGFKNSPTLFQMQLASILQPIRQAFPQCVILQYMDDILLASPSPEDLQQLSEATMASLISH GLPVSQDKTQQTPGTIKFLGQIISPNHITYDAVPTVPIRSRWALPELQALLGEIQWVSKGTPTLRQPLHSLYCALQGHTDPRDQIYLNPSQVQSLMQLQ QALSQNCRSRLAQTLPLLGAIMLTLTGTTTVVFQSKQQWPLVWLHAPLPHTSQCPWGQLLASAVLLLDKYTLQSYGLLCQTIHHNISIQTFNQFIQTSD HPSVPILLHHSHRFKNLGAQTGELWNTFLKTAAPLAPVKALTPVFTLSPIIINTAPCLFSDGSTSQAAYILWDKHILSQRSFPLPPPHKSAQQAELLGLLH GLSSARSWHCLNIFLDSKYLYHYLRTLAWGTFQGKSSQAPFQALLPRLLAHKVIYLHHVRSHTNLPDPISKLNALTDALLITPIL
HTL1L_P0C211_2mutB	8,037	GLEHLPRPPEISQFPLNPERLQALQHLVRKALEAGHIEPYTGPGNNPVFPVKKANGTWRFIHDLRATNSLTVDLSSSSPGPPDLSSPPTTLAHLQTIDLK DAFFQIPLPKQFQPYFAFTVPQQCNYGPGTRYAWKVLPQGFKNSPTLFQMQLASILQPIRQAFPQCVILQYMDDILLASPSPEDLQQLSEATMASLISH GLPVSQDKTQQTPGTIKFLGQIISPNHITYDAVPTVPIRSRWALPELQALLGEIQWVSKGTPTLRQPLHSLYCALQGHTDPRDQIYLNPSQVQSLMQLQ QALSQNCRSRLAQTLPLLGAIMLTLTGTTTVVFQSKQQWPLVWLHAPLPHTSQCPWGQLLASAVLLLDKYTLQSYGLLCQTIHHNISIQTFNQFIQTSD HPSVPILLHHSHRFKNLGAQTGELWNTFLKTAAPLAPVKALTPVFTLSPIIINTAPCLFSDGSTSQAAYILWDKHILSQRSFPLPPPHKSAQQAELLGLLH GLSSARSWHCLNIFLDSKYLYHYLRTLAWGTFQGKSSQAPFQALLPRLLAHKVIYLHHVRSHTNLPDPISKLNALTDALLITPIL
HTL32_Q0R5R2	8,038	GLEHLPPPPEVSQFPLNPERLQALTDLVSRALEAKHIEPYQGPGNNPIFPVKKPNGKWRFIHDLRATNSVTRDLASPSPGPPDLTSLPQGLPHLRTIDLT DAFFQIPLPTIFQPYFAFTLPQPNNYGPGTRYSWRVLPQGFKNSPTLFEQQLSHILTPVRKTFPNSLIIQYMDDILLASPAPGELAALTDKVTNALTKEGL PLSPEKTQATPGPIHFLGQVISQDCITYETLPSINVKSTWSLAELQSMLGELQWVSKGTPVLRSSLHQLYLALRGHRDPRDTIKLTSIQVQALRTIQKALT LNCRSRLVNQLPILALIMLRPTGTTAVLFQTKQKWPLVWLHTPHPATSLRPWGQLLANAVIILDKYSLQHYGQVCKSFHHNISNQALTYYLHTSDQSSV AILLQHSHRFHNLGAQPSGPWRSLLQMPQIFQNIDVLRPPFTISPVVINHAPCLFSDGSASKAAFIIWDRQVIHQQVLSLPSTCSAQAGELFGLLAGLQK SQPWVALNIFLDSKFLIGHLRRMALGAFPGPSTQCELHTQLLPLLQGKTVYVHHVRSHTLLQDPISRLNEATDALMLAPLLPL
HTL32_Q0R5R2_2mut	8,039	GLEHLPPPPEVSQFPLNPERLQALTDLVSRALEAKHIEPYQGPGNNPIFPVKKPNGKWRFIHDLRATNSVTRDLASPSPGPPDLTSLPQGLPHLRTIDLT DAFFQIPLPTIFQPYFAFTLPQPNNYGPGTRYSWRVLPQGFKNSPTLFQQQLSHILTPVRKTFPNSLIIQYMDDILLASPAPGELAALTDKVTNALTKEGL PLSPEKTQATPGPIHFLGQVISQDCITYETLPSINVKSTWSLAELQSMLGELQWVSKGTPVLRSSLHQLYLALRGHRDPRDTIKLTSIQVQALRTIQKALT LNCRSRLVNQLPILALIMLRPTGTTAVLFQTKQKWPLVWLHTPHPATSLRPWGQLLANAVIILDKYSLQHYGQVCKSFHHNISNQALTYYLHTSDQSSV AILLQHSHRFHNLGAQPSGPWRSLLQMPQIFQNIDVLRPPFTISPVVINHAPCLFSDGSASKAAFIIWDRQVIHQQVLSLPSTCSAQAGELFGLLAGLQK SQPWVALNIFLDSKFLIGHLRRMAWGAFPGPSTQCELHTQLLPLLQGKTVYVHHVRSHTLLQDPISRLNEATDALMLAPLLPL
HTL32_Q0R5R2_2mutB	8,040	GLEHLPPPPEVSQFPLNPERLQALTDLVSRALEAKHIEPYQGPGNNPIFPVKKPNGKWRFIHDLRATNSVTRDLASPSPGPPDLTSPPQGLPHLRTIDL TDAFFQIPLPTIFQPYFAFTLPQPNNYGPGTRYSWRVLPQGFKNSPTLFQQQLSHILTPVRKTFPNSLIIQYMDDILLASPAPGELAALTDKVTNALTKEG LPLSPEKTQATPGPIHFLGQVISQDCITYETLPSINVKSTWSLAELQSMLGELQWVSKGTPVLRSSLHQLYLALRGHRDPRDTIKLTSIQVQALRTIQKAL TLNCRSRLVNQLPILALIMLRPTGTTAVLFQTKQKWPLVWLHTPHPATSLRPWGQLLANAVIILDKYSLQHYGQVCKSFHHNISNQALTYYLHTSDQSS VAILLQHSHRFHNLGAQPSGPWRSLLQMPQIFQNIDVLRPPFTISPVVINHAPCLFSDGSASKAAFIIWDRQVIHQQVLSLPSTCSAQAGELFGLLAGLQ KSQPWVALNIFLDSKFLIGHLRRMAWGAFPGPSTQCELHTQLLPLLQGKTVYVHHVRSHTLLQDPISRLNEATDALMLAPLLPL
HTL3P_Q4U0X6	8,041	GLEHLPPPPEVSQFPLNPERLQALTDLVSRALEAKHIEPYQGPGNNPIFPVKKPNGKWRFIHDLRATNSLTRDLASPSPGPPDLTSLPQDLPHLRTIDLT DAFFQIPLPAVFQPYFAFTLPQPNNHGPGTRYSWRVLPQGFKNSPTLFEQQLSHILAPVRKAFPNSLIIQYMDDILLASPALRELTALTDKVTNALTKEGL PMSLEKTQATPGSIHFLGQVISPDCITYETLPSIHVKSIWSLAELQSMLGELQWVSKGTPVLRSSLHQLYLALRGHRDPRDTIELTSTQVQALKTIQKALA LNCRSRLVSQLPILALIILRPTGTTAVLFQTKQKWPLVWLHTPHPATSLRPWGQLLANAIITLDKYSLQHYGQICKSFHHNISNQALTYYLHTSDQSSVAIL LQHSHRFHNLGAQPSGPWRSLLQVPQIFQNIDVLRPPFIISPVVIDHAPCLFSDGATSKAAFILWDKQVIHQQVLPLPSTCSAQAGELFGLLAGLQKSKP WPALNIFLDSKFLIGHLRRMALGAFLGPSTQCDLHARLFPLLQGKTVYVHHVRSHTLLQDPISRLNEATDALMLAPLLPL

RT Name	SEQ ID NO:	RT amino acid sequence
HTL3P_Q4U0X6_2mut	8,042	GLEHLPPPPEVSQFPLNPERLQALTDLVSRALEAKHIEPYQGPGNNPIFPVKKPNGKWRFIHDLRATNSLTRDLASPSPGPPDLTSLPQDLPHLRTIDLT DAFFQIPLPAVFQPYFAFTLPQPNNHGPGTRYSWRVLPQGFKNSPTLFQQQLSHILAPVRKAFPNSLIIQYMDDILLASPALRELTALTDKVTNALTKEG LPMSLEKTQATPGSIHFLGQVISPDCITYETLPSIHVKSIWSLAELQSMLGELQWVSKGTPVLRSSLHQLYLALRGHRDPRDTIELTSTQVQALKTIQKAL ALNCRSRLVSQLPILALIILRPTGTTAVLFQTKQKWPLVWLHTPHPATSLRPWGQLLANAIITLDKYSLQHYGQICKSFHHNISNQALTYYLHTSDQSSVAI LLQHSHRFHNLGAQPSGPWRSLLQVPQIFQNIDVLRPPFIISPVVIDHAPCLFSDGATSKAAFILWDKQVIHQQVLPLPSTCSAQAGELFGLLAGLQKSK PWPALNIFLDSKFLIGHLRRMAWGAFLGPSTQCDLHARLFPLLQGKTVYVHHVRSHTLLQDPISRLNEATDALMLAPLLPL
HTL3P_Q4U0X6_2mutB	8,043	GLEHLPPPPEVSQFPLNPERLQALTDLVSRALEAKHIEPYQGPGNNPIFPVKKPNGKWRFIHDLRATNSLTRDLASPSPGPPDLTSPPQDLPHLRTIDLT DAFFQIPLPAVFQPYFAFTLPQPNNHGPGTRYSWRVLPQGFKNSPTLFQQQLSHILAPVRKAFPNSLIIQYMDDILLASPALRELTALTDKVTNALTKEG LPMSLEKTQATPGSIHFLGQVISPDCITYETLPSIHVKSIWSLAELQSMLGELQWVSKGTPVLRSSLHQLYLALRGHRDPRDTIELTSTQVQALKTIQKAL ALNCRSRLVSQLPILALIILRPTGTTAVLFQTKQKWPLVWLHTPHPATSLRPWGQLLANAIITLDKYSLQHYGQICKSFHHNISNQALTYYLHTSDQSSVAI LLQHSHRFHNLGAQPSGPWRSLLQVPQIFQNIDVLRPPFIISPVVIDHAPCLFSDGATSKAAFILWDKQVIHQQVLPLPSTCSAQAGELFGLLAGLQKSK PWPALNIFLDSKFLIGHLRRMAWGAFLGPSTQCDLHARLFPLLQGKTVYVHHVRSHTLLQDPISRLNEATDALMLAPLLPL
HTLV2_P03363_2mut	8,044	HLPPPPQVDQFPLNLPERLQALNDLVSKALEAGHIEPYSGPGNNPVFPVKKPNGKWRFIHDLRATNAITTTLTSPSPGPPDLTSLPTALPHLQTIDLTDA FFQIPLPKQYQPYFAFTIPQPCNYGPGTRYAWTVLPQGFKNSPTLFQQQLAAVLNPMRKMFPTSTIVQYMDDILLASPTNEELQQLSQLTLQALTTHGL PISQEKTQQTPGQIRFLGQVISPNHITYESTPTIPIKSQWTLTELQVILGEIQWVSKGTPILRKHLQSLYSALHPYRDPRACITLTPQQLHALHAIQQALQH NCRGRLNPALPLLGLISLSTSGTTSVIFQPKQNWPLAWLHTPHPPTSLCPWGHLLACTILTLDKYTLQHYGQLCQSFHHNMSKQALCDFLRNSPHPSV GILIHHMGRFHNLGSQPSGPWKTLLHLPTLLQEPRLLRPIFTLSPVVLDTAPCLFSDGSPQKAAYVLWDQTILQQDITPLPSHETHSAQKGELLALICGLR AAKPWPSLNIFLDSKYLIKYLHSLAIGAFLGTSAHQTLQAALPPLLQGKTIYLHHVRSHTNLPDPISTFNEYTDSLILAPLVPL
JSRV_P31623	8,045	PLGTSDSPVTHADPIDWKSEEPVWVDQWPLTQEKLSAAQQLVQEQLRLGHIEPSTSAWNSPIFVIKKKSGKWRLLQDLRKVNETMMHMGALQPGLPT PSAIPDKSYIIVIDLKDCFYTIPLAPQDCKRFAFSLPSVNFKEPMQRYQWRVLPQGMTNSPTLCQKFVATAIAPVRQRFPQLYLVHYMDDILLAHTDEHLL YQAFSILKQHLSLNGLVIADEKIQTHFPYNYLGFSLYPRVYNTQLVKLQTDHLKTLNDFQKLLGDINWIRPYLKLPTYTLQPLFDILKGDSDPASPRTLSLE GRTALQSIEEAIRQQQITYCDYQRSWGLYILPTPRAPTGVLYQDKPLRWIYLSATPTKHLLPYYELVAKIIAKGRHEAIQYFGMEPPFICVPYALEQQDWL FQFSDNWSIAFANYPGQITHHYPSDKLLQFASSHAFIFPKIVRRQPIPEATLIFTDGSSNGTAALIINHQTYYAQTSFSSAQVVELFAVHQALLTVPTSFNL FTDSSYVVGALQMIETVPIIGTTSPEVLNLFTLIQQVLHCRQHPCFFGHIRAHSTLPGALVQGNHTADVLTKQVFFQS
JSRV_P31623_2mutB	8,046	PLGTSDSPVTHADPIDWKSEEPVWVDQWPLTQEKLSAAQQLVQEQLRLGHIEPSTSAWNSPIFVIKKKSGKWRLLQDLRKVNETMMHMGALQPGLPT PSPIPDKSYIIVIDLKDCFYTIPLAPQDCKRFAFSLPSVNFKEPMQRYQWRVLPQGMTNSPTLCQKFVATAIAPVRQRFPQLYLVHYMDDILLAHTDEHLL YQAFSILKQHLSLNGLVIADEKIQTHFPYNYLGFSLYPRVYNTQLVKLQTDHLKTLNDFQKLLGDINWIRPYLKLPTYTLQPLFDILKGDSDPASPRTLSLE GRTALQSIEEAIRQQQITYCDYQRSWGLYILPTPRAPTGVLYQDKPLRWIYLSATPTKHLLPYYELVAKIIAKGRHEAIQYFGMEPPFICVPYALEQQDWL FQFSDNWSIAFANYPGQITHHYPSDKLLQFASSHAFIFPKIVRRQPIPEATLIFTDGSSNGTAALIINHQTYYAQTSFSSAQVVELFAVHQALLTVPTSFNL FTDSSYVVGALQMIETVPIIGTTSPEVLNLFTLIQQVLHCRQHPCFFGHIRAHSTLPGALVQGNHTADVLTKQVFFQS
KORV_Q9TTC1	8,047	TLGDQGSRGSDPLPEPRVTLTVEGIPTEFLVNTGAEHSVLTKPMGKMGSKRTVVAGATGSKVYPWTTKRLLKIGQKQVTHSFLVIPECPAPLLGRDLLT KLKAQIQFSTEGPQVTWEDRPAMCLVLNLEEEYRLHEKPVPPSIDPSWLQLFPMVWAEKAGMGLANQVPPVVVELKSDASPVAVRQYPMSKEAREGI RPHIQRFLDLGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVQDIHPTVPNPYNLLSSLPPSHTWYSVLDLKDAFFCLKLHPNSQPLFAFEW RDPEKGNTGQLTWTRLPQGFKNSPTLFDEALHRDLASFRALNPQVVMLQYVDDLLVAAPTYRDCKEGTRRLLQELSKLGYRVSAKKAQLCREEVTYL GYLLKGGKRWLTPARKATVMKIPTPTTPRQVREFLGTAGFCRLWIPGFASLAAPLYPLTREKVPFTWTEAHQEAFGRIKEALLSAPALALPDLTKPFAL YVDEKEGVARGVLTQTLGPWRRPVAYLSKKLDPVASGWPTCLKAIAAVALLLKDADKLTLGQNVLVIAPHNLESIVRQPPDRWMTNARMTHYQSLLLN ERVSFAPPAILNPATLLPVESDDTPIHICSEILAEETGTRPDLRDQPLPGVPAWYTDGSSFIMDGRRQAGAAIVDNKRTVWASNLPEGTSAQKAELIALT QALRLAEGKSINIYTDSRYAFATAHVHGAIYKQRGLLTSAGKDIKNKEEILALLEAIHLPKRVAIIHCPGHQRGTDPVATGNRKADEAAKQAAQSTRILTET TKN
KORV_Q9TTC1_3mut	8,048	TLGDQGSRGSDPLPEPRVTLTVEGIPTEFLVNTGAEHSVLTKPMGKMGSKRTVVAGATGSKVYPWTTKRLLKIGQKQVTHSFLVIPECPAPLLGRDLLT KLKAQIQFSTEGPQVTWEDRPAMCLVLNLEEEYRLHEKPVPPSIDPSWLQLFPMVWAEKAGMGLANQVPPVVVELKSDASPVAVRQYPMSKEAREGI RPHIQRFLDLGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVQDIHPTVPNPYNLLSSLPPSHTWYSVLDLKDAFFCLKLHPNSQPLFAFEW RDPEKGNTGQLTWTRLPQGFKNSPTLFNEALHRDLASFRALNPQVVMLQYVDDLLVAAPTYRDCKEGTRRLLQELSKLGYRVSAKKAQLCREEVTYL GYLLKGGKRWLTPARKATVMKIPTPTTPRQVREFLGTAGFCRLWIPGFASLAAPLYPLTRPKVPFTWTEAHQEAFGRIKEALLSAPALALPDLTKPFAL YVDEKEGVARGVLTQTLGPWRRPVAYLSKKLDPVASGWPTCLKAIAAVALLLKDADKLTLGQNVLVIAPHNLESIVRQPPDRWMTNARMTHYQSLLLN ERVSFAPPAILNPATLLPVESDDTPIHICSEILAEETGTRPDLRDQPLPGVPAWYTDGSSFIMDGRRQAGAAIVDNKRTVWASNLPEGTSAQKAELIALT QALRLAEGKSINIYTDSRYAFATAHVHGAIYKQRGWLTSAGKDIKNKEEILALLEAIHLPKRVAIIHCPGHQRGTDPVATGNRKADEAAKQAAQSTRILTE TTKN
KORV_Q9TTC1_3mutA	8,049	TLGDQGSRGSDPLPEPRVTLTVEGIPTEFLVNTGAEHSVLTKPMGKMGSKRTVVAGATGSKVYPWTTKRLLKIGQKQVTHSFLVIPECPAPLLGRDLLT KLKAQIQFSTEGPQVTWEDRPAMCLVLNLEEEYRLHEKPVPPSIDPSWLQLFPMVWAEKAGMGLANQVPPVVVELKSDASPVAVRQYPMSKEAREGI RPHIQRFLDLGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVQDIHPTVPNPYNLLSSLPPSHTWYSVLDLKDAFFCLKLHPNSQPLFAFEW RDPEKGNTGQLTWTRLPQGFKNSPTLFNEALHRDLASFRALNPQVVMLQYVDDLLVAAPTYRDCKEGTRRLLQELSKLGYRVSAKKAQLCREEVTYL GYLLKGGKRWLTPARKATVMKIPTPTTPRQVREFLGKAGFCRLFIPGFASLAAPLYPLTRPKVPFTWTEAHQEAFGRIKEALLSAPALALPDLTKPFALY VDEKEGVARGVLTQTLGPWRRPVAYLSKKLDPVASGWPTCLKAIAAVALLLKDADKLTLGQNVLVIAPHNLESIVRQPPDRWMTNARMTHYQSLLLNE RVSFAPPAILNPATLLPVESDDTPIHICSEILAEETGTRPDLRDQPLPGVPAWYTDGSSFIMDGRRQAGAAIVDNKRTVWASNLPEGTSAQKAELIALTQ ALRLAEGKSINIYTDSRYAFATAHVHGAIYKQRGWLTSAGKDIKNKEEILALLEAIHLPKRVAIIHCPGHQRGTDPVATGNRKADEAAKQAAQSTRILTET TKN
KORV_Q9TTC1-Pro	8,050	LLGRDLLTKLKAQIQFSTEGPQVTWEDRPAMCLVLNLEEEYRLHEKPVPPSIDPSWLQLFPMVWAEKAGMGLANQVPPVVVELKSDASPVAVRQYPM SKEAREGIRPHIQRFLDLGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVQDIHPTVPNPYNLLSSLPPSHTWYSVLDLKDAFFCLKLHPNSQ PLFAFEWRDPEKGNTGQLTWTRLPQGFKNSPTLFDEALHRDLASFRALNPQVVMLQYVDDLLVAAPTYRDCKEGTRRLLQELSKLGYRVSAKKAQLC REEVTYLGYLLKGGKRWLTPARKATVMKIPTPTTPRQVREFLGTAGFCRLWIPGFASLAAPLYPLTREKVPFTWTEAHQEAFGRIKEALLSAPALALPD LTKPFALYVDEKEGVARGVLTQTLGPWRRPVAYLSKKLDPVASGWPTCLKAIAAVALLLKDADKLTLGQNVLVIAPHNLESIVRQPPDRWMTNARMTH YQSLLLNERVSFAPPAILNPATLLPVESDDTPIHICSEILAEETGTRPDLRDQPLPGVPAWYTDGSSFIMDGRRQAGAAIVDNKRTVWASNLPEGTSAQ KAELIALTQALRLAEGKSINIYTDSRYAFATAHVHGAIYKQRGLLTSAGKDIKNKEEILALLEAIHLPKRVAIIHCPGHQRGTDPVATGNRKADEAAKQAAQ STRILTETTKN
KORV_Q9TTC	8,051	LLGRDLLTKLKAQIQFSTEGPQVTWEDRPAMCLVLNLEEEYRLHEKPVPPSIDPSWLQLFPMVWAEKAGMGLANQVPPVVVELKSDASPVAVRQYPM SKEAREGIRPHIQRFLDLGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVQDIHPTVPNPYNLLSSLPPSHTWYSVLDLKDAFFCLKLHPNSQ

RT Name	SEQ ID NO:	RT amino acid sequence
1-Pro_3mut		PLFAFEWRDPEKGNTGQLTWTRLPQGFKNSPTLFNEALHRDLASFRALNPQVVMLQYVDDLLVAAPTYRDCKEGTRRLLQELSKLGYRVSAKKAQLC REEVTYLGYLLKGGKRWLTPARKATVMKIPTPTTPRQVREFLGTAGFCRLWIPGFASLAAPLYPLTRPKVPFTWTEAHQEAFGRIKEALLSAPALALPD LTKPFALYVDEKEGVARGVLTQTLGPWRRPVAYLSKKLDPVASGWPTCLKAIAAVALLLKDADKLTLGQNVLVIAPHNLESIVRQPPDRWMTNARMTH YQSLLLNERVSFAPPAILNPATLLPVESDDTPIHICSEILAEETGTRPDLRDQPLPGVPAWYTDGSSFIMDGRRQAGAAIVDNKRTVWASNLPEGTSAQ KAELIALTQALRLAEGKSINIYTDSRYAFATAHVHGAIYKQRGWLTSAGKDIKNKEEILALLEAIHLPKRVAIIHCPGHQRGTDPVATGNRKADEAAKQAA QSTRILTETTKN
KORV_Q9TTC1-Pro_3mutA	8,052	LLGRDLLTKLKAQIQFSTEGPQVTWEDRPAMCLVLNLEEEYRLHEKPVPPSIDPSWLQLFPMVWAEKAGMGLANQVPPVVVELKSDASPVAVRQYPM SKEAREGIRPHIQRFLDLGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVQDIHPTVPNPYNLLSSLPPSHTWYSVLDLKDAFFCLKLHPNSQ PLFAFEWRDPEKGNTGQLTWTRLPQGFKNSPTLFNEALHRDLASFRALNPQVVMLQYVDDLLVAAPTYRDCKEGTRRLLQELSKLGYRVSAKKAQLC REEVTYLGYLLKGGKRWLTPARKATVMKIPTPTTPRQVREFLGKAGFCRLFIPGFASLAAPLYPLTRPKVPFTWTEAHQEAFGRIKEALLSAPALALPDL TKPFALYVDEKEGVARGVLTQTLGPWRRPVAYLSKKLDPVASGWPTCLKAIAAVALLLKDADKLTLGQNVLVIAPHNLESIVRQPPDRWMTNARMTHY QSLLLNERVSFAPPAILNPATLLPVESDDTPIHICSEILAEETGTRPDLRDQPLPGVPAWYTDGSSFIMDGRRQAGAAIVDNKRTVWASNLPEGTSAQK AELIALTQALRLAEGKSINIYTDSRYAFATAHVHGAIYKQRGWLTSAGKDIKNKEEILALLEAIHLPKRVAIIHCPGHQRGTDPVATGNRKADEAAKQAAQ STRILTETTKN
MLVAV_P03356	8,053	TLNLEDEYRLYETSAEPEVSPGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEAKLGIKPHIQRLLDQGILVPCQSPWNTPLL PVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHRWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGMGISGQLTWTRLPQGFKNSP TLFDEALHRDLADFRIQHPDLILLQYVDDILLAATSELDCQQGTRALLLTLGNLGYRASAKKAQLCQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPK TPRQLREFLGTAGFCRLWIPGFAEMAAPLYPLTKTGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVA YLSKKLDPVAAGWPPCLRMVAAIAVLRKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEEG APHDCLEILAETHGTRPDLTDQPIPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKRLNVYTDSRYAF ATAHIHGEIYRRRGLLTSEGREIKNKSEILALLKALFLPKRLSIIHCLGHQKGDSAEARGNRLADQAAREAAIKTPPDTSTLL
MLVAV_P03356_3mut	8,054	TLNLEDEYRLYETSAEPEVSPGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEAKLGIKPHIQRLLDQGILVPCQSPWNTPLL PVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHRWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGMGISGQLTWTRLPQGFKNSP TLFNEALHRDLADFRIQHPDLILLQYVDDILLAATSELDCQQGTRALLLTLGNLGYRASAKKAQLCQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPK TPRQLREFLGTAGFCRLWIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPV AYLSKKLDPVAAGWPPCLRMVAAIAVLRKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEE GAPHDCLEILAETHGTRPDLTDQPIPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKRLNVYTDSRYA FATAHIHGEIYRRRGWLTSEGREIKNKSEILALLKALFLPKRLSIIHCLGHQKGDSAEARGNRLADQAAREAAIKTPPDTSTLL
MLVAV_P03356_3mutA	8,055	TLNLEDEYRLYETSAEPEVSPGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEAKLGIKPHIQRLLDQGILVPCQSPWNTPLL PVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHRWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGMGISGQLTWTRLPQGFKNSP TLFNEALHRDLADFRIQHPDLILLQYVDDILLAATSELDCQQGTRALLLTLGNLGYRASAKKAQLCQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPK TPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFSWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVA YLSKKLDPVAAGWPPCLRMVAAIAVLRKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEEG APHDCLEILAETHGTRPDLTDQPIPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKRLNVYTDSRYAF ATAHIHGEIYRRRGWLTSEGREIKNKSEILALLKALFLPKRLSIIHCLGHQKGDSAEARGNRLADQAAREAAIKTPPDTSTLL
MLVBM_Q7SVK7	8,056	TLGIEDEYRLHETSTEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIQQYPMSHEARLGIKPHIQRLLDQGILVPCQSPWNTPLLP VKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGMGISGQLTWTRLPQGFKNSPT LFDEALHRDLADFRIQHPDLILLQYVDDILLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLREGQRWLTEARKETVMGQPVPKT PRQLREFLGTAGFCRLWIPGFAEMAAPLYPLTKTGTLFSWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAY LSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEEGAP HDCLEILAETHGTRPDLTDQPIPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVIWAGALPAGTSAQRAELIALTQALKMAEGKRLNVYTDSRYAFAT AHIHGEIYRRRGLLTSEGREIKNKSEILALLKALFLPKRLSIIHCLGHQKGDSAEARGNRLADQAAREAAIKTPPDTSTLL
MLVBM_Q7SVK7	8,057	TLGIEDEYRLHETSTEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIQQYPMSHEARLGIKPHIQRLLDQGILVPCQSPWNTPLLP VKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGMGISGQLTWTRLPQGFKNSPT LFDEALHRDLADFRIQHPDLILLQYVDDILLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLREGQRWLTEARKETVMGQPVPKT PRQLREFLGTAGFCRLWIPGFAEMAAPLYPLTKTGTLFSWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAY LSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEEGAP HDCLEILAETHGTRPDLTDQPIPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVIWAGALPAGTSAQRAELIALTQALKMAEGKRLNVYTDSRYAFAT AHIHGEIYRRRGLLTSEGREIKNKSEILALLKALFLPKRLSIIHCLGHQKGDSAEARGNRLADQAAREAAIKTPPDTSTLL
MLVBM_Q7SVK7_3mut	8,058	TLGIEDEYRLHETSTEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIQQYPMSHEARLGIKPHIQRLLDQGILVPCQSPWNTPLLP VKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGMGISGQLTWTRLPQGFKNSPT LFNEALHRDLADFRIQHPDLILLQYVDDILLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLREGQRWLTEARKETVMGQPVPKT PRQLREFLGTAGFCRLWIPGFAEMAAPLYPLTKPGTLFSWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVA YLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEEGA PHDCLEILAETHGTRPDLTDQPIPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVIWAGALPAGTSAQRAELIALTQALKMAEGKRLNVYTDSRYAFA TAHIHGEIYRRRGWLTSEGREIKNKSEILALLKALFLPKRLSIIHCLGHQKGDSAEARGNRLADQAAREAAIKTPPDTSTLL
MLVBM_Q7SVK7_3mut	8,059	TLGIEDEYRLHETSTEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIQQYPMSHEARLGIKPHIQRLLDQGILVPCQSPWNTPLLP VKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGMGISGQLTWTRLPQGFKNSPT LFNEALHRDLADFRIQHPDLILLQYVDDILLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLREGQRWLTEARKETVMGQPVPKT PRQLREFLGTAGFCRLWIPGFAEMAAPLYPLTKPGTLFSWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVA YLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEEGA PHDCLEILAETHGTRPDLTDQPIPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVIWAGALPAGTSAQRAELIALTQALKMAEGKRLNVYTDSRYAFA TAHIHGEIYRRRGWLTSEGREIKNKSEILALLKALFLPKRLSIIHCLGHQKGDSAEARGNRLADQAAREAAIKTPPDTSTLL
MLVBM_Q7SVK7_3	8,060	LGIEDEYRLHETSTEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIQQYPMSHEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPV KKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGMGISGQLTWTRLPQGFKNSPTL FNEALHRDLADFRIQHPDLILLQYVDDILLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLREGQRWLTEARKETVMGQPVPKTP RQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFSWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYL

RT Name	SEQ ID NO:	RT amino acid sequence
mutA_WS		SKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEEGAP HDCLEILAETHGTRPDLTDQPIPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVIWAGALPAGTSAQRAELIALTQALKMAEGKRLNVYTDSRYAFAT AHIHGEIYRRRGWLTSEGREIKNKSEILALLKALFLPKRLSIIHCLGHQKGDSAEARGNRLADQAAREAAIKTPPDTSTLLI
MLVBM_Q7SVK7_3mutA_WS	8,061	LGIEDEYRLHETSTEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIQQYPMSHEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPV KKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGMGISGQLTWTRLPQGFKNSPTL FNEALHRDLADFRIQHPDLILLQYVDDILLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLREGQRWLTEARKETVMGQPVPKTP RQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFSWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYL SKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEEGAP HDCLEILAETHGTRPDLTDQPIPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVIWAGALPAGTSAQRAELIALTQALKMAEGKRLNVYTDSRYAFAT AHIHGEIYRRRGWLTSEGREIKNKSEILALLKALFLPKRLSIIHCLGHQKGDSAEARGNRLADQAAREAAIKTPPDTSTLLI
MLVCB_P08361	8,062	TLNIEDEYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLP VKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPT LFDEALHRDLAGFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPIPKT PRQLREFLGTAGFCRLWIPGFAEMAAPLYPLTKTGTLFNWGPDQQKAFQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAY LSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQ HDCLDILAEAHGTRSDLMDQPLPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFAT AHIHGEIYRRRGLLTSEGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGNSAEARGNRMADQAAREVATRETPETSTLL
MLVCB_P08361_3mut	8,063	TLNIEDEYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLP VKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPT LFNEALHRDLAGFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPIPKT PRQLREFLGTAGFCRLWIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAFQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVA YLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGL QHDCLDILAEAHGTRSDLMDQPLPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAF ATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGNSAEARGNRMADQAAREVATRETPETSTLL
MLVCB_P08361_3mutA	8,064	TLNIEDEYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLP VKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPT LFNEALHRDLAGFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPIPKT PRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAFQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAY LSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQ HDCLDILAEAHGTRSDLMDQPLPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFAT AHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGNSAEARGNRMADQAAREVATRETPETSTLL
MLVF5_P26810	8,065	TLNIEDEYRLHETSKGPDVPLGSTWLSDFPQAWAETGGMGLAFRQAPLIISLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLP VKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQSLFAFEWKDPEMGISGQLTWTRLPQGFKNSPT LFDEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKT PRQLREFLGTAGLCRLWIPGFAEMAAPLYPLTKTGTLFKWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAY LSKKLDPVAAGWPPCLRMVAAIAVLTKDVGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPIVALNPATLLPLPEEGLQ HDCLDILAEAHGTRPDLTDQPLPDADHTWYTDGSSFLQEGQRRAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAAGKKLNVYTDSRYAFAT AHIHGEIYRRRGLLTSEGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGNHAEARGNRMADQAAREVATRETPETSTLL
MLVF5_P26810_3mut	8,066	TLNIEDEYRLHETSKGPDVPLGSTWLSDFPQAWAETGGMGLAFRQAPLIISLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLP VKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQSLFAFEWKDPEMGISGQLTWTRLPQGFKNSPT LFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKT PRQLREFLGTAGLCRLWIPGFAEMAAPLYPLTKTGTLFKWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAY LSKKLDPVAAGWPPCLRMVAAIAVLTKDVGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPIVALNPATLLPLPEEGLQ HDCLDILAEAHGTRPDLTDQPLPDADHTWYTDGSSFLQEGQRRAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAAGKKLNVYTDSRYAFAT AHIHGEIYRRRGLLTSEGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGNHAEARGNRMADQAAREVATRETPETSTLL
MLVFF_P26809_3mut	8,068	TLNIEDEYRLHETSKGPDVPLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLP VKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQSLFAFEWRDPEMGISGQLTWTRLPQGFKNSPT LFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKT PRQLREFLGTAGFCRLWIPGFAEMAAPLYPLTKPGTLFEWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVA YLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPIVALNPATLLPLPEEGLQ HDCLDILAEAHGTRPDLTDQPLPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVVWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFA TAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGNRAEARGNRMADQAAREVATRETPETSTLL
MLVFF_P26809_3mutA	8,069	TLNIEDEYRLHETSKGPDVPLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLP VKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQSLFAFEWRDPEMGISGQLTWTRLPQGFKNSPT LFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKT PRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFEWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAY LSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPIVALNPATLLPLPEEGLQ HDCLDILAEAHGTRPDLTDQPLPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVVWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFA TAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGNRAEARGNRMADQAAREVATRETPETSTLL

RT Name	SEQ ID NO:	RT amino acid sequence
MLVM S_P03 355	8,070	TLNIEDEHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLP VKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPT LFDEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKT PRQLREFLGTAGFCRLWIPGFAEMAAPLYPLTKTGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVA YLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGL QHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFA TAHIHGEIYRRRGLLTSEGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLL
MLVM S_refer ence	8,137	TLNIEDEYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLP VKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPT LFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKT PRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAY LSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQ HNCLDILAEAHGTRPDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFAT AHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSP
MLVM S_P03 355	8,071	TLNIEDEHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLP VKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPT LFDEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKT PRQLREFLGTAGFCRLWIPGFAEMAAPLYPLTKTGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVA YLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGL QHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFA TAHIHGEIYRRRGLLTSEGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLL
MLVM S_P03 355_3 mut	8,072	TLNIEDEHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLP VKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPT LFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKT PRQLREFLGTAGFCRLWIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVA YLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGL QHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFA TAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLL
MLVM S_P03 355_3 mut	8,073	TLNIEDEHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLP VKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPT LFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKT PRQLREFLGTAGFCRLWIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVA YLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGL QHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFA TAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLL
MLVM S_P03 355_3 mutA_ WS	8,074	TLNIEDEHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLP VKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPT LFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKT PRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAY LSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQ HNCLDILAEAHGTRPDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFAT AHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLL
MLVM S_P03 355_3 mutA_ WS	8,075	TLNIEDEHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLP VKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPT LFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKT PRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAY LSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQ HNCLDILAEAHGTRPDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFAT AHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLL
MLVM S_P03 355_PL V919	8,076	TLNIEDEYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLP VKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPT LFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKT PRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAY LSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQ HNCLDILAEAHGTRPDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFAT AHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSPSGGSKRTADGSEF E
MLVM S_P03 355_PL V919	8,077	TLNIEDEYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLP VKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPT LFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKT PRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAY LSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQ HNCLDILAEAHGTRPDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFAT AHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSPSGGSKRTADGSEF E

RT Name	SEQ ID NO:	RT amino acid sequence
MLVRD_P11227	8,078	TLNIEDEYRLHEISTEPDVSPGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEAKLGIKPHIQRLLDQGILVPCQSPWNTPLLP VKKPGTNDYRPVQGLREVNKRVEDIHPTVPNPYNLLSGLPTSHRWYTVLDLKDAFFCLRLHPTSQPLFASEWRDPGMGISGQLTWTRLPQGFKNSPT LFDEALHRGLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLKTLGNLGYRASAKKAQICQKQVKYLGYLLREGQRWLTEARKETVMGQPTPKT PRQLREFLGTAGFCRLWIPRFAEMAAPLYPLTKTGTLFNWGPDQQKAYHEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAY LSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEEGAP HDCLEILAETHGTEPDLTDQPIPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKRLNVYTDSRYAFATA HIHGEIYKRRGLLTSEGREIKNKSEILALLKALFLPKRLSIIHCLGHQKGDSAEARGNRLADQAAREAAIKTPPDTSTLL
MLVRD_P11227_3mut	8,079	TLNIEDEYRLHEISTEPDVSPGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEAKLGIKPHIQRLLDQGILVPCQSPWNTPLLP VKKPGTNDYRPVQGLREVNKRVEDIHPTVPNPYNLLSGLPTSHRWYTVLDLKDAFFCLRLHPTSQPLFASEWRDPGMGISGQLTWTRLPQGFKNSPT LFNEALHRGLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLKTLGNLGYRASAKKAQICQKQVKYLGYLLREGQRWLTEARKETVMGQPTPKT PRQLREFLGTAGFCRLWIPRFAEMAAPLYPLTKPGTLFNWGPDQQKAYHEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAY LSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEEGAP HDCLEILAETHGTEPDLTDQPIPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKRLNVYTDSRYAFATA HIHGEIYKRRGWLTSEGREIKNKSEILALLKALFLPKRLSIIHCLGHQKGDSAEARGNRLADQAAREAAIKTPPDTSTLL
MMTVB_P03365	8,080	WVQEISDSRPMLHIYLNGRRFLGLLNTGADKTCIAGRDWPANWPIHQTESSLQGLGMACGVARSSQPLRWQHEDKSGIIHPFVIPTLPFTLWGRDIMK DIKVRLMTDSPDDSQDLMIGAIESNLFADQISWKSDQPVWLNQWPLKQEKLQALQQLVTEQLQLGHLEESNSPWNTPVFVIKKKSGKWRLLQDLRAV NATMHDMGALQPGLPSPVAVPKGWEIIIIDLQDCFFNIKLHPEDCKRFAFSVPSPNFKRPYQRFQWKVLPQGMKNSPTLCQKFVDKAILTVRDKYQDS YIVHYMDDILLAHPSRSIVDEILTSMIQALNKHGLVVSTEKIQKYDNLKYLGTHIQGDSVSYQKLQIRTDKLRTLNDFQKLLGNINWIRPFLKLTTGELKPLF EILNGDSNPISTRKLTPEACKALQLMNERLSTARVKRLDLSQPWSLCILKTEYTPTACLWQDGVVEWIHLPHISPKVITPYDIFCTQLIIKGRHRSKELFSK DPDYIVVPYTKVQFDLLLQEKEDWPISLLGFLGEVHFHLPKDPLLTFTLQTAIIFPHMTSTTPLEKGIVIFTDGSANGRSVTYIQGREPIIKENTQNTAQQA EIVAVITAFEEVSQPFNLYTDSKYVTGLFPEIETATLSPRTKIYTELKHLQRLIHKRQEKFYIGHIRGHTGLPGPLAQGNAYADSLTRILT
MMTVB_P03365	8,081	WVQEISDSRPMLHIYLNGRRFLGLLNTGADKTCIAGRDWPANWPIHQTESSLQGLGMACGVARSSQPLRWQHEDKSGIIHPFVIPTLPFTLWGRDIMK DIKVRLMTDSPDDSQDLMIGAIESNLFADQISWKSDQPVWLNQWPLKQEKLQALQQLVTEQLQLGHLEESNSPWNTPVFVIKKKSGKWRLLQDLRAV NATMHDMGALQPGLPSPVAVPKGWEIIIIDLQDCFFNIKLHPEDCKRFAFSVPSPNFKRPYQRFQWKVLPQGMKNSPTLCQKFVDKAILTVRDKYQDS YIVHYMDDILLAHPSRSIVDEILTSMIQALNKHGLVVSTEKIQKYDNLKYLGTHIQGDSVSYQKLQIRTDKLRTLNDFQKLLGNINWIRPFLKLTTGELKPLF EILNGDSNPISTRKLTPEACKALQLMNERLSTARVKRLDLSQPWSLCILKTEYTPTACLWQDGVVEWIHLPHISPKVITPYDIFCTQLIIKGRHRSKELFSK DPDYIVVPYTKVQFDLLLQEKEDWPISLLGFLGEVHFHLPKDPLLTFTLQTAIIFPHMTSTTPLEKGIVIFTDGSANGRSVTYIQGREPIIKENTQNTAQQA EIVAVITAFEEVSQPFNLYTDSKYVTGLFPEIETATLSPRTKIYTELKHLQRLIHKRQEKFYIGHIRGHTGLPGPLAQGNAYADSLTRILT
MMTVB_P03365_2mut	8,082	WVQEISDSRPMLHIYLNGRRFLGLLNTGADKTCIAGRDWPANWPIHQTESSLQGLGMACGVARSSQPLRWQHEDKSGIIHPFVIPTLPFTLWGRDIMK DIKVRLMTDSPDDSQDLMIGAIESNLFADQISWKSDQPVWLNQWPLKQEKLQALQQLVTEQLQLGHLEESNSPWNTPVFVIKKKSGKWRLLQDLRAV NATMHDMGALQPGLPSPVAVPKGWEIIIIDLQDCFFNIKLHPEDCKRFAFSVPSPNFKRPYQRFQWKVLPQGMKNSPTLCQKFVDKAILTVRDKYQDS YIVHYMDDILLAHPSRSIVDEILTSMIQALNKHGLVVSTEKIQKYDNLKYLGTHIQGDSVSYQKLQIRTDKLRTLNDFQKLLGNINWIRPFLKLTTGELKPLF EILNPDSNPISTRKLTPEACKALQLMNERLSTARVKRLDLSQPWSLCILKTEYTPTACLWQDGVVEWIHLPHISPKVITPYDIFCTQLIIKGRHRSKELFSK DPDYIVVPYTKVQFDLLLQEKEDWPISLLGFLGEVHFHLPKDPLLTFTLQTAIIFPHMTSTTPLEKGIVIFTDGSANGRSVTYIQGREPIIKENTQNTAQQA EIVAVITAFEEVSQPFNLYTDSKYVTGLFPEIETATLSPRTKIYTELKHLQRLIHKRQEKFYIGHIRGHTGLPGPLAQGNAYADSLTRILT
MMTVB_P03365_2mut_WS	8,083	VQEISDSRPMLHIYLNGRRFLGLLDTGADKTCIAGRDWPANWPIHQTESSLQGLGMACGVARSSQPLRWQHEDKSGIIHPFVIPTLPFTLWGRDIMKDI KVRLMTDSPDDSQDLMIGAIESNLFADQISWKSDQPVWLNQWPLKQEKLQALQQLVTEQLQLGHLEESNSPWNTPVFVIKKKSGKWRLLQDLRAVNA TMHDMGALQPGLPSPVAVPKGWEIIIIDLQDCFFNIKLHPEDCKRFAFSVPSPNFKRPYQRFQWKVLPQGMKNSPTLCQKFVDKAILTVRDKYQDSYIV HYMDDILLAHPSRSIVDEILTSMIQALNKHGLVVSTEKIQKYDNLKYLGTHIQGDSVSYQKLQIRTDKLRTLNDFQKLLGNINWIRPFLKLTTGELKPLFEIL NPDSNPISTRKLTPEACKALQLMNERLSTARVKRLDLSQPWSLCILKTEYTPTACLWQDGVVEWIHLPHISPKVITPYDIFCTQLIIKGRHRSKELFSKDP DYIVVPYTKVQFDLLLQEKEDWPISLLGFLGEVHFHLPKDPLLTFTLQTAIIFPHMTSTTPLEKGIVIFTDGSANGRSVTYIQGREPIIKENTQNTAQQAEIV AVITAFEEVSQPFNLYTDSKYVTGLFPEIETATLSPRTKIYTELKHLQRLIHKRQEKFYIGHIRGHTGLPGPLAQGNAYADSLTRILTA
MMTVB_P03365_2mut_WS	8,084	VQEISDSRPMLHIYLNGRRFLGLLDTGADKTCIAGRDWPANWPIHQTESSLQGLGMACGVARSSQPLRWQHEDKSGIIHPFVIPTLPFTLWGRDIMKDI KVRLMTDSPDDSQDLMIGAIESNLFADQISWKSDQPVWLNQWPLKQEKLQALQQLVTEQLQLGHLEESNSPWNTPVFVIKKKSGKWRLLQDLRAVNA TMHDMGALQPGLPSPVAVPKGWEIIIIDLQDCFFNIKLHPEDCKRFAFSVPSPNFKRPYQRFQWKVLPQGMKNSPTLCQKFVDKAILTVRDKYQDSYIV HYMDDILLAHPSRSIVDEILTSMIQALNKHGLVVSTEKIQKYDNLKYLGTHIQGDSVSYQKLQIRTDKLRTLNDFQKLLGNINWIRPFLKLTTGELKPLFEIL NPDSNPISTRKLTPEACKALQLMNERLSTARVKRLDLSQPWSLCILKTEYTPTACLWQDGVVEWIHLPHISPKVITPYDIFCTQLIIKGRHRSKELFSKDP DYIVVPYTKVQFDLLLQEKEDWPISLLGFLGEVHFHLPKDPLLTFTLQTAIIFPHMTSTTPLEKGIVIFTDGSANGRSVTYIQGREPIIKENTQNTAQQAEIV AVITAFEEVSQPFNLYTDSKYVTGLFPEIETATLSPRTKIYTELKHLQRLIHKRQEKFYIGHIRGHTGLPGPLAQGNAYADSLTRILTA
MMTVB_P03365_2mutB	8,085	WVQEISDSRPMLHIYLNGRRFLGLLNTGADKTCIAGRDWPANWPIHQTESSLQGLGMACGVARSSQPLRWQHEDKSGIIHPFVIPTLPFTLWGRDIMK DIKVRLMTDSPDDSQDLMIGAIESNLFADQISWKSDQPVWLNQWPLKQEKLQALQQLVTEQLQLGHLEESNSPWNTPVFVIKKKSGKWRLLQDLRAV NATMHDMGALQPGLPSPVAPPKGWEIIIIDLQDCFFNIKLHPEDCKRFAFSVPSPNFKRPYQRFQWKVLPQGMKNSPTLCQKFVDKAILTVRDKYQDS YIVHYMDDILLAHPSRSIVDEILTSMIQALNKHGLVVSTEKIQKYDNLKYLGTHIQGDSVSYQKLQIRTDKLRTLNDFQKLLGNINWIRPFLKLTTGELKPLF EILNPDSNPISTRKLTPEACKALQLMNERLSTARVKRLDLSQPWSLCILKTEYTPTACLWQDGVVEWIHLPHISPKVITPYDIFCTQLIIKGRHRSKELFSK DPDYIVVPYTKVQFDLLLQEKEDWPISLLGFLGEVHFHLPKDPLLTFTLQTAIIFPHMTSTTPLEKGIVIFTDGSANGRSVTYIQGREPIIKENTQNTAQQA EIVAVITAFEEVSQPFNLYTDSKYVTGLFPEIETATLSPRTKIYTELKHLQRLIHKRQEKFYIGHIRGHTGLPGPLAQGNAYADSLTRILT
MMTVB_P03365_2mutB	8,086	WVQEISDSRPMLHIYLNGRRFLGLLNTGADKTCIAGRDWPANWPIHQTESSLQGLGMACGVARSSQPLRWQHEDKSGIIHPFVIPTLPFTLWGRDIMK DIKVRLMTDSPDDSQDLMIGAIESNLFADQISWKSDQPVWLNQWPLKQEKLQALQQLVTEQLQLGHLEESNSPWNTPVFVIKKKSGKWRLLQDLRAV NATMHDMGALQPGLPSPVAPPKGWEIIIIDLQDCFFNIKLHPEDCKRFAFSVPSPNFKRPYQRFQWKVLPQGMKNSPTLCQKFVDKAILTVRDKYQDS YIVHYMDDILLAHPSRSIVDEILTSMIQALNKHGLVVSTEKIQKYDNLKYLGTHIQGDSVSYQKLQIRTDKLRTLNDFQKLLGNINWIRPFLKLTTGELKPLF EILNPDSNPISTRKLTPEACKALQLMNERLSTARVKRLDLSQPWSLCILKTEYTPTACLWQDGVVEWIHLPHISPKVITPYDIFCTQLIIKGRHRSKELFSK DPDYIVVPYTKVQFDLLLQEKEDWPISLLGFLGEVHFHLPKDPLLTFTLQTAIIFPHMTSTTPLEKGIVIFTDGSANGRSVTYIQGREPIIKENTQNTAQQA EIVAVITAFEEVSQPFNLYTDSKYVTGLFPEIETATLSPRTKIYTELKHLQRLIHKRQEKFYIGHIRGHTGLPGPLAQGNAYADSLTRILT
MMTVB_P03365_2	8,087	VQEISDSRPMLHIYLNGRRFLGLLDTGADKTCIAGRDWPANWPIHQTESSLQGLGMACGVARSSQPLRWQHEDKSGIIHPFVIPTLPFTLWGRDIMKDI KVRLMTDSPDDSQDLMIGAIESNLFADQISWKSDQPVWLNQWPLKQEKLQALQQLVTEQLQLGHLEESNSPWNTPVFVIKKKSGKWRLLQDLRAVNA TMHDMGALQPGLPSPPAVPKGWEIIIIDLQDCFFNIKLHPEDCKRFAFSVPSPNFKRPYQRFQWKVLPQGMKNSPTLCQKFVDKAILTVRDKYQDSYIV HYMDDILLAHPSRSIVDEILTSMIQALNKHGLVVSTEKIQKYDNLKYLGTHIQGDSVSYQKLQIRTDKLRTLNDFQKLLGNINWIRPFLKLTTGELKPLFEIL

RT Name	SEQ ID NO:	RT amino acid sequence
mutB_WS		NPDSNPISTRKLTPEACKALQLMNERLSTARVKRLDLSQPWSLCILKTEYTPTACLWQDGVVEWIHLPHISPKVITPYDIFCTQLIIKGRHRSKELFSKDP DYIVVPYTKVQFDLLLQEKEDWPISLLGFLGEVHFHLPKDPLLTFTLQTAIIFPHMTSTTPLEKGIVIFTDGSANGRSVTYIQGREPIIKENTQNTAQQAEIV AVITAFEEVSQPFNLYTDSKYVTGLFPEIETATLSPRTKIYTELKHLQRLIHKRQEKFYIGHIRGHTGLPGPLAQGNAYADSLTRILTA
MMTVB_P03365_2mutB_WS	8,088	VQEISDSRPMLHIYLNGRRFLGLLDTGADKTCIAGRDWPANWPIHQTESSLQGLGMACGVARSSQPLRWQHEDKSGIIHPFVIPTLPFTLWGRDIMKDI KVRLMTDSPDDSQDLMIGAIESNLFADQISWKSDQPVWLNQWPLKQEKLQALQQLVTEQLQLGHLEESNSPWNTPVFVIKKKSGKWRLLQDLRAVNA TMHDMGALQPGLPSPPAVPKGWEIIIIDLQDCFFNIKLHPEDCKRFAFSVPSPNFKRPYQRFQWKVLPQGMKNSPTLCQKFVDKAILTVRDKYQDSYIV HYMDDILLAHPSRSIVDEILTSMIQALNKHGLVVSTEKIQKYDNLKYLGTHIQGDSVSYQKLQIRTDKLRTLNDFQKLLGNINWIRPFLKLTTGELKPLFEIL NPDSNPISTRKLTPEACKALQLMNERLSTARVKRLDLSQPWSLCILKTEYTPTACLWQDGVVEWIHLPHISPKVITPYDIFCTQLIIKGRHRSKELFSKDP DYIVVPYTKVQFDLLLQEKEDWPISLLGFLGEVHFHLPKDPLLTFTLQTAIIFPHMTSTTPLEKGIVIFTDGSANGRSVTYIQGREPIIKENTQNTAQQAEIV AVITAFEEVSQPFNLYTDSKYVTGLFPEIETATLSPRTKIYTELKHLQRLIHKRQEKFYIGHIRGHTGLPGPLAQGNAYADSLTRILTA
MMTVB_P03365_WS	8,089	VQEISDSRPMLHIYLNGRRFLGLLDTGADKTCIAGRDWPANWPIHQTESSLQGLGMACGVARSSQPLRWQHEDKSGIIHPFVIPTLPFTLWGRDIMKDI KVRLMTDSPDDSQDLMIGAIESNLFADQISWKSDQPVWLNQWPLKQEKLQALQQLVTEQLQLGHLEESNSPWNTPVFVIKKKSGKWRLLQDLRAVNA TMHDMGALQPGLPSPVAVPKGWEIIIIDLQDCFFNIKLHPEDCKRFAFSVPSPNFKRPYQRFQWKVLPQGMKNSPTLCQKFVDKAILTVRDKYQDSYIV HYMDDILLAHPSRSIVDEILTSMIQALNKHGLVVSTEKIQKYDNLKYLGTHIQGDSVSYQKLQIRTDKLRTLNDFQKLLGNINWIRPFLKLTTGELKPLFEIL NGDSNPISTRKLTPEACKALQLMNERLSTARVKRLDLSQPWSLCILKTEYTPTACLWQDGVVEWIHLPHISPKVITPYDIFCTQLIIKGRHRSKELFSKDP DYIVVPYTKVQFDLLLQEKEDWPISLLGFLGEVHFHLPKDPLLTFTLQTAIIFPHMTSTTPLEKGIVIFTDGSANGRSVTYIQGREPIIKENTQNTAQQAEIV AVITAFEEVSQPFNLYTDSKYVTGLFPEIETATLSPRTKIYTELKHLQRLIHKRQEKFYIGHIRGHTGLPGPLAQGNAYADSLTRILTA
MMTVB_P03365_WS	8,090	VQEISDSRPMLHIYLNGRRFLGLLDTGADKTCIAGRDWPANWPIHQTESSLQGLGMACGVARSSQPLRWQHEDKSGIIHPFVIPTLPFTLWGRDIMKDI KVRLMTDSPDDSQDLMIGAIESNLFADQISWKSDQPVWLNQWPLKQEKLQALQQLVTEQLQLGHLEESNSPWNTPVFVIKKKSGKWRLLQDLRAVNA TMHDMGALQPGLPSPVAVPKGWEIIIIDLQDCFFNIKLHPEDCKRFAFSVPSPNFKRPYQRFQWKVLPQGMKNSPTLCQKFVDKAILTVRDKYQDSYIV HYMDDILLAHPSRSIVDEILTSMIQALNKHGLVVSTEKIQKYDNLKYLGTHIQGDSVSYQKLQIRTDKLRTLNDFQKLLGNINWIRPFLKLTTGELKPLFEIL NGDSNPISTRKLTPEACKALQLMNERLSTARVKRLDLSQPWSLCILKTEYTPTACLWQDGVVEWIHLPHISPKVITPYDIFCTQLIIKGRHRSKELFSKDP DYIVVPYTKVQFDLLLQEKEDWPISLLGFLGEVHFHLPKDPLLTFTLQTAIIFPHMTSTTPLEKGIVIFTDGSANGRSVTYIQGREPIIKENTQNTAQQAEIV AVITAFEEVSQPFNLYTDSKYVTGLFPEIETATLSPRTKIYTELKHLQRLIHKRQEKFYIGHIRGHTGLPGPLAQGNAYADSLTRILTA
MMTVB_P03365-Pro	8,091	GRDIMKDIKVRLMTDSPDDSQDLMIGAIESNLFADQISWKSDQPVWLNQWPLKQEKLQALQQLVTEQLQLGHLEESNSPWNTPVFVIKKKSGKWRLL QDLRAVNATMHDMGALQPGLPSPVAVPKGWEIIIIDLQDCFFNIKLHPEDCKRFAFSVPSPNFKRPYQRFQWKVLPQGMKNSPTLCQKFVDKAILTVR DKYQDSYIVHYMDDILLAHPSRSIVDEILTSMIQALNKHGLVVSTEKIQKYDNLKYLGTHIQGDSVSYQKLQIRTDKLRTLNDFQKLLGNINWIRPFLKLTT GELKPLFEILNGDSNPISTRKLTPEACKALQLMNERLSTARVKRLDLSQPWSLCILKTEYTPTACLWQDGVVEWIHLPHISPKVITPYDIFCTQLIIKGRHR SKELFSKDPDYIVVPYTKVQFDLLLQEKEDWPISLLGFLGEVHFHLPKDPLLTFTLQTAIIFPHMTSTTPLEKGIVIFTDGSANGRSVTYIQGREPIIKENTQ NTAQQAEIVAVITAFEEVSQPFNLYTDSKYVTGLFPEIETATLSPRTKIYTELKHLQRLIHKRQEKFYIGHIRGHTGLPGPLAQGNAYADSLTRILT
MMTVB_P03365-Pro	8,092	GRDIMKDIKVRLMTDSPDDSQDLMIGAIESNLFADQISWKSDQPVWLNQWPLKQEKLQALQQLVTEQLQLGHLEESNSPWNTPVFVIKKKSGKWRLL QDLRAVNATMHDMGALQPGLPSPVAVPKGWEIIIIDLQDCFFNIKLHPEDCKRFAFSVPSPNFKRPYQRFQWKVLPQGMKNSPTLCQKFVDKAILTVR DKYQDSYIVHYMDDILLAHPSRSIVDEILTSMIQALNKHGLVVSTEKIQKYDNLKYLGTHIQGDSVSYQKLQIRTDKLRTLNDFQKLLGNINWIRPFLKLTT GELKPLFEILNGDSNPISTRKLTPEACKALQLMNERLSTARVKRLDLSQPWSLCILKTEYTPTACLWQDGVVEWIHLPHISPKVITPYDIFCTQLIIKGRHR SKELFSKDPDYIVVPYTKVQFDLLLQEKEDWPISLLGFLGEVHFHLPKDPLLTFTLQTAIIFPHMTSTTPLEKGIVIFTDGSANGRSVTYIQGREPIIKENTQ NTAQQAEIVAVITAFEEVSQPFNLYTDSKYVTGLFPEIETATLSPRTKIYTELKHLQRLIHKRQEKFYIGHIRGHTGLPGPLAQGNAYADSLTRILT
MMTVB_P03365-Pro_2mut	8,093	GRDIMKDIKVRLMTDSPDDSQDLMIGAIESNLFADQISWKSDQPVWLNQWPLKQEKLQALQQLVTEQLQLGHLEESNSPWNTPVFVIKKKSGKWRLL QDLRAVNATMHDMGALQPGLPSPVAVPKGWEIIIIDLQDCFFNIKLHPEDCKRFAFSVPSPNFKRPYQRFQWKVLPQGMKNSPTLCQKFVDKAILTVR DKYQDSYIVHYMDDILLAHPSRSIVDEILTSMIQALNKHGLVVSTEKIQKYDNLKYLGTHIQGDSVSYQKLQIRTDKLRTLNDFQKLLGNINWIRPFLKLTT GELKPLFEILNPDSNPISTRKLTPEACKALQLMNERLSTARVKRLDLSQPWSLCILKTEYTPTACLWQDGVVEWIHLPHISPKVITPYDIFCTQLIIKGRHR SKELFSKDPDYIVVPYTKVQFDLLLQEKEDWPISLLGFLGEVHFHLPKDPLLTFTLQTAIIFPHMTSTTPLEKGIVIFTDGSANGRSVTYIQGREPIIKENTQ NTAQQAEIVAVITAFEEVSQPFNLYTDSKYVTGLFPEIETATLSPRTKIYTELKHLQRLIHKRQEKFYIGHIRGHTGLPGPLAQGNAYADSLTRILT
MMTVB_P03365-Pro_2mutB	8,094	GRDIMKDIKVRLMTDSPDDSQDLMIGAIESNLFADQISWKSDQPVWLNQWPLKQEKLQALQQLVTEQLQLGHLEESNSPWNTPVFVIKKKSGKWRLL QDLRAVNATMHDMGALQPGLPSPVAVPKGWEIIIIDLQDCFFNIKLHPEDCKRFAFSVPSPNFKRPYQRFQWKVLPQGMKNSPTLCQKFVDKAILTVR DKYQDSYIVHYMDDILLAHPSRSIVDEILTSMIQALNKHGLVVSTEKIQKYDNLKYLGTHIQGDSVSYQKLQIRTDKLRTLNDFQKLLGNINWIRPFLKLTT GELKPLFEILNPDSNPISTRKLTPEACKALQLMNERLSTARVKRLDLSQPWSLCILKTEYTPTACLWQDGVVEWIHLPHISPKVITPYDIFCTQLIIKGRHR SKELFSKDPDYIVVPYTKVQFDLLLQEKEDWPISLLGFLGEVHFHLPKDPLLTFTLQTAIIFPHMTSTTPLEKGIVIFTDGSANGRSVTYIQGREPIIKENTQ NTAQQAEIVAVITAFEEVSQPFNLYTDSKYVTGLFPEIETATLSPRTKIYTELKHLQRLIHKRQEKFYIGHIRGHTGLPGPLAQGNAYADSLTRILT
MMTVB_P03365-Pro_2mutB	8,095	GRDIMKDIKVRLMTDSPDDSQDLMIGAIESNLFADQISWKSDQPVWLNQWPLKQEKLQALQQLVTEQLQLGHLEESNSPWNTPVFVIKKKSGKWRLL QDLRAVNATMHDMGALQPGLPSPVAPPKGWEIIIIDLQDCFFNIKLHPEDCKRFAFSVPSPNFKRPYQRFQWKVLPQGMKNSPTLCQKFVDKAILTVR DKYQDSYIVHYMDDILLAHPSRSIVDEILTSMIQALNKHGLVVSTEKIQKYDNLKYLGTHIQGDSVSYQKLQIRTDKLRTLNDFQKLLGNINWIRPFLKLTT GELKPLFEILNPDSNPISTRKLTPEACKALQLMNERLSTARVKRLDLSQPWSLCILKTEYTPTACLWQDGVVEWIHLPHISPKVITPYDIFCTQLIIKGRHR SKELFSKDPDYIVVPYTKVQFDLLLQEKEDWPISLLGFLGEVHFHLPKDPLLTFTLQTAIIFPHMTSTTPLEKGIVIFTDGSANGRSVTYIQGREPIIKENTQ NTAQQAEIVAVITAFEEVSQPFNLYTDSKYVTGLFPEIETATLSPRTKIYTELKHLQRLIHKRQEKFYIGHIRGHTGLPGPLAQGNAYADSLTRILT
MMTVB_P03365-Pro_2mutB	8,096	GRDIMKDIKVRLMTDSPDDSQDLMIGAIESNLFADQISWKSDQPVWLNQWPLKQEKLQALQQLVTEQLQLGHLEESNSPWNTPVFVIKKKSGKWRLL QDLRAVNATMHDMGALQPGLPSPVAPPKGWEIIIIDLQDCFFNIKLHPEDCKRFAFSVPSPNFKRPYQRFQWKVLPQGMKNSPTLCQKFVDKAILTVR DKYQDSYIVHYMDDILLAHPSRSIVDEILTSMIQALNKHGLVVSTEKIQKYDNLKYLGTHIQGDSVSYQKLQIRTDKLRTLNDFQKLLGNINWIRPFLKLTT GELKPLFEILNPDSNPISTRKLTPEACKALQLMNERLSTARVKRLDLSQPWSLCILKTEYTPTACLWQDGVVEWIHLPHISPKVITPYDIFCTQLIIKGRHR SKELFSKDPDYIVVPYTKVQFDLLLQEKEDWPISLLGFLGEVHFHLPKDPLLTFTLQTAIIFPHMTSTTPLEKGIVIFTDGSANGRSVTYIQGREPIIKENTQ NTAQQAEIVAVITAFEEVSQPFNLYTDSKYVTGLFPEIETATLSPRTKIYTELKHLQRLIHKRQEKFYIGHIRGHTGLPGPLAQGNAYADSLTRILT
MPMV_P07572	8,097	LTAAIDILAPQQCAEPITWKSDEPVWVDQWPLTNDKLAAAQQLVQEQLEAGHITESSSPWNTPIFVIKKKSGKWRLLQDLRAVNATMVLMGALQPGLP SPVAIPQGYLKIIIDLKDCFFSIPLHPSDQKRFAFSLPSTNFKEPMQRFQWKVLPQGMANSPTLCQKYVATAIHKVRHAWKQMYIIHYMDDILIAGKDGQ QVLQCFDQLKQELTAAGLHIAPEKVQLQDPYTYLGFELNGPKITNQKAVIRKDKLQTLNDFQKLLGDINWLRPYLKLTTGDLKPLFDTLKGDSDPNSHR SLSKEALASLEKVETAIAEQFVTHINYSLPLIFLIFNTALTPTGLFWQDNPIMWIHLPASPKKVLLPYYDAIADLIILGRDHSKKYFGIEPSTIIQPYSKSQIDW LMQNTEMWPIACASFVGILDNHYPPNKLIQFCKLHTFVFPQIISKTPLNNALLVFTDGSSTGMAAYTLTDTTIKFQTNLNSAQLVELQALIAVLSAFPNQPL NIYTDSAYLAHSIPLLETVAQIKHISETAKLFLQCQQLIYNRSIPFYIGHVRAHSGLPGPIAQGNQRADLATKIVASNINT

RT Name	SEQ ID NO:	RT amino acid sequence
MPMV_P07572_2mutB	8,098	LTAAIDILAPQQCAEPITWKSDEPVWVDQWPLTNDKLAAAQQLVQEQLEAGHITESSSPWNTPIFVIKKKSGKWRLLQDLRAVNATMVLMGALQPGLP SPVAPPQGYLKIIIDLKDCFFSIPLHPSDQKRFAFSLPSTNFKEPMQRFQWKVLPQGMANSPTLCQKYVATAIHKVRHAWKQMYIIHYMDDILIAGKDGQ QVLQCFDQLKQELTAAGLHIAPEKVQLQDPYTYLGFELNGPKITNQKAVIRKDKLQTLNDFQKLLGDINWLRPYLKLTTGDLKPLFDTLKPDSDPNSHRS LSKEALASLEKVETAIAEQFVTHINYSLPIFLIFNTALTPTGLFWQDNPIMWIHLPASPKKVLLPYYDAIADLIILGRDHSKKYFGIEPSTIIQPYSKSQIDWL MQNTEMWPIACASFVGILDNHYPPNKLIQFCKLHTFVFPQIISKTPLNNALLVFTDGSSTGMAAYTLTDTTIKFQTNLNSAQLVELQALIAVLSAFPNQPL NIYTDSAYLAHSIPLLETVAQIKHISETAKLFLQCQQLIYNRSIPFYIGHVRAHSGLPGPIAQGNQRADLATKIVASNINT
PERV_Q4VFZ2	8,099	TLQLDDEYRLYSPLVKPDQNIQFWLEQFPQAWAETAGMGLAKQVPPQVIQLKASATPVSVRQYPLSKEAQEGIRPHVQRLIQQGILVPVQSPWNTPLL PVRKPGTNDYRPVQDLREVNKRVQDIHPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGTGRTGQLTWTRLPQGFKNS PTIFDEALHRDLANFRIQHPQVTLLQYVDDLLLAGATKQDCLEGTKALLLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWLTEARKKTVVQIPAPT TAKQVREFLGTAGFCRLWIPGFATLAAPLYPLTKEKGEFSWAPEHQKAFDAIKKALLSAPALALPDVTKPFTLYVDERKGVARGVLTQTLGPWRRPVA YLSKKLDPVASGWPVCLKAIAAVAILVKDADKLTLGQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNPATLLPEETDEPVTH DCHQLLIEETGVRKDLTDIPLTGEVLTWFTDGSSYVVEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSINIYTDSRYAFATAH VHGAIYKQRGLLTSAGREIKNKEEILSLLEALHLPKRLAIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLL
PERV_Q4VFZ2_3mut	8,101	TLQLDDEYRLYSPLVKPDQNIQFWLEQFPQAWAETAGMGLAKQVPPQVIQLKASATPVSVRQYPLSKEAQEGIRPHVQRLIQQGILVPVQSPWNTPLL PVRKPGTNDYRPVQDLREVNKRVQDIHPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGTGRTGQLTWTRLPQGFKNS PTIFNEALHRDLANFRIQHPQVTLLQYVDDLLLAGATKQDCLEGTKALLLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWLTEARKKTVVQIPAPT TAKQVREFLGTAGFCRLWIPGFATLAAPLYPLTKPKGEFSWAPEHQKAFDAIKKALLSAPALALPDVTKPFTLYVDERKGVARGVLTQTLGPWRRPVA YLSKKLDPVASGWPVCLKAIAAVAILVKDADKLTLGQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNPATLLPEETDEPVTH DCHQLLIEETGVRKDLTDIPLTGEVLTWFTDGSSYVVEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSINIYTDSRYAFATAH VHGAIYKQRGWLTSAGREIKNKEEILSLLEALHLPKRLAIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLL
PERV_Q4VFZ2_3mut	8,102	TLQLDDEYRLYSPLVKPDQNIQFWLEQFPQAWAETAGMGLAKQVPPQVIQLKASATPVSVRQYPLSKEAQEGIRPHVQRLIQQGILVPVQSPWNTPLL PVRKPGTNDYRPVQDLREVNKRVQDIHPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGTGRTGQLTWTRLPQGFKNS PTIFNEALHRDLANFRIQHPQVTLLQYVDDLLLAGATKQDCLEGTKALLLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWLTEARKKTVVQIPAPT TAKQVREFLGTAGFCRLWIPGFATLAAPLYPLTKPKGEFSWAPEHQKAFDAIKKALLSAPALALPDVTKPFTLYVDERKGVARGVLTQTLGPWRRPVA YLSKKLDPVASGWPVCLKAIAAVAILVKDADKLTLGQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNPATLLPEETDEPVTH DCHQLLIEETGVRKDLTDIPLTGEVLTWFTDGSSYVVEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSINIYTDSRYAFATAH VHGAIYKQRGWLTSAGREIKNKEEILSLLEALHLPKRLAIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLL
PERV_Q4VFZ2_3mutA_WS	8,103	LDDEYRLYSPLVKPDQNIQFWLEQFPQAWAETAGMGLAKQVPPQVIQLKASATPVSVRQYPLSKEAQEGIRPHVQRLIQQGILVPVQSPWNTPLLPVR KPGTNDYRPVQDLREVNKRVQDIHPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGTGRTGQLTWTRLPQGFKNSPTIF NEALHRDLANFRIQHPQVTLLQYVDDLLLAGATKQDCLEGTKALLLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWLTEARKKTVVQIPAPTTAK QVREFLGKAGFCRLFIPGFATLAAPLYPLTKPKGEFSWAPEHQKAFDAIKKALLSAPALALPDVTKPFTLYVDERKGVARGVLTQTLGPWRRPVAYLSK KLDPVASGWPVCLKAIAAVAILVKDADKLTLGQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNPATLLPEETDEPVTHDCHQ LLIEETGVRKDLTDIPLTGEVLTWFTDGSSYVVEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSINIYTDSRYAFATAHVHGAI YKQRGWLTSAGREIKNKEEILSLLEALHLPKRLAIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLP
PERV_Q4VFZ2_3mutA_WS	8,104	LDDEYRLYSPLVKPDQNIQFWLEQFPQAWAETAGMGLAKQVPPQVIQLKASATPVSVRQYPLSKEAQEGIRPHVQRLIQQGILVPVQSPWNTPLLPVR KPGTNDYRPVQDLREVNKRVQDIHPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGTGRTGQLTWTRLPQGFKNSPTIF NEALHRDLANFRIQHPQVTLLQYVDDLLLAGATKQDCLEGTKALLLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWLTEARKKTVVQIPAPTTAK QVREFLGKAGFCRLFIPGFATLAAPLYPLTKPKGEFSWAPEHQKAFDAIKKALLSAPALALPDVTKPFTLYVDERKGVARGVLTQTLGPWRRPVAYLSK KLDPVASGWPVCLKAIAAVAILVKDADKLTLGQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNPATLLPEETDEPVTHDCHQ LLIEETGVRKDLTDIPLTGEVLTWFTDGSSYVVEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSINIYTDSRYAFATAHVHGAI YKQRGWLTSAGREIKNKEEILSLLEALHLPKRLAIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLP
SFV1_P23074	8,105	MDPLQLLQPLEAEIKGTKLKAHWNSGATITCVPEAFLEDERPIQTMLIKTIHGEKQQDVYYLTFKVQGRKVEAEVLASPYDYILLNPSDVPWLMKKPLQL TVLVPLHEYQERLLQQTALPKEQKELLQKLFLKYDALWQHWENQVGHRRIKPHNIATGTLAPRPQKQYPINPKAKPSIQIVIDDLLKQGVLIQQNSTMNT PVYPVPKPDGKWRMVLDYREVNKTIPLIAAQNQHSAGILSSIYRGKYKTTLDLTNGFWAHPITPESYWLTAFTWQGKQYCWTRLPQGFLNSPALFTAD VVDLLKEIPNVQAYVDDIYISHDDPQEHLEQLEKIFSILLNAGYVVSLKKSEIAQREVEFLGFNITKEGRGLTDTFKQKLLNITPPKDLKQLQSILGLLNFAR NFIPNYSELVKPLYTIVANANGKFISWTEDNSNQLQHIISVLNQADNLEERNPETRLIIKVNSSPSAGYIRYYNEGSKRPIMYVNYIFSKAEAKFTQTEKLL TTMHKGLIKAMDLAMGQEILVYSPIVSMTKIQRTPLPERKALPVRWITWMTYLEDPRIQFHYDKSLPELQQIPNVTEDVIAKTKHPSEFAMVFYTDGSAIK HPDVNKSHSAGMGIAQVQFIPEYKIVHQWSIPLGDHTAQLAEIAAVEFACKKALKISGPVLIVTDSFYVAESANKELPYWKSNGFLNNKKKPLRHVSKW KSIAECLQLKPDIIIMHEKGHQQPMTTLHTEGNNLADKLATQGSYVVH
SFV1_P23074_2mut	8,106	MDPLQLLQPLEAEIKGTKLKAHWNSGATITCVPEAFLEDERPIQTMLIKTIHGEKQQDVYYLTFKVQGRKVEAEVLASPYDYILLNPSDVPWLMKKPLQL TVLVPLHEYQERLLQQTALPKEQKELLQKLFLKYDALWQHWENQVGHRRIKPHNIATGTLAPRPQKQYPINPKAKPSIQIVIDDLLKQGVLIQQNSTMNT PVYPVPKPDGKWRMVLDYREVNKTIPLIAAQNQHSAGILSSIYRGKYKTTLDLTNGFWAHPITPESYWLTAFTWQGKQYCWTRLPQGFLNSPALFNAD VVDLLKEIPNVQAYVDDIYISHDDPQEHLEQLEKIFSILLNAGYVVSLKKSEIAQREVEFLGFNITKEGRGLTDTFKQKLLNITPPKDLKQLQSILGLLNFAR NFIPNYSELVKPLYTIVAPANGKFISWTEDNSNQLQHIISVLNQADNLEERNPETRLIIKVNSSPSAGYIRYYNEGSKRPIMYVNYIFSKAEAKFTQTEKLLT TMHKGLIKAMDLAMGQEILVYSPIVSMTKIQRTPLPERKALPVRWITWMTYLEDPRIQFHYDKSLPELQQIPNVTEDVIAKTKHPSEFAMVFYTDGSAIKH PDVNKSHSAGMGIAQVQFIPEYKIVHQWSIPLGDHTAQLAEIAAVEFACKKALKISGPVLIVTDSFYVAESANKELPYWKSNGFLNNKKKPLRHVSKWK SIAECLQLKPDIIIMHEKGHQQPMTTLHTEGNNLADKLATQGSYVVH
SFV1_P23074_2mutA	8,107	MDPLQLLQPLEAEIKGTKLKAHWNSGATITCVPEAFLEDERPIQTMLIKTIHGEKQQDVYYLTFKVQGRKVEAEVLASPYDYILLNPSDVPWLMKKPLQL TVLVPLHEYQERLLQQTALPKEQKELLQKLFLKYDALWQHWENQVGHRRIKPHNIATGTLAPRPQKQYPINPKAKPSIQIVIDDLLKQGVLIQQNSTMNT PVYPVPKPDGKWRMVLDYREVNKTIPLIAAQNQHSAGILSSIYRGKYKTTLDLTNGFWAHPITPESYWLTAFTWQGKQYCWTRLPQGFLNSPALFNAD

RT Name	SEQ ID NO:	RT amino acid sequence
		VVDLLKEIPNVQAYVDDIYISHDDPQEHLEQLEKIFSILLNAGYVVSLKKSEIAQREVEFLGFNITKEGRGLTDTFKQKLLNITPPKDLKQLQSILGKLNFAR NFIPNYSELVKPLYTIVAPANGKFISWTEDNSNQLQHIISVLNQADNLEERNPETRLIIKVNSSPSAGYIRYYNEGSKRPIMYVNYIFSKAEAKFTQTEKLLT TMHKGLIKAMDLAMGQEILVYSPIVSMTKIQRTPLPERKALPVRWITWMTYLEDPRIQFHYDKSLPELQQIPNVTEDVIAKTKHPSEFAMVFYTDGSAIKH PDVNKSHSAGMGIAQVQFIPEYKIVHQWSIPLGDHTAQLAEIAAVEFACKKALKISGPVLIVTDSFYVAESANKELPYWKSNGFLNNKKKPLRHVSKWK SIAECLQLKPDIIIMHEKGHQQPMTTLHTEGNNLADKLATQGSYVVH
SFV1_P23074-Pro	8,108	VPWLMKKPLQLTVLVPLHEYQERLLQQTALPKEQKELLQKLFLKYDALWQHWENQVGHRRIKPHNIATGTLAPRPQKQYPINPKAKPSIQIVIDDLLKQ GVLIQQNSTMNTPVYPVPKPDGKWRMVLDYREVNKTIPLIAAQNQHSAGILSSIYRGKYKTTLDLTNGFWAHPITPESYWLTAFTWQGKQYCWTRLPQ GFLNSPALFTADVVDLLKEIPNVQAYVDDIYISHDDPQEHLEQLEKIFSILLNAGYVVSLKKSEIAQREVEFLGFNITKEGRGLTDTFKQKLLNITPPKDLKQ LQSILGLLNFARNFIPNYSELVKPLYTIVANANGKFISWTEDNSNQLQHIISVLNQADNLEERNPETRLIIKVNSSPSAGYIRYYNEGSKRPIMYVNYIFSKA EAKFTQTEKLLTTMHKGLIKAMDLAMGQEILVYSPIVSMTKIQRTPLPERKALPVRWITWMTYLEDPRIQFHYDKSLPELQQIPNVTEDVIAKTKHPSEFA MVFYTDGSAIKHPDVNKSHSAGMGIAQVQFIPEYKIVHQWSIPLGDHTAQLAEIAAVEFACKKALKISGPVLIVTDSFYVAESANKELPYWKSNGFLNNK KKPLRHVSKWKSIAECLQLKPDIIIMHEKGHQQPMTTLHTEGNNLADKLATQGSYVVH
SFV1_P23074-Pro_2mut	8,109	VPWLMKKPLQLTVLVPLHEYQERLLQQTALPKEQKELLQKLFLKYDALWQHWENQVGHRRIKPHNIATGTLAPRPQKQYPINPKAKPSIQIVIDDLLKQ GVLIQQNSTMNTPVYPVPKPDGKWRMVLDYREVNKTIPLIAAQNQHSAGILSSIYRGKYKTTLDLTNGFWAHPITPESYWLTAFTWQGKQYCWTRLPQ GFLNSPALFNADVVDLLKEIPNVQAYVDDIYISHDDPQEHLEQLEKIFSILLNAGYVVSLKKSEIAQREVEFLGFNITKEGRGLTDTFKQKLLNITPPKDLK QLQSILGLLNFARNFIPNYSELVKPLYTIVAPANGKFISWTEDNSNQLQHIISVLNQADNLEERNPETRLIIKVNSSPSAGYIRYYNEGSKRPIMYVNYIFSK AEAKFTQTEKLLTTMHKGLIKAMDLAMGQEILVYSPIVSMTKIQRTPLPERKALPVRWITWMTYLEDPRIQFHYDKSLPELQQIPNVTEDVIAKTKHPSEF AMVFYTDGSAIKHPDVNKSHSAGMGIAQVQFIPEYKIVHQWSIPLGDHTAQLAEIAAVEFACKKALKISGPVLIVTDSFYVAESANKELPYWKSNGFLNN KKKPLRHVSKWKSIAECLQLKPDIIIMHEKGHQQPMTTLHTEGNNLADKLATQGSYVVH
SFV1_P23074-Pro_2mutA	8,110	VPWLMKKPLQLTVLVPLHEYQERLLQQTALPKEQKELLQKLFLKYDALWQHWENQVGHRRIKPHNIATGTLAPRPQKQYPINPKAKPSIQIVIDDLLKQ GVLIQQNSTMNTPVYPVPKPDGKWRMVLDYREVNKTIPLIAAQNQHSAGILSSIYRGKYKTTLDLTNGFWAHPITPESYWLTAFTWQGKQYCWTRLPQ GFLNSPALFNADVVDLLKEIPNVQAYVDDIYISHDDPQEHLEQLEKIFSILLNAGYVVSLKKSEIAQREVEFLGFNITKEGRGLTDTFKQKLLNITPPKDLK QLQSILGKLNFARNFIPNYSELVKPLYTIVAPANGKFISWTEDNSNQLQHIISVLNQADNLEERNPETRLIIKVNSSPSAGYIRYYNEGSKRPIMYVNYIFSK AEAKFTQTEKLLTTMHKGLIKAMDLAMGQEILVYSPIVSMTKIQRTPLPERKALPVRWITWMTYLEDPRIQFHYDKSLPELQQIPNVTEDVIAKTKHPSEF AMVFYTDGSAIKHPDVNKSHSAGMGIAQVQFIPEYKIVHQWSIPLGDHTAQLAEIAAVEFACKKALKISGPVLIVTDSFYVAESANKELPYWKSNGFLNN KKKPLRHVSKWKSIAECLQLKPDIIIMHEKGHQQPMTTLHTEGNNLADKLATQGSYVVH
SFV3L_P27401	8,111	MDPLQLLQPLEAEIKGTKLKAHWNSGATITCVPQAFLEEEVPIKNIWIKTIHGEKEQPVYYLTFKIQGRKVEAEVISSPYDYILVSPSDIPWLMKKPLQLTT LVPLQEYEERLLKQTMLTGSYKEKLQSLFLKYDALWQHWENQVGHRRIKPHHIATGTVNPRPQKQYPINPKAKASIQTVINDLLKQGVLIQQNSIMNTP VYPVPKPDGKWRMVLDYREVNKTIPLIAAQNQHSAGILSSIFRGKYKTTLDLSNGFWAHSITPESYWLTAFTWLGQQYCWTRLPQGFLNSPALFTADV VDLLKEVPNVQVYVDDIYISHDDPREHLEQLEKVFSLLLNAGYVVSLKKSEIAQHEVEFLGFNITKEGRGLTETFKQKLLNITPPRDLKQLQSILGLLNFAR NFIPNFSELVKPLYNIIATANGKYITWTTDNSQQLQNIISMLNSAENLEERNPEVRLIMKVNTSPSAGYIRFYNEFAKRPIMYLNYVYTKAEVKFTNTEKLL TTIHKGLIKALDLGMGQEILVYSPIVSMTKIQKTPLPERKALPIRWITWMSYLEDPRIQFHYDKTLPELQQVPTVTDDIIAKIKHPSEFSMVFYTDGSAIKHP NVNKSHNAGMGIAQVQFKPEFTVINTWSIPLGDHTAQLAEVAAVEFACKKALKIDGPVLIVTDSFYVAESVNKELPYWQSNGFFNNKKKPLKHVSKWK SIADCIQLKPDIIIIHEKGHQPTASTFHTEGNNLADKLATQGSYVVN
SFV3L_P27401_2mut	8,112	MDPLQLLQPLEAEIKGTKLKAHWNSGATITCVPQAFLEEEVPIKNIWIKTIHGEKEQPVYYLTFKIQGRKVEAEVISSPYDYILVSPSDIPWLMKKPLQLTT LVPLQEYEERLLKQTMLTGSYKEKLQSLFLKYDALWQHWENQVGHRRIKPHHIATGTVNPRPQKQYPINPKAKASIQTVINDLLKQGVLIQQNSIMNTP VYPVPKPDGKWRMVLDYREVNKTIPLIAAQNQHSAGILSSIFRGKYKTTLDLSNGFWAHSITPESYWLTAFTWLGQQYCWTRLPQGFLNSPALFNADV VDLLKEVPNVQVYVDDIYISHDDPREHLEQLEKVFSLLLNAGYVVSLKKSEIAQHEVEFLGFNITKEGRGLTETFKQKLLNITPPRDLKQLQSILGLLNFAR NFIPNFSELVKPLYNIIATAPGKYITWTTDNSQQLQNIISMLNSAENLEERNPEVRLIMKVNTSPSAGYIRFYNEFAKRPIMYLNYVYTKAEVKFTNTEKLL TTIHKGLIKALDLGMGQEILVYSPIVSMTKIQKTPLPERKALPIRWITWMSYLEDPRIQFHYDKTLPELQQVPTVTDDIIAKIKHPSEFSMVFYTDGSAIKHP NVNKSHNAGMGIAQVQFKPEFTVINTWSIPLGDHTAQLAEVAAVEFACKKALKIDGPVLIVTDSFYVAESVNKELPYWQSNGFFNNKKKPLKHVSKWK SIADCIQLKPDIIIIHEKGHQPTASTFHTEGNNLADKLATQGSYVVN
SFV3L_P27401_2mutA	8,113	MDPLQLLQPLEAEIKGTKLKAHWNSGATITCVPQAFLEEEVPIKNIWIKTIHGEKEQPVYYLTFKIQGRKVEAEVISSPYDYILVSPSDIPWLMKKPLQLTT LVPLQEYEERLLKQTMLTGSYKEKLQSLFLKYDALWQHWENQVGHRRIKPHHIATGTVNPRPQKQYPINPKAKASIQTVINDLLKQGVLIQQNSIMNTP VYPVPKPDGKWRMVLDYREVNKTIPLIAAQNQHSAGILSSIFRGKYKTTLDLSNGFWAHSITPESYWLTAFTWLGQQYCWTRLPQGFLNSPALFNADV VDLLKEVPNVQVYVDDIYISHDDPREHLEQLEKVFSLLLNAGYVVSLKKSEIAQHEVEFLGFNITKEGRGLTETFKQKLLNITPPRDLKQLQSILGKLNFA RNFIPNFSELVKPLYNIIATAPGKYITWTTDNSQQLQNIISMLNSAENLEERNPEVRLIMKVNTSPSAGYIRFYNEFAKRPIMYLNYVYTKAEVKFTNTEKL LTTIHKGLIKALDLGMGQEILVYSPIVSMTKIQKTPLPERKALPIRWITWMSYLEDPRIQFHYDKTLPELQQVPTVTDDIIAKIKHPSEFSMVFYTDGSAIKH PNVNKSHNAGMGIAQVQFKPEFTVINTWSIPLGDHTAQLAEVAAVEFACKKALKIDGPVLIVTDSFYVAESVNKELPYWQSNGFFNNKKKPLKHVSKW KSIADCIQLKPDIIIIHEKGHQPTASTFHTEGNNLADKLATQGSYVVN
SFV3L_P27401-Pro	8,114	IPWLMKKPLQLTTLVPLQEYEERLLKQTMLTGSYKEKLQSLFLKYDALWQHWENQVGHRRIKPHHIATGTVNPRPQKQYPINPKAKASIQTVINDLLKQ GVLIQQNSIMNTPVYPVPKPDGKWRMVLDYREVNKTIPLIAAQNQHSAGILSSIFRGKYKTTLDLSNGFWAHSITPESYWLTAFTWLGQQYCWTRLPQ GFLNSPALFTADVVDLLKEVPNVQVYVDDIYISHDDPREHLEQLEKVFSLLLNAGYVVSLKKSEIAQHEVEFLGFNITKEGRGLTETFKQKLLNITPPRDL KQLQSILGLLNFARNFIPNFSELVKPLYNIIATANGKYITWTTDNSQQLQNIISMLNSAENLEERNPEVRLIMKVNTSPSAGYIRFYNEFAKRPIMYLNYVY TKAEVKFTNTEKLLTTIHKGLIKALDLGMGQEILVYSPIVSMTKIQKTPLPERKALPIRWITWMSYLEDPRIQFHYDKTLPELQQVPTVTDDIIAKIKHPSEF SMVFYTDGSAIKHPNVNKSHNAGMGIAQVQFKPEFTVINTWSIPLGDHTAQLAEVAAVEFACKKALKIDGPVLIVTDSFYVAESVNKELPYWQSNGFFN NKKKPLKHVSKWKSIADCIQLKPDIIIIHEKGHQPTASTFHTEGNNLADKLATQGSYVVN
SFV3L_P27401-Pro_2mut	8,115	IPWLMKKPLQLTTLVPLQEYEERLLKQTMLTGSYKEKLQSLFLKYDALWQHWENQVGHRRIKPHHIATGTVNPRPQKQYPINPKAKASIQTVINDLLKQ GVLIQQNSIMNTPVYPVPKPDGKWRMVLDYREVNKTIPLIAAQNQHSAGILSSIFRGKYKTTLDLSNGFWAHSITPESYWLTAFTWLGQQYCWTRLPQ GFLNSPALFNADVVDLLKEVPNVQVYVDDIYISHDDPREHLEQLEKVFSLLLNAGYVVSLKKSEIAQHEVEFLGFNITKEGRGLTETFKQKLLNITPPRDL KQLQSILGLLNFARNFIPNFSELVKPLYNIIATAPGKYITWTTDNSQQLQNIISMLNSAENLEERNPEVRLIMKVNTSPSAGYIRFYNEFAKRPIMYLNYVY TKAEVKFTNTEKLLTTIHKGLIKALDLGMGQEILVYSPIVSMTKIQKTPLPERKALPIRWITWMSYLEDPRIQFHYDKTLPELQQVPTVTDDIIAKIKHPSEF SMVFYTDGSAIKHPNVNKSHNAGMGIAQVQFKPEFTVINTWSIPLGDHTAQLAEVAAVEFACKKALKIDGPVLIVTDSFYVAESVNKELPYWQSNGFFN NKKKPLKHVSKWKSIADCIQLKPDIIIIHEKGHQPTASTFHTEGNNLADKLATQGSYVVN
SFV3L_P27401-	8,116	IPWLMKKPLQLTTLVPLQEYEERLLKQTMLTGSYKEKLQSLFLKYDALWQHWENQVGHRRIKPHHIATGTVNPRPQKQYPINPKAKASIQTVINDLLKQ GVLIQQNSIMNTPVYPVPKPDGKWRMVLDYREVNKTIPLIAAQNQHSAGILSSIFRGKYKTTLDLSNGFWAHSITPESYWLTAFTWLGQQYCWTRLPQ GFLNSPALFNADVVDLLKEVPNVQVYVDDIYISHDDPREHLEQLEKVFSLLLNAGYVVSLKKSEIAQHEVEFLGFNITKEGRGLTETFKQKLLNITPPRDL

RT Name	SEQ ID NO:	RT amino acid sequence
Pro_2mutA		KQLQSILGKLNFARNFIPNFSELVKPLYNIIATAPGKYITWTTDNSQQLQNIISMLNSAENLEERNPEVRLIMKVNTSPSAGYIRFYNEFAKRPIMYLNYVY TKAEVKFTNTEKLLTTIHKGLIKALDLGMGQEILVYSPIVSMTKIQKTPLPERKALPIRWITWMSYLEDPRIQFHYDKTLPELQQVPTVTDDIIAKIKHPSEF SMVFYTDGSAIKHPNVNKSHNAGMGIAQVQFKPEFTVINTWSIPLGDHTAQLAEVAAVEFACKKALKIDGPVLIVTDSFYVAESVNKELPYWQSNGFFN NKKKPLKHVSKWKSIADCIQLKPDIIIIIHEKGHQPTASTFHTEGNNLADKLATQGSYVVN
SFVCP_Q87040	8,117	MNPLQLLQPLPAEVKGTKLLAHWNSGATITCIPESFLEDEQPIKQTLIKTIHGEKQQNVYYLTFKVKGRKVEAEVIASPYEYILLSPTDVPWLTQQPLQLTI LVPLQEYQDRILNKTALPEEQKQQLKALFTKYDNLWQHWENQVGHRKIRPHNIATGDYPPRPQKQYPINPKAKPSIQIVIDDLLKQGVLTPQNSTMNTP VYPVPKPDGRWRMVLDYREVNKTIPLTAAQNQHSAGILATIVRQKYKTTLDLANGFWAHPITPDSYWLTAFTWQGKQYCWTRLPQGFLNSPALFTAD AVDLLKEVPNVQVYVDDIYLSHDNPHEHIQQLEKVFQILLQAGYVVSLKKSEIGQRTVEFLGFNITKEGRGLTDTFKTKLLNVTPPKDLKQLQSILGLLNF ARNFIPNFAELVQTLYNLIASSKGKYIEWTEDNTKQLNKVIEALNTASNLEERLPDQRLVIKVNTSPSAGYVRYYNESGKKPIMYLNYVFSKAELKFSMLE KLLTTMHKALIKAMDLAMGQEILVYSPIVSMTKIQKTPLPERKALPIRWITWMTYLEDPRIQFHYDKTLPELKHIPDVYTSSIPPLKHPSQYEGVFCTDGSA IKSPDPTKSNNAGMGIVHAIYNPEYKILNQWSIPLGHHTAQMAEIAAVEFACKKALKVPGPVLVITDSFYVAESANKELPYWKSNGFVNNKKEPLKHISK WKSIAECLSIKPDITIQHEKGHQPINTSIHTEGNALADKLATQGSYVVN
SFVCP_Q87040_2mut	8,118	MNPLQLLQPLPAEVKGTKLLAHWNSGATITCIPESFLEDEQPIKQTLIKTIHGEKQQNVYYLTFKVKGRKVEAEVIASPYEYILLSPTDVPWLTQQPLQLTI LVPLQEYQDRILNKTALPEEQKQQLKALFTKYDNLWQHWENQVGHRKIRPHNIATGDYPPRPQKQYPINPKAKPSIQIVIDDLLKQGVLTPQNSTMNTP VYPVPKPDGRWRMVLDYREVNKTIPLTAAQNQHSAGILATIVRQKYKTTLDLANGFWAHPITPDSYWLTAFTWQGKQYCWTRLPQGFLNSPALFNAD AVDLLKEVPNVQVYVDDIYLSHDNPHEHIQQLEKVFQILLQAGYVVSLKKSEIGQRTVEFLGFNITKEGRGLTDTFKTKLLNVTPPKDLKQLQSILGLLNF ARNFIPNFAELVQTLYNLIASSPGKYIEWTEDNTKQLNKVIEALNTASNLEERLPDQRLVIKVNTSPSAGYVRYYNESGKKPIMYLNYVFSKAELKFSMLE KLLTTMHKALIKAMDLAMGQEILVYSPIVSMTKIQKTPLPERKALPIRWITWMTYLEDPRIQFHYDKTLPELKHIPDVYTSSIPPLKHPSQYEGVFCTDGSA IKSPDPTKSNNAGMGIVHAIYNPEYKILNQWSIPLGHHTAQMAEIAAVEFACKKALKVPGPVLVITDSFYVAESANKELPYWKSNGFVNNKKEPLKHISK WKSIAECLSIKPDITIQHEKGHQPINTSIHTEGNALADKLATQGSYVVN
SFVCP_Q87040_2mutA	8,119	MNPLQLLQPLPAEVKGTKLLAHWNSGATITCIPESFLEDEQPIKQTLIKTIHGEKQQNVYYLTFKVKGRKVEAEVIASPYEYILLSPTDVPWLTQQPLQLTI LVPLQEYQDRILNKTALPEEQKQQLKALFTKYDNLWQHWENQVGHRKIRPHNIATGDYPPRPQKQYPINPKAKPSIQIVIDDLLKQGVLTPQNSTMNTP VYPVPKPDGRWRMVLDYREVNKTIPLTAAQNQHSAGILATIVRQKYKTTLDLANGFWAHPITPDSYWLTAFTWQGKQYCWTRLPQGFLNSPALFNAD AVDLLKEVPNVQVYVDDIYLSHDNPHEHIQQLEKVFQILLQAGYVVSLKKSEIGQRTVEFLGFNITKEGRGLTDTFKTKLLNVTPPKDLKQLQSILGLLNF ARNFIPNFAELVQTLYNLIASSPGKYIEWTEDNTKQLNKVIEALNTASNLEERLPDQRLVIKVNTSPSAGYVRYYNESGKKPIMYLNYVFSKAELKFSMLE KLLTTMHKALIKAMDLAMGQEILVYSPIVSMTKIQKTPLPERKALPIRWITWMTYLEDPRIQFHYDKTLPELKHIPDVYTSSIPPLKHPSQYEGVFCTDGSA IKSPDPTKSNNAGMGIVHAIYNPEYKILNQWSIPLGHHTAQMAEIAAVEFACKKALKVPGPVLVITDSFYVAESANKELPYWKSNGFVNNKKEPLKHISK WKSIAECLSIKPDITIQHEKGHQPINTSIHTEGNALADKLATQGSYVVN
SFVCP_Q87040-Pro	8,120	VPWLTQQPLQLTILVPLQEYQDRILNKTALPEEQKQQLKALFTKYDNLWQHWENQVGHRKIRPHNIATGDYPPRPQKQYPINPKAKPSIQIVIDDLLKQG VLTPQNSTMNTPVYPVPKPDGRWRMVLDYREVNKTIPLTAAQNQHSAGILATIVRQKYKTTLDLANGFWAHPITPDSYWLTAFTWQGKQYCWTRLPQ GFLNSPALFTADAVDLLKEVPNVQVYVDDIYLSHDNPHEHIQQLEKVFQILLQAGYVVSLKKSEIGQRTVEFLGFNITKEGRGLTDTFKTKLLNVTPPKDL KQLQSILGLLNFARNFIPNFAELVQTLYNLIASSKGKYIEWTEDNTKQLNKVIEALNTASNLEERLPDQRLVIKVNTSPSAGYVRYYNESGKKPIMYLNYV FSKAELKFSMLEKLLTTMHKALIKAMDLAMGQEILVYSPIVSMTKIQKTPLPERKALPIRWITWMTYLEDPRIQFHYDKTLPELKHIPDVYTSSIPPLKHPS QYEGVFCTDGSAIKSPDPTKSNNAGMGIVHAIYNPEYKILNQWSIPLGHHTAQMAEIAAVEFACKKALKVPGPVLVITDSFYVAESANKELPYWKSNGF VNNKKEPLKHISKWKSIAECLSIKPDITIQHEKGHQPINTSIHTEGNALADKLATQGSYVVN
SFVCP_Q87040-Pro_2mut	8,121	VPWLTQQPLQLTILVPLQEYQDRILNKTALPEEQKQQLKALFTKYDNLWQHWENQVGHRKIRPHNIATGDYPPRPQKQYPINPKAKPSIQIVIDDLLKQG VLTPQNSTMNTPVYPVPKPDGRWRMVLDYREVNKTIPLTAAQNQHSAGILATIVRQKYKTTLDLANGFWAHPITPDSYWLTAFTWQGKQYCWTRLPQ GFLNSPALFNADAVDLLKEVPNVQVYVDDIYLSHDNPHEHIQQLEKVFQILLQAGYVVSLKKSEIGQRTVEFLGFNITKEGRGLTDTFKTKLLNVTPPKDL KQLQSILGLLNFARNFIPNFAELVQTLYNLIASSPGKYIEWTEDNTKQLNKVIEALNTASNLEERLPDQRLVIKVNTSPSAGYVRYYNESGKKPIMYLNYV FSKAELKFSMLEKLLTTMHKALIKAMDLAMGQEILVYSPIVSMTKIQKTPLPERKALPIRWITWMTYLEDPRIQFHYDKTLPELKHIPDVYTSSIPPLKHPS QYEGVFCTDGSAIKSPDPTKSNNAGMGIVHAIYNPEYKILNQWSIPLGHHTAQMAEIAAVEFACKKALKVPGPVLVITDSFYVAESANKELPYWKSNGF VNNKKEPLKHISKWKSIAECLSIKPDITIQHEKGHQPINTSIHTEGNALADKLATQGSYVVN
SFVCP_Q87040-Pro_2mutA	8,122	VPWLTQQPLQLTILVPLQEYQDRILNKTALPEEQKQQLKALFTKYDNLWQHWENQVGHRKIRPHNIATGDYPPRPQKQYPINPKAKPSIQIVIDDLLKQG VLTPQNSTMNTPVYPVPKPDGRWRMVLDYREVNKTIPLTAAQNQHSAGILATIVRQKYKTTLDLANGFWAHPITPDSYWLTAFTWQGKQYCWTRLPQ GFLNSPALFNADAVDLLKEVPNVQVYVDDIYLSHDNPHEHIQQLEKVFQILLQAGYVVSLKKSEIGQRTVEFLGFNITKEGRGLTDTFKTKLLNVTPPKDL KQLQSILGKLNFARNFIPNFAELVQTLYNLIASSPGKYIEWTEDNTKQLNKVIEALNTASNLEERLPDQRLVIKVNTSPSAGYVRYYNESGKKPIMYLNYV FSKAELKFSMLEKLLTTMHKALIKAMDLAMGQEILVYSPIVSMTKIQKTPLPERKALPIRWITWMTYLEDPRIQFHYDKTLPELKHIPDVYTSSIPPLKHPS QYEGVFCTDGSAIKSPDPTKSNNAGMGIVHAIYNPEYKILNQWSIPLGHHTAQMAEIAAVEFACKKALKVPGPVLVITDSFYVAESANKELPYWKSNGF VNNKKEPLKHISKWKSIAECLSIKPDITIQHEKGHQPINTSIHTEGNALADKLATQGSYVVN
SMRVH_P03364	8,123	PRSRAIDIPVPHADKISWKITDPVWVDQWPLTYEKTLAAIALVQEQLAAGHIEPTNSPWNTPIFIIKKKSGSWRLLQDLRAVNKVMVPMGALQPGLPSPV AIPLNYHKIVIDLKDCFFTIPLHPEDRPYFAFSVPQINFQSPMPRYQWKVLPQGMANSPTLCQKFVAAAIAPVRSQWPEAYILHYMDDILLACDSAEAAK ACYAHIISCLTSYGLKIAPDKVQVSEPFSYLGFELHHQQVFTPRVCLKTDHLKTLNDFQKLLGDIQWLRPYLKLPTSALVPLNNILKGDPNPLSVRALTPE AKQSLALINKAIQNQSVQQISYNLPLVLLLLPTPHTPTAVFWQPNGTDPTKNGSPLLWLHLPASPSKVLLTYPSLLAMLIIKGRYTGRQLFGRDPHSIIIPY TQDQLTWLLQTSDEWAIALSSFTGDIDNHYPSDPVIQFAKLHQFIFPKITKCAPIPQATLVFTDGSSNGIAAYVIDNQPISIKSPYLSAQLVELYAILQVFTV LAHQPFNLYTDSAYIAQSVPLLETVPFIKSSTNATPLFSKLQQLILNRQHPFFIGHLRAHLNLPGPLAEGNALADAATQIFPIISD
SMRVH_P03364_2mut	8,124	PRSRAIDIPVPHADKISWKITDPVWVDQWPLTYEKTLAAIALVQEQLAAGHIEPTNSPWNTPIFIIKKKSGSWRLLQDLRAVNKVMVPMGALQPGLPSPV AIPLNYHKIVIDLKDCFFTIPLHPEDRPYFAFSVPQINFQSPMPRYQWKVLPQGMANSPTLCQKFVAAAIAPVRSQWPEAYILHYMDDILLACDSAEAAK ACYAHIISCLTSYGLKIAPDKVQVSEPFSYLGFELHHQQVFTPRVCLKTDHLKTLNDFQKLLGDIQWLRPYLKLPTSALVPLNNILKPDPNPLSVRALTPE AKQSLALINKAIQNQSVQQISYNLPLVLLLLPTPHTPTAVFWQPNGTDPTKNGSPLLWLHLPASPSKVLLTYPSLLAMLIIKGRYTGRQLFGRDPHSIIIPY TQDQLTWLLQTSDEWAIALSSFTGDIDNHYPSDPVIQFAKLHQFIFPKITKCAPIPQATLVFTDGSSNGIAAYVIDNQPISIKSPYLSAQLVELYAILQVFTV LAHQPFNLYTDSAYIAQSVPLLETVPFIKSSTNATPLFSKLQQLILNRQHPFFIGHLRAHLNLPGPLAEGNALADAATQIFPIISD
SMRVH_P03364_2mutB	8,125	PRSRAIDIPVPHADKISWKITDPVWVDQWPLTYEKTLAAIALVQEQLAAGHIEPTNSPWNTPIFIIKKKSGSWRLLQDLRAVNKVMVPMGALQPGLPSPV APPLNYHKIVIDLKDCFFTIPLHPEDRPYFAFSVPQINFQSPMPRYQWKVLPQGMANSPTLCQKFVAAAIAPVRSQWPEAYILHYMDDILLACDSAEAAK ACYAHIISCLTSYGLKIAPDKVQVSEPFSYLGFELHHQQVFTPRVCLKTDHLKTLNDFQKLLGDIQWLRPYLKLPTSALVPLNNILKPDPNPLSVRALTPE AKQSLALINKAIQNQSVQQISYNLPLVLLLLPTPHTPTAVFWQPNGTDPTKNGSPLLWLHLPASPSKVLLTYPSLLAMLIIKGRYTGRQLFGRDPHSIIIPY TQDQLTWLLQTSDEWAIALSSFTGDIDNHYPSDPVIQFAKLHQFIFPKITKCAPIPQATLVFTDGSSNGIAAYVIDNQPISIKSPYLSAQLVELYAILQVFTV LAHQPFNLYTDSAYIAQSVPLLETVPFIKSSTNATPLFSKLQQLILNRQHPFFIGHLRAHLNLPGPLAEGNALADAATQIFPIISD

RT Name	SEQ ID NO:	RT amino acid sequence
SRV2_P51517	8,126	LATAVDILAPQRYADPITWKSDEPVWVDQWPLTQEKLAAAQQLVQEQLQAGHIIESNSPWNTPIFVIKKKSGKWRLLQDLRAVNATMVLMGALQPGLP SPVAIPQGYFKIVIDLKDCFFTIPLQPVDQKRFAFSLPSTNFKQPMKRYQWKVLPQGMANSPTLCQKYVAAAIEPVRKSWAQMYIIHYMDDILIAGKLGE QVLQCFAQLKQALTTTGLQIAPEKVQLQDPYTYLGFQINGPKITNQKAVIRRDKLQTLNDFQKLLGDINWLRPYLHLTTGDLKPLFDILKGDSNPNSPRS LSEAALASLQKVETAIAEQFVTQIDYTQPLTFLIFNTTLTPTGLFWQNNPVMWVHLPASPKKVLLPYYDAIADLIILGRDNSKKYFGLEPSTIIQPYSKSQIH WLMQNTETWPIACASYAGNIDNHYPPNKLIQFCKLHAVVFPRIISKTPLDNALLVFTDGSSTGIAAYTFEKTTVRFKTSHTSAQLVELQALIAVLSAFPHR ALNVYTDSAYLAHSIPLLETVSHIKHISDTAKFFLQCQQLIYNRSIPFYLGHIRAHSGLPGPLSQGNHITDLATKVVATTLTT
SRV2_P51517_2mutB	8,127	LATAVDILAPQRYADPITWKSDEPVWVDQWPLTQEKLAAAQQLVQEQLQAGHIIESNSPWNTPIFVIKKKSGKWRLLQDLRAVNATMVLMGALQPGLP SPVAPPQGYFKIVIDLKDCFFTIPLQPVDQKRFAFSLPSTNFKQPMKRYQWKVLPQGMANSPTLCQKYVAAAIEPVRKSWAQMYIIHYMDDILIAGKLGE QVLQCFAQLKQALTTTGLQIAPEKVQLQDPYTYLGFQINGPKITNQKAVIRRDKLQTLNDFQKLLGDINWLRPYLHLTTGDLKPLFDILKGDSNPNSPRS LSEAALASLQKVETAIAEQFVTQIDYTQPLTFLIFNTTLTPTGLFWQNNPVMWVHLPASPKKVLLPYYDAIADLIILGRDNSKKYFGLEPSTIIQPYSKSQIH WLMQNTETWPIACASYAGNIDNHYPPNKLIQFCKLHAVVFPRIISKTPLDNALLVFTDGSSTGIAAYTFEKTTVRFKTSHTSAQLVELQALIAVLSAFPHR ALNVYTDSAYLAHSIPLLETVSHIKHISDTAKFFLQCQQLIYNRSIPFYLGHIRAHSGLPGPLSQGNHITDLATKVVATTLTT
WDSV_O92815	8,128	SCQTKNTLNIDEYLLQFPDQLWASLPTDIGRMLVPPITIKIKDNASLPSIRQYPLPKDKTEGLRPLISSLENQGILIKCHSPCNTPIFPIKKAGRDEYRMIHD LRAINNIVAPLTAVVASPTTVLSNLAPSLHWFTVIDLSNAFFSVPIHKDSQYLFAFTFEGHQYTWTVLPQGFIHSPTLFSQALYQSLHKIKFKISSEICIYMD DVLIASKDRDTNLKDTAVMLQHLASEGHKVSKKKLQLCQQEVVYLGQLLTPEGRKILPDRKVTVSQFQQPTTIRQIRAFLGLVGYCRHWIPEFSIHSKFL EKQLKKDTAEPFQLDDQQVEAFNKLKHAITTAPVLVVPDPAKPFQLYTSHSEHASIAVLTQKHAGRTRPIAFLSSKFDAIESGLPPCLKACASIHRSLTQA DSFILGAPLIIYTTHAICTLLQRDRSQLVTASRFSKWEADLLRPELTFVACSAVSPAHLYMQSCENNIPPHDCVLLTHTISRPRPDLSDLPIPDPDMTLFSD GSYTTGRGGAAVVMHRPVTDDFIIIHQQPGGASAQTAELLALAAACHLATDKTVNIYTDSRYAYGVVHDFGHLWMHRGFVTSAGTPIKNHKEIEYLLKQ IMKPKQVSVIKIEAHTKGVSMEVRGNAAADEAAKNAVFLVQR
WDSV_O92815_2mut	8,129	SCQTKNTLNIDEYLLQFPDQLWASLPTDIGRMLVPPITIKIKDNASLPSIRQYPLPKDKTEGLRPLISSLENQGILIKCHSPCNTPIFPIKKAGRDEYRMIHD LRAINNIVAPLTAVVASPTTVLSNLAPSLHWFTVIDLSNAFFSVPIHKDSQYLFAFTFEGHQYTWTVLPQGFIHSPTLFNQALYQSLHKIKFKISSEICIYMD DVLIASKDRDTNLKDTAVMLQHLASEGHKVSKKKLQLCQQEVVYLGQLLTPEGRKILPDRKVTVSQFQQPTTIRQIRAFLGLVGYCRHWIPEFSIHSKFL EKQLKPDTAEPFQLDDQQVEAFNKLKHAITTAPVLVVPDPAKPFQLYTSHSEHASIAVLTQKHAGRTRPIAFLSSKFDAIESGLPPCLKACASIHRSLTQA DSFILGAPLIIYTTHAICTLLQRDRSQLVTASRFSKWEADLLRPELTFVACSAVSPAHLYMQSCENNIPPHDCVLLTHTISRPRPDLSDLPIPDPDMTLFSD GSYTTGRGGAAVVMHRPVTDDFIIIHQQPGGASAQTAELLALAAACHLATDKTVNIYTDSRYAYGVVHDFGHLWMHRGFVTSAGTPIKNHKEIEYLLKQ IMKPKQVSVIKIEAHTKGVSMEVRGNAAADEAAKNAVFLVQR
WDSV_O92815_2mutA	8,130	SCQTKNTLNIDEYLLQFPDQLWASLPTDIGRMLVPPITIKIKDNASLPSIRQYPLPKDKTEGLRPLISSLENQGILIKCHSPCNTPIFPIKKAGRDEYRMIHD LRAINNIVAPLTAVVASPTTVLSNLAPSLHWFTVIDLSNAFFSVPIHKDSQYLFAFTFEGHQYTWTVLPQGFIHSPTLFNQALYQSLHKIKFKISSEICIYMD DVLIASKDRDTNLKDTAVMLQHLASEGHKVSKKKLQLCQQEVVYLGQLLTPEGRKILPDRKVTVSQFQQPTTIRQIRAFLGKVGYCRHFIPEFSIHSKFL EKQLKPDTAEPFQLDDQQVEAFNKLKHAITTAPVLVVPDPAKPFQLYTSHSEHASIAVLTQKHAGRTRPIAFLSSKFDAIESGLPPCLKACASIHRSLTQA DSFILGAPLIIYTTHAICTLLQRDRSQLVTASRFSKWEADLLRPELTFVACSAVSPAHLYMQSCENNIPPHDCVLLTHTISRPRPDLSDLPIPDPDMTLFSD GSYTTGRGGAAVVMHRPVTDDFIIIHQQPGGASAQTAELLALAAACHLATDKTVNIYTDSRYAYGVVHDFGHLWMHRGFVTSAGTPIKNHKEIEYLLKQ IMKPKQVSVIKIEAHTKGVSMEVRGNAAADEAAKNAVFLVQR
WMSV_P03359	8,131	VLNLEEEYRLHEKPVPSSIDPSWLQLFPTVWAERAGMGLANQVPPVVVELRSGASPVAVRQYPMSKEAREGIRPHIQRFLDLGVLVPCQSPWNTPLL PVKKPGTNDYRPVQDLREINKRVQDIHPTVPNPYNLLSSLPPSHTWYSVLDLKDAFFCLKLHPNSQPLFAFEWRDPEKGNTGQLTWTRLPQGFKNSP TLFDEALHRDLAPFRALNPQVVLLQYVDDLLVAAPTYRDCKEGTQKLLQELSKLGYRVSAKKAQLCQKEVTYLGYLLKEGKRWLTPARKATVMKIPPP TTPRQVREFLGTAGFCRLWIPGFASLAAPLYPLTKESIPFIWTEEHQKAFDRIKEALLSAPALALPDLTKPFTLYVDERAGVARGVLTQTLGPWRRPVAY LSKKLDPVASGWPTCLKAVAAVALLLKDADKLTLGQNVTVIASHSLESIVRQPPDRWMTNARMTHYQSLLLNERVSFAPPAVLNPATLLPVESEATPVH RCSEILAEETGTRRDLKDQPLPGVPAWYTDGSSFIAEGKRRAGAAIVDGKRTVWASSLPEGTSAQKAELVALTQALRLAEGKDINIYTDSRYAFATAHI HGAIYKQRGLLTSAGKDIKNKEEILALLEAIHLPKRVAIIHCPGHQKGNDPVATGNRRADEAAKQAALSTRVLAETTKP
WMSV_P03359_3mut	8,132	VLNLEEEYRLHEKPVPSSIDPSWLQLFPTVWAERAGMGLANQVPPVVVELRSGASPVAVRQYPMSKEAREGIRPHIQRFLDLGVLVPCQSPWNTPLL PVKKPGTNDYRPVQDLREINKRVQDIHPTVPNPYNLLSSLPPSHTWYSVLDLKDAFFCLKLHPNSQPLFAFEWRDPEKGNTGQLTWTRLPQGFKNSP TLFNEALHRDLAPFRALNPQVVLLQYVDDLLVAAPTYRDCKEGTQKLLQELSKLGYRVSAKKAQLCQKEVTYLGYLLKEGKRWLTPARKATVMKIPPP TTPRQVREFLGTAGFCRLWIPGFASLAAPLYPLTKPSIPFIWTEEHQKAFDRIKEALLSAPALALPDLTKPFTLYVDERAGVARGVLTQTLGPWRRPVAY LSKKLDPVASGWPTCLKAVAAVALLLKDADKLTLGQNVTVIASHSLESIVRQPPDRWMTNARMTHYQSLLLNERVSFAPPAVLNPATLLPVESEATPVH RCSEILAEETGTRRDLKDQPLPGVPAWYTDGSSFIAEGKRRAGAAIVDGKRTVWASSLPEGTSAQKAELVALTQALRLAEGKDINIYTDSRYAFATAHI HGAIYKQRGWLTSAGKDIKNKEEILALLEAIHLPKRVAIIHCPGHQKGNDPVATGNRRADEAAKQAALSTRVLAETTKP
WMSV_P03359_3mutA	8,133	VLNLEEEYRLHEKPVPSSIDPSWLQLFPTVWAERAGMGLANQVPPVVVELRSGASPVAVRQYPMSKEAREGIRPHIQRFLDLGVLVPCQSPWNTPLL PVKKPGTNDYRPVQDLREINKRVQDIHPTVPNPYNLLSSLPPSHTWYSVLDLKDAFFCLKLHPNSQPLFAFEWRDPEKGNTGQLTWTRLPQGFKNSP TLFNEALHRDLAPFRALNPQVVLLQYVDDLLVAAPTYRDCKEGTQKLLQELSKLGYRVSAKKAQLCQKEVTYLGYLLKEGKRWLTPARKATVMKIPPP TTPRQVREFLGKAGFCRLFIPGFASLAAPLYPLTKPSIPFIWTEEHQKAFDRIKEALLSAPALALPDLTKPFTLYVDERAGVARGVLTQTLGPWRRPVAY LSKKLDPVASGWPTCLKAVAAVALLLKDADKLTLGQNVTVIASHSLESIVRQPPDRWMTNARMTHYQSLLLNERVSFAPPAVLNPATLLPVESEATPVH RCSEILAEETGTRRDLKDQPLPGVPAWYTDGSSFIAEGKRRAGAAIVDGKRTVWASSLPEGTSAQKAELVALTQALRLAEGKDINIYTDSRYAFATAHI HGAIYKQRGWLTSAGKDIKNKEEILALLEAIHLPKRVAIIHCPGHQKGNDPVATGNRRADEAAKQAALSTRVLAETTKP
XMRV6_A1Z651	8,134	TLNIEDEYRLHETSKEPDVPLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLP VKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPT LFDEALHRDLADFRIQHPDLILLQYVDDLLLAATSEQDCQRGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPK TPRQLREFLGTAGFCRLWIPGFAEMAAPLYPLTKTGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVA YLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEKEA PHDCLEILAETHGTRPDLTDQPIPDADYTWYTDGSSFLQEGQRRAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFAT AHVHGEIYRRRGLLTSEGREIKNKNEILALLKALFLPKRLSIIHCPGHQKGNSAEARGNRMADQAARE AAMKAVLETSTLL
XMRV6_A1Z651_3mut	8,135	TLNIEDEYRLHETSKEPDVPLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLP VKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPT LFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSEQDCQRGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPK TPRQLREFLGTAGFCRLWIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPV AYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEKE

RT Name	SEQ ID NO:	RT amino acid sequence
		APHDCLEILAETHGTRPDLTDQPIPDADYTWYTDGSSFLQEGQRRAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAF ATAHVHGEIYRRRGWLTSEGREIKNKNEILALLKALFLPKRLSIIHCPGHQKGNSAEARGNRMADQAAREAAMKAVLETSTLL
XMRV6_A1Z651_3mutA	8,136	TLNIEDEYRLHETSKEPDVPLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLP VKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPT LFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSEQDCQRGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPK TPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVA YLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEKEA PHDCLEILAETHGTRPDLTDQPIPDADYTWYTDGSSFLQEGQRRAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFAT AHVHGEIYRRRGWLTSEGREIKNKNEILALLKALFLPKRLSIIHCPGHQKGNSAEARGNRMADQAAREAAMKAVLETSTLL

In some embodiments, reverse transcriptase domains are modified, for example by site-specific mutation. In some embodiments, reverse transcriptase domains are engineered to have improved properties, e.g. SuperScript IV (SSIV) reverse transcriptase derived from the MMLV RT. In some embodiments, the reverse transcriptase domain may be engineered to have lower error rates, e.g., as described in WO2001068895, incorporated herein by reference. In some embodiments, the reverse transcriptase domain may be engineered to be more thermostable. In some embodiments, the reverse transcriptase domain may be engineered to be more processive. In some embodiments, the reverse transcriptase domain may be engineered to have tolerance to inhibitors. In some embodiments, the reverse transcriptase domain may be engineered to be faster. In some embodiments, the reverse transcriptase domain may be engineered to better tolerate modified nucleotides in the RNA template. In some embodiments, the reverse transcriptase domain may be engineered to insert modified DNA nucleotides. In some embodiments, the reverse transcriptase domain is engineered to bind a template RNA. In some embodiments, one or more mutations are chosen from D200N, L603W, T330P, D524G, E562Q, D583N, P51L, S67R, E67K, T197A, H204R, E302K, F309N, W313F, L435G, N454K, H594Q, L671P, E69K, H8Y, T306K, or D653N in the RT domain of murine leukemia virus reverse transcriptase or a corresponding mutation at a corresponding position of another RT domain.

In some embodiments, a gene modifying polypeptide comprises the RT domain from a retroviral reverse transcriptase, e.g., a wild-type M-MLV RT, e.g., comprising the following sequence:

M-MLV (WT):

TLNIEDEYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSI KQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNK

RVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGIS
GQLTWTRLPQGFKNSPTLFDEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQG
TRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKT
PRQLREFLGTAGFCRLWIPGFAEMAAPLYPLTKTGTLFNWGPDQQKAYQEIKQALLTAP
ALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRM
VAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDR
VQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDGSSL
LQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRY
AFATAHIHGEIYRRRGLLTSEGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEAR
GNRMADQAARKAAITETPDTSTLLI (SEQ ID NO: 5002)

In some embodiments, a gene modifying polypeptide comprises the RT domain from a retroviral reverse transcriptase, e.g., an M-MLV RT, e.g., comprising the following sequence:
TLNIEDEHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSI
KQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNK
RVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGIS
GQLTWTRLPQGFKNSPTLFDEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQG
TRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKT
PRQLREFLGTAGFCRLWIPGFAEMAAPLYPLTKTGTLFNWGPDQQKAYQEIKQALLTAP
ALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRM
VAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDR
VQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDGSSL
LQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRY
AFATAHIHGEIYRRRGLLTSEGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEAR
GNRMADQAARKAAITETPDTSTLL (SEQ ID NO: 5003)

In some embodiments, a gene modifying polypeptide comprises the RT domain from a retroviral reverse transcriptase comprising the sequence of amino acids 659-1329 of NP_057933. In embodiments, the gene modifying polypeptide further comprises one additional amino acid at the N-terminus of the sequence of amino acids 659-1329 of NP_057933, e.g., as shown below:

TLNIEDEHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSI
KQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLP**VKKPGTNDYRPVQDLREVN**
KRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDP
EMGISGQLTWTRLPQGFKNSPTLFDEALHRDLADFRIQHPDLILLQYVDDLLLAAT
SELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKE
TVMGQPTPKTPRQLREFLGTAGFCRLWIPGFAEMAAPLYPLTKTGTLFNWGPDQQKAY
QEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPV
AAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTH
YQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDAD
HTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGK
KLNVYTDSRYAFATAHIHGEIYRRRGLLTSEGKEIKNKDEILALLKALFLPKRLSIIHCPG
HQKGHSAEARGNRMADQAARKAA (SEQ ID NO: 5004)

Core RT (bold), annotated per above
RNAseH (underlined), annotated per above

In embodiments, the gene modifying polypeptide further comprises one additional amino acid at the C-terminus of the sequence of amino acids 659-1329 of NP_057933. In embodiments, the gene modifying polypeptide comprises an RNaseH1 domain (e.g., amino acids 1178-1318 of NP_057933).

In some embodiments, a retroviral reverse transcriptase domain, e.g., M-MLV RT, may comprise one or more mutations from a wild-type sequence that may improve features of the RT, e.g., thermostability, processivity, and/or template binding. In some embodiments, an M-MLV RT domain comprises, relative to the M-MLV (WT) sequence above, one or more mutations, e.g., selected from D200N, L603W, T330P, T306K, W313F, D524G, E562Q, D583N, P51L, S67R, E67K, T197A, H204R, E302K, F309N, L435G, N454K, H594Q, D653N, R110S, K103L, e.g., a combination of mutations, such as D200N, L603W, and T330P, optionally further including T306K and W313F. In some embodiments, an M-MLV RT used herein comprises the mutations D200N, L603W, T330P, T306K and W313F. In embodiments, the mutant M-MLV RT comprises the following amino acid sequence:

M-MLV (PE2):

TLNIEDEYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSI
KQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNK
RVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGIS
GQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQG

TRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKT
PRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAP
ALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRM
VAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDR
VQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDGSSL
LQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRY
AFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEAR
GNRMADQAARKAAITETPDTSTLLI (SEQ ID NO: 5005)

In some embodiments, a writing domain (e.g., RT domain) comprises an RNA-binding domain, e.g., that specifically binds to an RNA sequence. In some embodiments, a template RNA comprises an RNA sequence that is specifically bound by the RNA-binding domain of the writing domain.

In some embodiments, the reverse transcription domain only recognizes and reverse transcribes a specific template, e.g., a template RNA of the system. In some embodiments, the template comprises a sequence or structure that enables recognition and reverse transcription by a reverse transcription domain. In some embodiments, the template comprises a sequence or structure that enables association with an RNA-binding domain of a polypeptide component of a genome engineering system described herein. In some embodiments, the genome engineering system reverse preferably transcribes a template comprising an association sequence over a template lacking an association sequence.

The writing domain may also comprise DNA-dependent DNA polymerase activity, e.g., comprise enzymatic activity capable of writing DNA into the genome from a template DNA sequence. In some embodiments, DNA-dependent DNA polymerization is employed to complete second-strand synthesis of a target site edit. In some embodiments, the DNA-dependent DNA polymerase activity is provided by a DNA polymerase domain in the polypeptide. In some embodiments, the DNA-dependent DNA polymerase activity is provided by a reverse transcriptase domain that is also capable of DNA-dependent DNA polymerization, e.g., second-strand synthesis. In some embodiments, the DNA-dependent DNA polymerase activity is provided by a second polypeptide of the system. In some embodiments, the DNA-

dependent DNA polymerase activity is provided by an endogenous host cell polymerase that is optionally recruited to the target site by a component of the genome engineering system.

In some embodiments, the reverse transcriptase domain has a lower probability of premature termination rate (P_{off}) *in vitro* relative to a reference reverse transcriptase domain. In some embodiments, the reference reverse transcriptase domain is a viral reverse transcriptase domain, e.g., the RT domain from M-MLV.

In some embodiments, the reverse transcriptase domain has a lower probability of premature termination rate (P_{off}) *in vitro* of less than about 5×10^{-3}/nt, 5×10^{-4}/nt, or 5×10^{-6}/nt, e.g., as measured on a 1094 nt RNA. In embodiments, the *in vitro* premature termination rate is determined as described in Bibillo and Eickbush (2002) J Biol Chem 277(38):34836-34845 (incorporated by reference herein its entirety).

In some embodiments, the reverse transcriptase domain is able to complete at least about 30% or 50% of integrations in cells. The percent of complete integrations can be measured by dividing the number of substantially full-length integration events (e.g., genomic sites that comprise at least 98% of the expected integrated sequence) by the number of total (including substantially full-length and partial) integration events in a population of cells. In embodiments, the integrations in cells is determined (e.g., across the integration site) using long-read amplicon sequencing, e.g., as described in Karst et al. (2020) *bioRxiv* doi.org/10.1101/645903 (incorporated by reference herein in its entirety).

In embodiments, quantifying integrations in cells comprises counting the fraction of integrations that contain at least about 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% of the DNA sequence corresponding to the template RNA (e.g., a template RNA having a length of at least 0.05, 0.1, 0.5, 0.6, 0.7, 0.8, 0.9, 1, 1.5, 2, 3, 4, or 5 kb, e.g., a length between 0.5-0.6, 0.6-0.7, 0.7-0.8, 0.8-0.9, 1.0-1.2, 1.2-1.4, 1.4-1.6, 1.6-1.8, 1.8-2.0, 2-3, 3-4, or 4-5 kb).

In some embodiments, the reverse transcriptase domain is capable of polymerizing dNTPs *in vitro*. In embodiments, the reverse transcriptase domain is capable of polymerizing dNTPs *in vitro* at a rate between 0.1 – 50 nt/sec (e.g., between 0.1-1, 1-10, or 10-50 nt/sec). In embodiments, polymerization of dNTPs by the reverse transcriptase domain is measured by a single-molecule assay, e.g., as described in Schwartz and Quake (2009) *PNAS* 106(48):20294-20299 (incorporated by reference in its entirety).

In some embodiments, the reverse transcriptase domain has an *in vitro* error rate (e.g., misincorporation of nucleotides) of between $1 \times 10^{-3} – 1 \times 10^{-4}$ or $1 \times 10^{-4} – 1 \times 10^{-5}$ substitutions/nt , e.g., as described in Yasukawa et al. (2017) *Biochem Biophys Res Commun* 492(2):147-153 (incorporated herein by reference in its entirety). In some embodiments, the reverse transcriptase domain has an error rate (e.g., misincorporation of nucleotides) in cells (e.g., HEK293T cells) of between $1 \times 10^{-3} – 1 \times 10^{-4}$ or $1 \times 10^{-4} – 1 \times 10^{-5}$ substitutions/nt, e.g., by long-read amplicon sequencing, e.g., as described in Karst et al. (2020) *bioRxiv* doi.org/10.1101/645903 (incorporated by reference herein in its entirety).

In some embodiments, the reverse transcriptase domain is capable of performing reverse transcription of a target RNA *in vitro*. In some embodiments, the reverse transcriptase requires a primer of at least 3 nucleotides to initiate reverse transcription of a template. In some embodiments, reverse transcription of the target RNA is determined by detection of cDNA from the target RNA (e.g., when provided with a ssDNA primer, e.g., which anneals to the target with at least 3, 4, 5, 6, 7, 8, 9, or 10 nt at the 3´ end), e.g., as described in Bibillo and Eickbush (2002) *J Biol Chem* 277(38):34836-34845 (incorporated herein by reference in its entirety).

In some embodiments, the reverse transcriptase domain performs reverse transcription at least 5 or 10 times more efficiently (e.g., by cDNA production), e.g., when converting its RNA template to cDNA, for example, as compared to an RNA template lacking the protein binding motif (e.g., a 3´ UTR). In embodiments, efficiency of reverse transcription is measured as described in Yasukawa et al. (2017) *Biochem Biophys Res Commun* 492(2):147-153 (incorporated by reference herein in its entirety).

In some embodiments, the reverse transcriptase domain specifically binds a specific RNA template with higher frequency (e.g., about 5 or 10-fold higher frequency) than any endogenous cellular RNA, e.g., when expressed in cells (e.g., HEK293T cells). In embodiments, frequency of specific binding between the reverse transcriptase domain and the template RNA are measured by CLIP-seq, e.g., as described in Lin and Miles (2019) *Nucleic Acids Res* 47(11):5490-5501 (incorporated herein by reference in its entirety).

In some embodiments, an RT domain (e.g., as listed in Table 6) comprises one or more mutations as listed in Table 2 below. In some embodiment, an RT domain as listed in Table 6 comprises one, two, three, four, five, or six of the mutations listed in the corresponding row of Table 2 below.

Table 2. Exemplary RT domain mutations (relative to corresponding wild-type sequences as listed in the corresponding row of Table 6)

RT Domain Name	Mutation(s)					
AVIRE_P03360						
AVIRE_P03360_3mut	D200N	G330P	L605W			
AVIRE_P03360_3mutA	D200N	G330P	L605W	T306K	W313F	
BAEVM_P10272						
BAEVM_P10272_3mut	D198N	E328P	L602W			
BAEVM_P10272_3mutA	D198N	E328P	L602W	T304K	W311F	
BLVAU_P25059						
BLVAU_P25059_2mut	E159Q	G286P				
BLVJ_P03361						
BLVJ_P03361_2mut	E159Q	L524W				
BLVJ_P03361_2mutB	E159Q	L524W	I97P			
FFV_O93209	D21N					
FFV_O93209_2mut	D21N	T293N	T419P			
FFV_O93209_2mutA	D21N	T293N	T419P	L393K		
FFV_O93209-Pro						
FFV_O93209-Pro_2mut	T207N	T333P				
FFV_O93209-Pro_2mutA	T207N	T333P	L307K			
FLV_P10273						
FLV_P10273_3mut	D199N	L602W				
FLV_P10273_3mutA	D199N	L602W	T305K	W312F		
FOAMV_P14350	D24N					
FOAMV_P14350_2mut	D24N	T296N	S420P			
FOAMV_P14350_2mutA	D24N	T296N	S420P	L396K		
FOAMV_P14350-Pro						
FOAMV_P14350-Pro_2mut	T207N	S331P				
FOAMV_P14350-Pro_2mutA	T207N	S331P	L307K			
GALV_P21414						
GALV_P21414_3mut	D198N	E328P	L600W			
GALV_P21414_3mutA	D198N	E328P	L600W	T304K	W311F	
HTL1A_P03362						
HTL1A_P03362_2mut	E152Q	R279P				
HTL1A_P03362_2mutB	E152Q	R279P	L90P			
HTL1C_P14078						
HTL1C_P14078_2mut	E152Q	R279P				
HTL1L_P0C211						

HTL1L_P0C211_2mut	E149Q	L527W				
HTL1L_P0C211_2mutB	E149Q	L527W	L87P			
HTL32_Q0R5R2						
HTL32_Q0R5R2_2mut	E149Q	L526W				
HTL32_Q0R5R2_2mutB	E149Q	L526W	L87P			
HTL3P_Q4U0X6						
HTL3P_Q4U0X6_2mut	E149Q	L526W				
HTL3P_Q4U0X6_2mutB	E149Q	L526W	L87P			
HTLV2_P03363_2mut	E147Q	G274P				
JSRV_P31623						
JSRV_P31623_2mutB	A100P					
KORV_Q9TTC1	D32N					
KORV_Q9TTC1_3mut	D32N	D322N	E452P	L724W		
KORV_Q9TTC1_3mutA	D32N	D322N	E452P	L724W	T428K	W435F
KORV_Q9TTC1-Pro						
KORV_Q9TTC1-Pro_3mut	D231N	E361P	L633W			
KORV_Q9TTC1-Pro_3mutA	D231N	E361P	L633W	T337K	W344F	
MLVAV_P03356						
MLVAV_P03356_3mut	D200N	T330P	L603W			
MLVAV_P03356_3mutA	D200N	T330P	L603W	T306K	W313F	
MLVBM_Q7SVK7						
MLVBM_Q7SVK7						
MLVBM_Q7SVK7_3mut	D200N	T330P	L603W			
MLVBM_Q7SVK7_3mut	D200N	T330P	L603W			
MLVBM_Q7SVK7_3mutA_WS	D199N	T329P	L602W	T305K	W312F	
MLVBM_Q7SVK7_3mutA_WS	D199N	T329P	L602W	T305K	W312F	
MLVCB_P08361						
MLVCB_P08361_3mut	D200N	T330P	L603W			
MLVCB_P08361_3mutA	D200N	T330P	L603W	T306K	W313F	
MLVF5_P26810						
MLVF5_P26810_3mut	D200N	T330P	L603W			
MLVF5_P26810_3mutA	D200N	T330P	L603W	T306K	W313F	
MLVFF_P26809_3mut	D200N	T330P	L603W			
MLVFF_P26809_3mutA	D200N	T330P	L603W	T306K	W313F	
MLVMS_P03355						
MLVMS_P03355						
MLVMS_P03355_3mut	D200N	T330P	L603W			
MLVMS_P03355_3mut	D200N	T330P	L603W			
MLVMS_P03355_3mutA_WS	D200N	T330P	L603W	T306K	W313F	

MLVMS_P03355_3mutA_WS	D200N	T330P	L603W	T306K	W313F	
MLVMS_P03355_PLV919	D200N	T330P	L603W	T306K	W313F	H8Y
MLVMS_P03355_PLV919	D200N	T330P	L603W	T306K	W313F	H8Y
MLVRD_P11227						
MLVRD_P11227_3mut	D200N	T330P	L603W			
MMTVB_P03365	D26N					
MMTVB_P03365	D26N					
MMTVB_P03365_2mut	D26N	G401P				
MMTVB_P03365_2mut_WS	G400P					
MMTVB_P03365_2mut_WS	G400P					
MMTVB_P03365_2mutB	D26N	G401P	V215P			
MMTVB_P03365_2mutB	D26N	G401P	V215P			
MMTVB_P03365_2mutB_WS	G400P	V212P				
MMTVB_P03365_2mutB_WS	G400P	V212P				
MMTVB_P03365_WS						
MMTVB_P03365_WS						
MMTVB_P03365-Pro						
MMTVB_P03365-Pro						
MMTVB_P03365-Pro_2mut	G309P					
MMTVB_P03365-Pro_2mut	G309P					
MMTVB_P03365-Pro_2mutB	G309P	V123P				
MMTVB_P03365-Pro_2mutB	G309P	V123P				
MPMV_P07572						
MPMV_P07572_2mutB	G289P	I103P				
PERV_Q4VFZ2						
PERV_Q4VFZ2						
PERV_Q4VFZ2_3mut	D199N	E329P	L602W			
PERV_Q4VFZ2_3mut	D199N	E329P	L602W			
PERV_Q4VFZ2_3mutA_WS	D196N	E326P	L599W	T302K	W309F	
PERV_Q4VFZ2_3mutA_WS	D196N	E326P	L599W	T302K	W309F	
SFV1_P23074	D24N					
SFV1_P23074_2mut	D24N	T296N	N420P			
SFV1_P23074_2mutA	D24N	T296N	N420P	L396K		
SFV1_P23074-Pro						
SFV1_P23074-Pro_2mut	T207N	N331P				
SFV1_P23074-Pro_2mutA	T207N	N331P	L307K			
SFV3L_P27401	D24N					
SFV3L_P27401_2mut	D24N	T296N	N422P			
SFV3L_P27401_2mutA	D24N	T296N	N422P	L396K		

SFV3L_P27401-Pro						
SFV3L_P27401-Pro_2mut	T307N	N333P				
SFV3L_P27401-Pro_2mutA	T307N	N333P	L307K			
SFVCP_Q87040	D24N					
SFVCP_Q87040_2mut	D24N	T296N	K422P			
SFVCP_Q87040_2mutA	D24N	T296N	K422P	L396K		
SFVCP_Q87040-Pro						
SFVCP_Q87040-Pro_2mut	T207N	K333P				
SFVCP_Q87040-Pro_2mutA	T207N	K333P	L307K			
SMRVH_P03364						
SMRVH_P03364_2mut	G288P					
SMRVH_P03364_2mutB	G288P	I102P				
SRV2_P51517						
SRV2_P51517_2mutB	I103P					
WDSV_O92815						
WDSV_O92815_2mut	S183N	K312P				
WDSV_O92815_2mutA	S183N	K312P	L288K	W295F		
WMSV_P03359						
WMSV_P03359_3mut	D198N	E328P	L600W			
WMSV_P03359_3mutA	D198N	E328P	L600W	T304K	W311F	
XMRV6_A1Z651						
XMRV6_A1Z651_3mut	D200N	T330P	L603W			
XMRV6_A1Z651_3mutA	D200N	T330P	L603W	T306K	W313F	

Template nucleic acid binding domain

The gene modifying polypeptide typically contains regions capable of associating with the template nucleic acid (e.g., template RNA). In some embodiments, the template nucleic acid binding domain is an RNA binding domain. In some embodiments, the RNA binding domain is a modular domain that can associate with RNA molecules containing specific signatures, e.g., structural motifs. In other embodiments, the template nucleic acid binding domain (e.g., RNA binding domain) is contained within the reverse transcription domain, e.g., the reverse transcriptase-derived component has a known signature for RNA preference.

In other embodiments, the template nucleic acid binding domain (e.g., RNA binding domain) is contained within the target DNA binding domain. For example, in some embodiments, the DNA binding domain is a CRISPR-associated protein that recognizes the

structure of a template nucleic acid (e.g., template RNA) comprising a gRNA. In some embodiments, a gene modifying polypeptide comprises a DNA-binding domain comprising a CRISPR-associated protein that associates with a gRNA scaffold that allows the DNA-binding domain to bind a target genomic DNA sequence. In some embodiments, the gRNA scaffold and gRNA spacer is comprised within the template nucleic acid (e.g., template RNA), thus the DNA-binding domain is also the template nucleic acid binding domain. In some embodiments, the polypeptide possesses RNA binding function in multiple domains, e.g., can bind a gRNA structure in a CRISPR-associated DNA binding domain and an additional sequence or structure in a reverse transcriptase domain.

In some embodiments, the RNA binding domain is capable of binding to a template RNA with greater affinity than a reference RNA binding domain. In some embodiments, the reference RNA binding domain is an RNA binding domain from Cas9 of S. pyogenes. In some embodiments, the RNA binding domain is capable of binding to a template RNA with an affinity between 100 pM – 10 nM (e.g., between 100 pM-1 nM or 1 nM – 10 nM). In some embodiments, the affinity of a RNA binding domain for its template RNA is measured *in vitro,* e.g., by thermophoresis, e.g., as described in Asmari et al. Methods 146:107-119 (2018) (incorporated by reference herein in its entirety). In some embodiments, the affinity of a RNA binding domain for its template RNA is measured in cells (e.g., by FRET or CLIP-Seq).

In some embodiments, the RNA binding domain is associated with the template RNA *in vitro* at a frequency at least about 5-fold or 10-fold higher than with a scrambled RNA. In some embodiments, the frequency of association between the RNA binding domain and the template RNA or scrambled RNA is measured by CLIP-seq, e.g., as described in Lin and Miles (2019) *Nucleic Acids Res* 47(11):5490-5501 (incorporated by reference herein in its entirety). In some embodiments, the RNA binding domain is associated with the template RNA in cells (e.g., in HEK293T cells) at a frequency at least about 5-fold or 10-fold higher than with a scrambled RNA. In some embodiments, the frequency of association between the RNA binding domain and the template RNA or scrambled RNA is measured by CLIP-seq, e.g., as described in Lin and Miles (2019), *supra.*

Endonuclease domains and DNA binding domains

In some embodiments, a gene modifying polypeptide possesses the function of DNA target site cleavage via an endonuclease domain. In some embodiments, a gene modifying polypeptide comprises a DNA binding domain, e.g., for binding to a target nucleic acid. In some embodiments, a domain (e.g., a Cas domain) of the gene modifying polypeptide comprises two or more smaller domains, e.g., a DNA binding domain and an endonuclease domain. It is understood that when a DNA binding domain (e.g., a Cas domain) is said to bind to a target nucleic acid sequence, in some embodiments, the binding is mediated by a gRNA.

In some embodiments, a domain has two functions. For example, in some embodiments, the endonuclease domain is also a DNA-binding domain. In some embodiments, the endonuclease domain is also a template nucleic acid (e.g., template RNA) binding domain. For example, in some embodiments, a polypeptide comprises a CRISPR-associated endonuclease domain that binds a template RNA comprising a gRNA, binds a target DNA sequence (e.g., with complementarity to a portion of the gRNA), and cuts the target DNA sequence. In some embodiments, an endonuclease domain or endonuclease/DNA-binding domain from a heterologous source can be used or can be modified (e.g., by insertion, deletion, or substitution of one or more residues) in a gene modifying system described herein.

In some embodiments, a nucleic acid encoding the endonuclease domain or endonuclease/DNA binding domain is altered from its natural sequence to have altered codon usage, e.g. improved for human cells. In some embodiments, the endonuclease element is a heterologous endonuclease element, such as a Cas endonuclease (e.g., Cas9), a type-II restriction endonuclease (e.g., Fok1), a meganuclease (e.g., I-SceI), or other endonuclease domain.

In certain aspects, the DNA-binding domain of a gene modifying polypeptide described herein is selected, designed, or constructed for binding to a desired host DNA target sequence. In certain embodiments, the DNA-binding domain of the polypeptide is a heterologous DNA-binding element. In some embodiments the heterologous DNA binding element is a zinc-finger element or a TAL effector element, e.g., a zinc-finger or TAL polypeptide or functional fragment thereof. In some embodiments the heterologous DNA binding element is a sequence-guided DNA binding element, such as Cas9, Cpf1, or other CRISPR-related protein that has been altered to have no endonuclease activity. In some embodiments the heterologous DNA binding element retains endonuclease activity. In some embodiments, the heterologous DNA binding element retains partial endonuclease activity to cleave ssDNA, e.g., possesses nickase activity. In

specific embodiments, the heterologous DNA-binding domain can be any one or more of Cas9, TAL domain, ZF domain, Myb domain, combinations thereof, or multiples thereof.

In some embodiments, DNA-binding domains are modified, for example by site-specific mutation, increasing or decreasing DNA-binding elements (for example, number and/or specificity of zinc fingers), etc., to alter DNA-binding specificity and affinity. In some embodiments a nucleic acid sequence encoding the DNA binding domain is altered from its natural sequence to have altered codon usage, e.g. improved for human cells. In embodiments, the DNA binding domain comprises one or more modifications relative to a wild-type DNA binding domain, e.g., a modification via directed evolution, e.g., phage-assisted continuous evolution (PACE).

In some embodiments, the DNA binding domain comprises a meganuclease domain (e.g., as described herein, e.g., in the endonuclease domain section), or a functional fragment thereof. In some embodiments, the meganuclease domain possesses endonuclease activity, e.g., double-strand cleavage and/or nickase activity. In other embodiments, the meganuclease domain has reduced activity, e.g., lacks endonuclease activity, e.g., the meganuclease is catalytically inactive. In some embodiments, a catalytically inactive meganuclease is used as a DNA binding domain, e.g., as described in Fonfara et al. Nucleic Acids Res 40(2):847-860 (2012), incorporated herein by reference in its entirety.

In some embodiments, a gene modifying polypeptide comprises a modification to a DNA-binding domain, e.g., relative to the wild-type polypeptide. In some embodiments, the DNA-binding domain comprises an addition, deletion, replacement, or modification to the amino acid sequence of the original DNA-binding domain. In some embodiments, the DNA-binding domain is modified to include a heterologous functional domain that binds specifically to a target nucleic acid (e.g., DNA) sequence of interest. In some embodiments, the functional domain replaces at least a portion (e.g., the entirety of) the prior DNA-binding domain of the polypeptide. In some embodiments, the functional domain comprises a zinc finger (e.g., a zinc finger that specifically binds to the target nucleic acid (e.g., DNA) sequence of interest. In some embodiments, the functional domain comprises a Cas domain (e.g., a Cas domain that specifically binds to the target nucleic acid (e.g., DNA) sequence of interest. In some embodiments, the Cas domain comprises a Cas9 or a mutant or variant thereof (e.g., as described herein). In embodiments, the Cas domain is associated with a guide RNA (gRNA), e.g., as

described herein. In embodiments, the Cas domain is directed to a target nucleic acid (e.g., DNA) sequence of interest by the gRNA. In embodiments, the Cas domain is encoded in the same nucleic acid (e.g., RNA) molecule as the gRNA. In embodiments, the Cas domain is encoded in a different nucleic acid (e.g., RNA) molecule from the gRNA.

In some embodiments, the DNA binding domain is capable of binding to a target sequence (e.g., a dsDNA target sequence) with greater affinity than a reference DNA binding domain. In some embodiments, the reference DNA binding domain is a DNA binding domain from Cas9 of S. pyogenes. In some embodiments, the DNA binding domain is capable of binding to a target sequence (e.g., a dsDNA target sequence) with an affinity between 100 pM – 10 nM (e.g., between 100 pM-1 nM or 1 nM – 10 nM).

In some embodiments, the affinity of a DNA binding domain for its target sequence (e.g., dsDNA target sequence) is measured in vitro, e.g., by thermophoresis, e.g., as described in Asmari et al. Methods 146:107-119 (2018) (incorporated by reference herein in its entirety).

In embodiments, the DNA binding domain is capable of binding to its target sequence (e.g., dsDNA target sequence), e.g, with an affinity between 100 pM – 10 nM (e.g., between 100 pM-1 nM or 1 nM – 10 nM) in the presence of a molar excess of scrambled sequence competitor dsDNA, e.g., of about 100-fold molar excess.

In some embodiments, the DNA binding domain is found associated with its target sequence (e.g., dsDNA target sequence) more frequently than any other sequence in the genome of a target cell, e.g., human target cell, e.g., as measured by ChIP-seq (e.g., in HEK293T cells), e.g., as described in He and Pu (2010) *Curr. Protoc Mol Biol* Chapter 21 (incorporated herein by reference in its entirety). In some embodiments, the DNA binding domain is found associated with its target sequence (e.g., dsDNA target sequence) at least about 5-fold or 10-fold, more frequently than any other sequence in the genome of a target cell, e.g., as measured by ChIP-seq (e.g., in HEK293T cells), e.g., as described in He and Pu (2010), *supra*.

In some embodiments, the endonuclease domain has nickase activity and cleaves one strand of a target DNA. In some embodiments, nickase activity reduces the formation of double-stranded breaks at the target site. In some embodiments, the endonuclease domain creates a staggered nick structure in the first and second strands of a target DNA. In some embodiments, a staggered nick structure generates free 3’ overhangs at the target site. In some embodiments,

free 3’ overhangs at the target site improve editing efficiency, e.g., by enhancing access and annealing of a 3’ homology region of a template nucleic acid. In some embodiments, a staggered nick structure reduces the formation of double-stranded breaks at the target site.

In some embodiments, the endonuclease domain cleaves both strands of a target DNA, e.g., results in blunt-end cleavage of a target with no ssDNA overhangs on either side of the cut-site. The amino acid sequence of an endonuclease domain of a gene modifying system described herein may be at least about 50%, at least about 60%, at least about 70%, at least about 80%, at least about 85%, at least about 90%, at least about 95%, at least about 96%, at least about 97%, at least about 98%, at least about 99% identical to the amino acid sequence of an endonuclease domain described herein, e.g., an endonuclease domain from Table 8.

In certain embodiments, the heterologous endonuclease is Fok1 or a functional fragment thereof. In certain embodiments, the heterologous endonuclease is a Holliday junction resolvase or homolog thereof, such as the Holliday junction resolving enzyme from Sulfolobus solfataricus—Ssol Hje (Govindaraju et al., *Nucleic Acids Research* 44:7, 2016). In certain embodiments, the heterologous endonuclease is the endonuclease of the large fragment of a spliceosomal protein, such as Prp8 (Mahbub et al., *Mobile DNA* 8:16, 2017). In certain embodiments, the heterologous endonuclease is derived from a CRISPR-associated protein, e.g., Cas9. In certain embodiments, the heterologous endonuclease is engineered to have only ssDNA cleavage activity, e.g., only nickase activity, e.g., be a Cas9 nickase, e.g., SpCas9 with D10A, H840A, or N863A mutations. Table 8 provides exemplary Cas proteins and mutations associated with nickase activity. In still other embodiments, homologous endonuclease domains are modified, for example by site-specific mutation, to alter DNA endonuclease activity. In still other embodiments, endonuclease domains are modified to reduce DNA-sequence specificity, e.g., by truncation to remove domains that confer DNA-sequence specificity or mutation to inactivate regions conferring DNA-sequence specificity.

In some embodiments, the endonuclease domain has nickase activity and does not form double-stranded breaks. In some embodiments, the endonuclease domain forms single-stranded breaks at a higher frequency than double-stranded breaks, e.g., at least 90%, 95%, 96%, 97%, 98%, or 99% of the breaks are single-stranded breaks, or less than 10%, 5%, 4%, 3%, 2%, or 1% of the breaks are double-stranded breaks. In some embodiments, the endonuclease forms

substantially no double-stranded breaks. In some embodiments, the endonuclease does not form detectable levels of double-stranded breaks.

In some embodiments, the endonuclease domain has nickase activity that nicks the target site DNA of the first strand; e.g., in some embodiments, the endonuclease domain cuts the genomic DNA of the target site near to the site of alteration on the strand that will be extended by the writing domain. In some embodiments, the endonuclease domain has nickase activity that nicks the target site DNA of the first strand and does not nick the target site DNA of the second strand. For example, when a polypeptide comprises a CRISPR-associated endonuclease domain having nickase activity, in some embodiments, said CRISPR-associated endonuclease domain nicks the target site DNA strand containing the PAM site (e.g., and does not nick the target site DNA strand that does not contain the PAM site). As a further example, when a polypeptide comprises a CRISPR-associated endonuclease domain having nickase activity, in some embodiments, said CRISPR-associated endonuclease domain nicks the target site DNA strand not containing the PAM site (e.g., and does not nick the target site DNA strand that contains the PAM site).

In some other embodiments, the endonuclease domain has nickase activity that nicks the target site DNA of the first strand and the second strand. Without wishing to be bound by theory, after a writing domain (e.g., RT domain) of a polypeptide described herein polymerizes (e.g., reverse transcribes) from the heterologous object sequence of a template nucleic acid (e.g., template RNA), the cellular DNA repair machinery must repair the nick on the first DNA strand. The target site DNA now contains two different sequences for the first DNA strand: one corresponding to the original genomic DNA (e.g., having a free 5′ end) and a second corresponding to that polymerized from the heterologous object sequence (e.g., having a free 3′ end). It is thought that the two different sequences equilibrate with one another, first one hybridizing the second strand, then the other, and which sequence the cellular DNA repair apparatus incorporates into its repaired target site may be a stochastic process. Without wishing to be bound by theory, it is thought that introducing an additional nick to the second-strand may bias the cellular DNA repair machinery to adopt the heterologous object sequence-based sequence more frequently than the original genomic sequence (Anzalone et al. Nature 576:149-157 (2019)). In some embodiments, the additional nick is positioned at least 10, 15, 20, 25, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, 100, 105, 110, 115, 120, 125, 130, 135, 140,

145, or 150 nucleotides 5′ or 3′ of the target site modification (e.g., the insertion, deletion, or substitution) or to the nick on the first strand.

Alternatively or additionally, without wishing to be bound by theory, it is thought that an additional nick to the second strand may promote second-strand synthesis. In some embodiments, where the gene modifying system has inserted or substituted a portion of the first strand, synthesis of a new sequence corresponding to the insertion/substitution in the second strand is necessary.

In some embodiments, the polypeptide comprises a single domain having endonuclease activity (e.g., a single endonuclease domain) and said domain nicks both the first strand and the second strand. For example, in such an embodiment the endonuclease domain may be a CRISPR-associated endonuclease domain, and the template nucleic acid (e.g., template RNA) comprises a gRNA spacer that directs nicking of the first strand and an additional gRNA spacer that directs nicking of the second strand. In some embodiments, the polypeptide comprises a plurality of domains having endonuclease activity, and a first endonuclease domain nicks the first strand and a second endonuclease domain nicks the second strand (optionally, the first endonuclease domain does not (e.g., cannot) nick the second strand and the second endonuclease domain does not (e.g., cannot) nick the first strand).

In some embodiments, the endonuclease domain is capable of nicking a first strand and a second strand. In some embodiments, the first and second strand nicks occur at the same position in the target site but on opposite strands. In some embodiments, the second strand nick occurs in a staggered location, e.g., upstream or downstream, from the first nick. In some embodiments, the endonuclease domain generates a target site deletion if the second strand nick is upstream of the first strand nick. In some embodiments, the endonuclease domain generates a target site duplication if the second strand nick is downstream of the first strand nick. In some embodiments, the endonuclease domain generates no duplication and/or deletion if the first and second strand nicks occur in the same position of the target site. In some embodiments, the endonuclease domain has altered activity depending on protein conformation or RNA-binding status, e.g., which promotes the nicking of the first or second strand (e.g., as described in Christensen et al. PNAS 2006; incorporated by reference herein in its entirety).

In some embodiments, the endonuclease domain comprises a meganuclease, or a functional fragment thereof. In some embodiments, the endonuclease domain comprises a

homing endonuclease, or a functional fragment thereof. In some embodiments, the endonuclease domain comprises a meganuclease from the LAGLIDADG (SEQ ID NO: 37638), GIY-YIG, HNH, His-Cys Box, or PD-(D/E) XK families, or a functional fragment or variant thereof, e.g., which possess conserved amino acid motifs, e.g., as indicated in the family names. In some embodiments, the endonuclease domain comprises a meganuclease, or fragment thereof, chosen from, e.g., I-SmaMI (Uniprot F7WD42), I-SceI (Uniprot P03882), I-AniI (Uniprot P03880), I-DmoI (Uniprot P21505), I-CreI (Uniprot P05725), I-TevI (Uniprot P13299), I-OnuI (Uniprot Q4VWW5), or I-BmoI (Uniprot Q9ANR6). In some embodiments, the meganuclease is naturally monomeric, e.g., I-SceI, I-TevI, or dimeric, e.g., I-CreI, in its functional form. For example, the LAGLIDADG meganucleases (SEQ ID NO: 37638) with a single copy of the LAGLIDADG motif (SEQ ID NO: 37638) generally form homodimers, whereas members with two copies of the LAGLIDADG motif (SEQ ID NO: 37638) are generally found as monomers. In some embodiments, a meganuclease that normally forms as a dimer is expressed as a fusion, e.g., the two subunits are expressed as a single ORF and, optionally, connected by a linker, e.g., an I-CreI dimer fusion (Rodriguez-Fornes et al. Gene Therapy 2020; incorporated by reference herein in its entirety). In some embodiments, a meganuclease, or a functional fragment thereof, is altered to favor nickase activity for one strand of a double-stranded DNA molecule, e.g., I-SceI (K122I and/or K223I) (Niu et al. J Mol Biol 2008), I-AniI (K227M) (McConnell Smith et al. PNAS 2009), I-DmoI (Q42A and/or K120M) (Molina et al. J Biol Chem 2015). In some embodiments, a meganuclease or functional fragment thereof possessing this preference for single-strand cleavage is used as an endonuclease domain, e.g., with nickase activity. In some embodiments, an endonuclease domain comprises a meganuclease, or a functional fragment thereof, which naturally targets or is engineered to target a safe harbor site, e.g., an I-CreI targeting SH6 site (Rodriguez-Fornes et al., *supra*). In some embodiments, an endonuclease domain comprises a meganuclease, or a functional fragment thereof, with a sequence tolerant catalytic domain, e.g., I-TevI recognizing the minimal motif CNNNG (Kleinstiver et al. PNAS 2012). In some embodiments, a target sequence tolerant catalytic domain is fused to a DNA binding domain, e.g., to direct activity, e.g., by fusing I-TevI to: (i) zinc fingers to create Tev-ZFEs (Kleinstiver et al. PNAS 2012), (ii) other meganucleases to create MegaTevs (Wolfs et al. Nucleic Acids Res 2014), and/or (iii) Cas9 to create TevCas9 (Wolfs et al. PNAS 2016).

In some embodiments, the endonuclease domain comprises a restriction enzyme, e.g., a Type IIS or Type IIP restriction enzyme. In some embodiments, the endonuclease domain comprises a Type IIS restriction enzyme, e.g., FokI, or a fragment or variant thereof. In some embodiments, the endonuclease domain comprises a Type IIP restriction enzyme, e.g., PvuII, or a fragment or variant thereof. In some embodiments, a dimeric restriction enzyme is expressed as a fusion such that it functions as a single chain, e.g., a FokI dimer fusion (Minczuk et al. Nucleic Acids Res 36(12):3926-3938 (2008)).

The use of additional endonuclease domains is described, for example, in Guha and Edgell Int J Mol Sci 18(22):2565 (2017), which is incorporated herein by reference in its entirety.

In some embodiments, a gene modifying polypeptide comprises a modification to an endonuclease domain, e.g., relative to a wild-type Cas protein. In some embodiments, the endonuclease domain comprises an addition, deletion, replacement, or modification to the amino acid sequence of the wild-type Cas protein. In some embodiments, the endonuclease domain is modified to include a heterologous functional domain that binds specifically to and/or induces endonuclease cleavage of a target nucleic acid (e.g., DNA) sequence of interest. In some embodiments, the endonuclease domain comprises a zinc finger. In embodiments, the endonuclease domain comprising the Cas domain is associated with a guide RNA (gRNA), e.g., as described herein. In some embodiments, the endonuclease domain is modified to include a functional domain that does not target a specific target nucleic acid (e.g., DNA) sequence. In embodiments, the endonuclease domain comprises a Fok1 domain.

In some embodiments, the endonuclease domain is associated with the target dsDNA *in vitro* at a frequency at least about 5-fold or 10-fold higher than with a scrambled dsDNA. In some embodiments, the endonuclease domain is associated with the target dsDNA *in vitro* at a frequency at least about 5-fold or 10-fold higher than with a scrambled dsDNA, e.g., in a cell (e.g., a HEK293T cell). In some embodiments, the frequency of association between the endonuclease domain and the target DNA or scrambled DNA is measured by ChIP-seq, e.g., as described in He and Pu (2010) *Curr. Protoc Mol Biol* Chapter 21 (incorporated by reference herein in its entirety).

In some embodiments, the endonuclease domain can catalyze the formation of a nick at a target sequence, e.g., to an increase of at least about 5-fold or 10-fold relative to a non-target

sequence (e.g., relative to any other genomic sequence in the genome of the target cell). In some embodiments, the level of nick formation is determined using NickSeq, e.g., as described in Elacqua et al. (2019) *bioRxiv* doi.org/10.1101/867937 (incorporated herein by reference in its entirety).

In some embodiments, the endonuclease domain is capable of nicking DNA *in vitro*. In embodiments, the nick results in an exposed base. In embodiments, the exposed base can be detected using a nuclease sensitivity assay, e.g., as described in Chaudhry and Weinfeld (1995) *Nucleic Acids Res* 23(19):3805-3809 (incorporated by reference herein in its entirety). In embodiments, the level of exposed bases (e.g., detected by the nuclease sensitivity assay) is increased by at least 10%, 50%, or more relative to a reference endonuclease domain. In some embodiments, the reference endonuclease domain is an endonuclease domain from Cas9 of S. pyogenes.

In some embodiments, the endonuclease domain is capable of nicking DNA in a cell. In embodiments, the endonuclease domain is capable of nicking DNA in a HEK293T cell. In embodiments, an unrepaired nick that undergoes replication in the absence of Rad51 results in increased NHEJ rates at the site of the nick, which can be detected, e.g., by using a Rad51 inhibition assay, e.g., as described in Bothmer et al. (2017) *Nat Commun* 8:13905 (incorporated by reference herein in its entirety). In embodiments, NHEJ rates are increased above 0-5%. In embodiments, NHEJ rates are increased to 20-70% (e.g., between 30%-60% or 40-50%), e.g., upon Rad51 inhibition.

In some embodiments, the endonuclease domain releases the target after cleavage. In some embodiments, release of the target is indicated indirectly by assessing for multiple turnovers by the enzyme, e.g., as described in Yourik at al. RNA 25(1):35-44 (2019) (incorporated herein by reference in its entirety) and shown in FIG. 2. In some embodiments, the k_{exp} of an endonuclease domain is $1 \times 10^{-3} - 1 \times 10^{-}5$ min-1 as measured by such methods.

In some embodiments, the endonuclease domain has a catalytic efficiency (k_{cat}/K_m) greater than about 1×10^8 s^{-1} M^{-1} *in vitro*. In embodiments, the endonuclease domain has a catalytic efficiency greater than about 1×10^5, 1×10^6, 1×10^7, or 1×10^8, s^{-1} M^{-1} *in vitro*. In embodiments, catalytic efficiency is determined as described in Chen et al. (2018) *Science* 360(6387):436-439 (incorporated herein by reference in its entirety). In some embodiments, the endonuclease domain has a catalytic efficiency (k_{cat}/K_m) greater than about 1×10^8 s^{-1} M^{-1} in

cells. In embodiments, the endonuclease domain has a catalytic efficiency greater than about 1 x 10^5, 1 x 10^6, 1 x 10^7, or 1 x 10^8 s^{-1} M^{-1} in cells.

Gene modifying polypeptides comprising Cas domains

In some embodiments, a gene modifying polypeptide described herein comprises a Cas domain. In some embodiments, the Cas domain can direct the gene modifying polypeptide to a target site specified by a gRNA spacer, thereby modifying a target nucleic acid sequence in "cis". In some embodiments, a gene modifying polypeptide is fused to a Cas domain. In some embodiments, a gene modifying polypeptide comprises a CRISPR/Cas domain (also referred to herein as a CRISPR-associated protein). In some embodiments, a CRISPR/Cas domain comprises a protein involved in the clustered regulatory interspaced short palindromic repeat (CRISPR) system, e.g., a Cas protein, and optionally binds a guide RNA, e.g., single guide RNA (sgRNA).

CRISPR systems are adaptive defense systems originally discovered in bacteria and archaea. CRISPR systems use RNA-guided nucleases termed CRISPR-associated or "Cas" endonucleases (e. g., Cas9 or Cpf1) to cleave foreign DNA. For example, in a typical CRISPR-Cas system, an endonuclease is directed to a target nucleotide sequence (e. g., a site in the genome that is to be sequence-edited) by sequence-specific, non-coding "guide RNAs" that target single- or double-stranded DNA sequences. Three classes (I-III) of CRISPR systems have been identified. The class II CRISPR systems use a single Cas endonuclease (rather than multiple Cas proteins). One class II CRISPR system includes a type II Cas endonuclease such as Cas9, a CRISPR RNA ("crRNA"), and a trans-activating crRNA ("tracrRNA"). The crRNA contains a "spacer" sequence, a typically about 20-nucleotide RNA sequence that corresponds to a target DNA sequence ("protospacer"). In the wild-type system, and in some engineered systems, crRNA also contains a region that binds to the tracrRNA to form a partially double-stranded structure that is cleaved by RNase III, resulting in a crRNA/tracrRNA hybrid molecule. A crRNA/tracrRNA hybrid then directs the Cas endonuclease to recognize and cleave a target DNA sequence. A target DNA sequence is generally adjacent to a "protospacer adjacent motif" ("PAM") that is specific for a given Cas endonuclease and required for cleavage activity at a target site matching the spacer of the crRNA. CRISPR endonucleases identified from various prokaryotic species have unique PAM sequence requirements, e.g., as listed for exemplary Cas enzymes in Table 7; examples of PAM sequences include 5´-NGG (Streptococcus pyogenes), 5´-

NNAGAA (Streptococcus thermophilus CRISPR1), 5´-NGGNG (Streptococcus thermophilus CRISPR3), and 5´-NNNGATT (Neisseria meningiditis). Some endonucleases, e.g., Cas9 endonucleases, are associated with G-rich PAM sites, e. g., 5´-NGG), and perform blunt-end cleaving of the target DNA at a location 3 nucleotides upstream from (5´ from) the PAM site. Another class II CRISPR system includes the type V endonuclease Cpf1, which is smaller than Cas9; examples include AsCpf1 (from Acidaminococcus sp.) and LbCpf1 (from Lachnospiraceae sp.). Cpf1-associated CRISPR arrays are processed into mature crRNAs without the requirement of a tracrRNA; in other words, a Cpf1 system, in some embodiments, comprises only Cpf1 nuclease and a crRNA to cleave a target DNA sequence. Cpf1 endonucleases, are typically associated with T-rich PAM sites, e. g., 5´-TTN. Cpf1 can also recognize a 5´-CTA PAM motif. Cpf1 typically cleaves a target DNA by introducing an offset or staggered double-strand break with a 4- or 5-nucleotide 5´ overhang, for example, cleaving a target DNA with a 5-nucleotide offset or staggered cut located 18 nucleotides downstream from (3´ from) from a PAM site on the coding strand and 23 nucleotides downstream from the PAM site on the complimentary strand; the 5-nucleotide overhang that results from such offset cleavage allows more precise genome editing by DNA insertion by homologous recombination than by insertion at blunt-end cleaved DNA. See, e.g., Zetsche et al. (2015) Cell, 163:759 – 771.

A variety of CRISPR associated (Cas) genes or proteins can be used in the technologies provided by the present disclosure and the choice of Cas protein will depend upon the particular conditions of the method. Specific examples of Cas proteins include class II systems including Cas1, Cas2, Cas3, Cas4, Cas5, Cas6, Cas7, Cas8, Cas9, Cas10, Cpf1, C2C1, or C2C3. In some embodiments, a Cas protein, e.g., a Cas9 protein, may be from any of a variety of prokaryotic species. In some embodiments a particular Cas protein, e.g., a particular Cas9 protein, is selected to recognize a particular protospacer-adjacent motif (PAM) sequence. In some embodiments, a DNA-binding domain or endonuclease domain includes a sequence targeting polypeptide, such as a Cas protein, e.g., Cas9. In certain embodiments a Cas protein, e.g., a Cas9 protein, may be obtained from a bacteria or archaea or synthesized using known methods. In certain embodiments, a Cas protein may be from a gram-positive bacteria or a gram-negative bacteria. In certain embodiments, a Cas protein may be from a Streptococcus (e.g., a S. pyogenes, or a S. thermophilus), a Francisella (e.g., an F. novicida), a Staphylococcus (e.g., an S. aureus), an Acidaminococcus (e.g., an Acidaminococcus sp. BV3L6), a Neisseria (e.g., an N. meningitidis),

a Cryptococcus, a Corynebacterium, a Haemophilus, a Eubacterium, a Pasteurella, a Prevotella, a Veillonella, or a Marinobacter.

In some embodiments, a gene modifying polypeptide may comprise the amino acid sequence of SEQ ID NO: 4000 below, or a sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99% identity thereto. In embodiments, the amino acid sequence of SEQ ID NO: 4000 below, or the sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99% identity thereto, is positioned at the N-terminal end of the gene modifying polypeptide. In embodiments, the amino acid sequence of SEQ ID NO: 4000 below, or the sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99% identity thereto, is positioned within 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25, or 30 amino acids of the N-terminal end of the gene modifying polypeptide.

Exemplary N-terminal NLS-Cas9 domain

MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSI
KKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRLEE
SFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIK
FRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILSARLSKSRRLE
NLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIG
DQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQL
PEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQR
TFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAW
MTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNE
LTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISG
VEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLF
DDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDS
LTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVI
EMARENQTTQKGQKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGR
DMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKK
MKNYWRQLLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDS
RMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGT
ALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANG

EIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKESILPKRN
SDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSF
EKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYV
NFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSA
YNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITG
LYETRIDLSQLGGDGG (SEQ ID NO: 4000)

In some embodiments, a gene modifying polypeptide may comprise the amino acid sequence of SEQ ID NO: 4001 below, or a sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99% identity thereto. In embodiments, the amino acid sequence of SEQ ID NO: 4001 below, or the sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99% identity thereto, is positioned at the C-terminal end of the gene modifying polypeptide. In embodiments, the amino acid sequence of SEQ ID NO: 4001 below, or the sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99% identity thereto, is positioned within 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25, or 30 amino acids of the C-terminal end of the gene modifying polypeptide.

Exemplary C-terminal sequence comprising an NLS

AGKRTADGSEFEKRTADGSEFESPKKKAKVE (SEQ ID NO: 4001)

Exemplary benchmarking sequence

MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSI
KKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRLEE
SFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIK
FRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILSARLSKSRRLE
NLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIG
DQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQL
PEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQR
TFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAW
MTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNE
LTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISG
VEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLF

DDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDS
LTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVI
EMARENQTTQKGQKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGR
DMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKK
MKNYWRQLLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDS
RMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGT
ALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANG
EIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKESILPKRN
SDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSF
EKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYV
NFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSA
YNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITG
LYETRIDLSQLGGDGGSGGSSGGSSGSETPGTSESATPESSGGSSGGSSGGTLNIEDEYRL
HETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQE
ARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTV
PNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRL
PQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLG
NLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLG
KAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTK
PFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTK
DAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVAL
NPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDGSSLLQEGQRKAG
AAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHG
EIYRRRGWLTSEGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQA
ARKAAITETPDTSTLLIENSSPSGGSKRTADGSEFEAGKRTADGSEFEKRTADGSEFESPK
KKAKVE (SEQ ID NO: 4002)

In some embodiments, a gene modifying polypeptide may comprise a Cas domain as listed in Table 7 or 8, or a functional fragment thereof, or a sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99% identity thereto.

Table 7. CRISPR/Cas Proteins, Species, and Mutations

Name	*Enzyme*	*Species*	*# of AAs*	*PAM*	*Mutations to alter PAM recognition*	*Mutations to make catalytically dead*
FnCas9	Cas9	*Francisella novicida*	1629	5'-NGG-3'	Wt	D11A/H969A/N995A
FnCas9 RHA	Cas9	*Francisella novicida*	1629	5'-YG-3'	E1369R/E1449H/R1556A	D11A/H969A/N995A
SaCas9	Cas9	*Staphylococcus aureus*	1053	5'-NNGRRT-3'	Wt	D10A/H557A
SaCas9 KKH	Cas9	*Staphylococcus aureus*	1053	5'-NNNRRT-3'	E782K/N968K/R1015H	D10A/H557A
SpCas9	Cas9	*Streptococcus pyogenes*	1368	5'-NGG-3'	Wt	D10A/D839A/H840A/N863A
SpCas9 VQR	Cas9	*Streptococcus pyogenes*	1368	5'-NGA-3'	D1135V/R1335Q/T1337R	D10A/D839A/H840A/N863A
AsCpf1 RR	Cpf1	*Acidaminococcus sp. BV3L6*	1307	5'-TYCV-3'	S542R/K607R	E993A
AsCpf1 RVR	Cpf1	*Acidaminococcus sp. BV3L6*	1307	5'-TATV-3'	S542R/K548V/N552R	E993A
FnCpf1	Cpf1	*Francisella novicida*	1300	5'-NTTN-3'	Wt	D917A/E1006A/D1255A
NmCas9	Cas9	*Neisseria meningitidis*	1082	5'-NNNGATT-3'	Wt	D16A/D587A/H588A/N611A

Table 8 Amino Acid Sequences of CRISPR/Cas Proteins, Species, and Mutations

Variant	**Parental Host(s)**	**Protein Sequence**	**SEQ ID NO:**	**Nickase (HNH)**	**Nickase (HNH)**	**Nickase (RuvC)**
Nme2Cas9	Neisseria meningitidis	MAAFKPNPINYILGLDIGIASVGWAMVEIDEEENPIRLIDLGVRVFERAEVPK TGDSLAMARRLARSVRRLTRRRAHRLLRARRLLKREGVLQAADFDENGLIKS LPNTPWQLRAAALDRKLTPLEWSAVLLHLIKHRGYLSQRKNEGETADKELG ALLKGVANNAHALQTGDFRTPAELALNKFEKESGHIRNQRGDYSHTFSRKD LQAELILLFEKQKEFGNPHVSGGLKEGIETLLMTQRPALSGDAVQKMLGHCT FEPAEPKAAKNTYTAERFIWLTKLNNLRILEQGSERPLTDTERATLMDEPYRK SKLTYAQARKLLGLEDTAFFKGLRYGKDNAEASTLMEMKAYHAISRALEKEG LKDKKSPLNLSSELQDEIGTAFSLFKTDEDITGRLKDRVQPEILEALLKHISFDKF VQISLKALRRIVPLMEQGKRYDEACAEIYGDHYGKKNTEEKIYLPPIPADEIRN PVVLRALSQARKVINGVVRRYGSPARIHIETAREVGKSFKDRKEIEKRQEENR KDREKAAAKFREYFPNFVGEPKSKDILKLRLYEQQHGKCLYSGKEINLVRLNE KGYVEIDHALPFSRTWDDSFNNKVLVLGSENQNKGNQTPYEYFNGKDNSR EWQEFKARVETSRFPRSKKQRILLQKFDEDGFKECNLNDTRYVNRFLCQFVA DHILLTGKGKRRVFASNGQITNLLRGFWGLRKVRAENDRHHALDAVVVACS TVAMQQKITRFVRYKEMNAFDGKTIDKETGKVLHQKTHFPQPWEFFAQEV MIRVFGKPDGKPEFEEADTPEKLRTLLAEKLSSRPEAVHEYVTPLFVSRAPNR KMSGAHKDTLRSAKRFVKHNEKISVKRVWLTEIKLADLENMVNYKNGREIEL YEALKARLEAYGGNAKQAFDPKDNPFYKKGGQLVKAVRVEKTQESGVLLNK KNAYTIADNGDMVRVDVFCKVDKKGKNQYFIVPIYAWQVAENILPDIDCKG YRIDDSYTFCFSLHKYDLIAFQKDEKSKVEFAYYINCDSSNGRFYLAWHDKGS KEQQFRISTQNLVLIQKYQVNELGKEIRPCRLKKRPPVR	9,001	N611A	H588A	D16A
PpnCas9	Pasteurella pneumotropica	MQNNPLNYILGLDLGIASIGWAVVEIDEESSPIRLIDVGVRTFERAEVAKTGE SLALSRRLARSSRRLIKRRAERLKKAKRLLKAEKILHSIDEKLPINVWQLRVKGL KEKLERQEWAAVLLHLSKHRGYLSQRKNEGKSDNKELGALLSGIASNHQML QSSEYRTPAEIAVKKFQVEEGHIRNQRGSYTHTFSRLDLLAEMELLFQRQAEL GNSYTSTTLLENLTALLMWQKPALAGDAILKMLGKCTFEPSEYKAAKNSYSA ERFVWLTKLNNLRILENGTERALNDNERFALLEQPYEKSKLTYAQVRAMLAL SDNAIFKGVRYLGEDKKTVESKTTLIEMKFYHQIRKTLGSAELKKEWNELKGN SDLLDEIGTAFSLYKTDDDICRYLEGKLPERVLNALLENLNFDKFIQLSLKALHQ ILPLMLQGQRYDEAVSAIYGDHYGKKSTETTRLLPTIPADEIRNPVVLRTLTQA	9,002	N605A	H582A	D13A

		RKVINAVVRLYGSPARIHIETAREVGKSYQDRKKLEKQQEDNRKQRESAVKK FKEMFPHFVGEPKGKDILKMRLYELQQAKCLYSGKSLELHRLLEKGYVEVDH ALPFSRTWDDSFNNKVLVLANENQNKGNLTPYEWLDGKNNSERWQHFVV RVQTSGFSYAKKQRILNHKLDEKGFIERNLNDTRYVARFLCNFIADNMLLVG KGKRNVFASNGQITALLRHRWGLQKVREQNDRHHALDAVVVACSTVAMQ QKITRFVRYNEGNVFSGERIDRETGEIIPLHFPSPWAFFKENVEIRIFSENPKLE LENRLPDYPQYNHEWVQPLFVSRMPTRKMTGQGHMETVKSAKRLNEGLS VLKVPLTQLKLSDLERMVNRDREIALYESLKARLEQFGNDPAKAFAEPFYKKG GALVKAVRLEQTQKSGVLVRDGNGVADNASMVRVDVFTKGGKYFLVPIYT WQVAKGILPNRAATQGKDENDWDIMDEMATFQFSLCQNDLIKLVTKKKTI FGYFNGLNRATSNINIKEHDLDKSKGKLGIYLEVGVKLAISLEKYQVDELGKNI RPCRPTKRQHVR				
SauCas9	Staphylococcus aureus	MKRNYILGLDIGITSVGYGIIDYETRDVIDAGVRLFKEANVENNEGRRSKRGA RRLKRRRRHRIQRVKKLLFDYNLLTDHSELSGINPYEARVKGLSQKLSEEEFSA ALLHLAKRRGVHNVNEVEEDTGNELSTKEQISRNSKALEEKYVAELQLERLKK DGEVRGSINRFKTSDYVKEAKQLLKVQKAYHQLDQSFIDTYIDLLETRRTYYE GPGEGSPFGWKDIKEWYEMLMGHCTYFPEELRSVKYAYNADLYNALNDLN NLVITRDENEKLEYYEKFQIIENVFKQKKKPTLKQIAKEILVNEEDIKGYRVTST GKPEFTNLKVYHDIKDITARKEIIENAELLDQIAKILTIYQSSEDIQEELTNLNSE LTQEEIEQISNLKGYTGTHNLSLKAINLILDELWHTNDNQIAIFNRLKLVPKKV DLSQQKEIPTTLVDDFILSPVVKRSFIQSIKVINAIIKKYGLPNDIIIELAREKNSK DAQKMINEMQKRNRQTNERIEEIIRTTGKENAKYLIEKIKLHDMQEGKCLYS LEAIPLEDLLNNPFNYEVDHIIPRSVSFDNSFNNKVLVKQEENSKKGNRTPFQ YLSSSDSKISYETFKKHILNLAKGKGRISKTKKEYLLEERDINRFSVQKDFINRNL VDTRYATRGLMNLLRSYFRVNNLDVKVKSINGGFTSFLRRKWKFKKERNKG YKHHAEDALIIANADFIFKEWKKLDKAKKVMENQMFEEKQAESMPEIETEQ EYKEIFITPHQIKHIKDFKDYKYSHRVDKKPNRELINDTLYSTRKDDKGNTLIVN NLNGLYDKDNDKLKKLINKSPEKLLMYHHDPQTYQKLKLIMEQYGDEKNPL YKYYEETGNYLTKYSKKDNGPVIKKIKYYGNKLNAHLDITDDYPNSRNKVVKL SLKPYRFDVYLDNGVYKFVTVKNLDVIKKENYYEVNSKCYEEAKKLKKISNQA EFIASFYNNDLIKINGELYRVIGVNNDLLNRIEVNMIDITYREYLENMNDKRPP RIIKTIASKTQSIKKYSTDILGNLYEVKSKKHPQIIKKG	9,003	N580A	H557A	D10A
SauCas9-KKH	Staphylococcus aureus	MKRNYILGLDIGITSVGYGIIDYETRDVIDAGVRLFKEANVENNEGRRSKRGA RRLKRRRRHRIQRVKKLLFDYNLLTDHSELSGINPYEARVKGLSQKLSEEEFSA ALLHLAKRRGVHNVNEVEEDTGNELSTKEQISRNSKALEEKYVAELQLERLKK DGEVRGSINRFKTSDYVKEAKQLLKVQKAYHQLDQSFIDTYIDLLETRRTYYE GPGEGSPFGWKDIKEWYEMLMGHCTYFPEELRSVKYAYNADLYNALNDLN NLVITRDENEKLEYYEKFQIIENVFKQKKKPTLKQIAKEILVNEEDIKGYRVTST GKPEFTNLKVYHDIKDITARKEIIENAELLDQIAKILTIYQSSEDIQEELTNLNSE LTQEEIEQISNLKGYTGTHNLSLKAINLILDELWHTNDNQIAIFNRLKLVPKKV DLSQQKEIPTTLVDDFILSPVVKRSFIQSIKVINAIIKKYGLPNDIIIELAREKNSK DAQKMINEMQKRNRQTNERIEEIIRTTGKENAKYLIEKIKLHDMQEGKCLYS LEAIPLEDLLNNPFNYEVDHIIPRSVSFDNSFNNKVLVKQEENSKKGNRTPFQ YLSSSDSKISYETFKKHILNLAKGKGRISKTKKEYLLEERDINRFSVQKDFINRNL VDTRYATRGLMNLLRSYFRVNNLDVKVKSINGGFTSFLRRKWKFKKERNKG YKHHAEDALIIANADFIFKEWKKLDKAKKVMENQMFEEKQAESMPEIETEQ EYKEIFITPHQIKHIKDFKDYKYSHRVDKKPNRKLINDTLYSTRKDDKGNTLIV NNLNGLYDKDNDKLKKLINKSPEKLLMYHHDPQTYQKLKLIMEQYGDEKNP LYKYYEETGNYLTKYSKKDNGPVIKKIKYYGNKLNAHLDITDDYPNSRNKVVK LSLKPYRFDVYLDNGVYKFVTVKNLDVIKKENYYEVNSKCYEEAKKLKKISNQ AEFIASFYKNDLIKINGELYRVIGVNNDLLNRIEVNMIDITYREYLENMNDKRP PHIIKTIASKTQSIKKYSTDILGNLYEVKSKKHPQIIKKG	9,004	N580A	H557A	D10A
SauriCas9	Staphylococcus auricularis	MQENQQKQNYILGLDIGITSVGYGLIDSKTREVIDAGVRLFPEADSENNSNR RSKRGARRLKRRRIHRLNRVKDLLADYQMIDLNNVPKSTDPYTIRVKGLREPL TKEEFAIALLHIAKRRGLHNISVSMGDEEQDNELSTKQQLQKNAQQLQDKY VCELQLERLTNINKVRGEKNRFKTEDFVKEVKQLCETQRQYHNIDDQFIQQY IDLVSTRREYFEGPGNGSPYGWDGDLLKWYEKLMGRCTYFPEELRSVKYAYS ADLFNALNDLNNLVVTRDDNPKLEYYEKYHIIENVFKQKKNPTLKQIAKEIGV	9,005	N588A	H565A	D15A

		QDYDIRGYRITKSGKPQFTSFKLYHDLKNIFEQAKYLEDVEMLDEIAKILTIYQ DEISIKKALDQLPELLTESEKSQIAQLTGYTGTHRLSLKCIHIVIDELWESPENQ MEIFTRLNLKPKKVEMSEIDSIPTTLVDEFILSPVVKRAFIQSIKVINAVINRFGL PEDIIIELAREKNSKDRRKFINKLQKQNEATRKKIEQLLAKYGNTNAKYMIEKI KLHDMQEGKCLYSLEAIPLEDLLSNPTHYEVDHIIPRSVSFDNSLNNKVLVKQ SENSKKGNRTPYQYLSSNESKISYNQFKQHILNLSKAKDRISKKKRDMLLEER DINKFEVQKEFINRNLVDTRYATRELSNLLKTYFSTHDYAVKVKTINGGFTNH LRKVWDFKKHRNHGYKHHAEDALVIANADFLFKTHKALRRTDKILEQPGLE VNDTTVKVDTEEKYQELFETPKQVKNIKQFRDFKYSHRVDKKPNRQLINDTL YSTREIDGETYVVQTLKDLYAKDNEKVKKLFTERPQKILMYQHDPKTFEKLM TILNQYAEAKNPLAAYYEDKGEYVTKYAKKGNGPAIHKIKYIDKKLGSYLDVS NKYPETQNKLVKLSLKSFRFDIYKCEQGYKMVSIGYLDVLKKDNYYYIPKDKYE AEKQKKKIKESDLFVGSFYYNDLIMYEDELFRVIGVNSDINNLVELNMVDITY KDFCEVNNVTGEKRIKKTIGKRVVLIEKYTTDILGNLYKTPLPKKPQLIFKRGEL				
SauriCas9-KKH	Staphylococcus auricularis	MQENQQKQNYILGLDIGITSVGYGLIDSKTREVIDAGVRLFPEADSENNSNR RSKRGARRLKRRRIHRLNRVKDLLADYQMIDLNNVPKSTDPYTIRVKGLREPL TKEEFAIALLHIAKRRGLHNISVSMGDEEQDNELSTKQQLQKNAQQLQDKY VCELQLERLTNINKVRGEKNRFKTEDFVKEVKQLCETQRQYHNIDDQFIQQY IDLVSTRREYFEGPGNGSPYGWDGDLLKWYEKLMGRCTYFPEELRSVKYAYS ADLFNALNDLNNLVVTRDDNPKLEYYEKYHIIENVFKQKKNPTLKQIAKEIGV QDYDIRGYRITKSGKPQFTSFKLYHDLKNIFEQAKYLEDVEMLDEIAKILTIYQ DEISIKKALDQLPELLTESEKSQIAQLTGYTGTHRLSLKCIHIVIDELWESPENQ MEIFTRLNLKPKKVEMSEIDSIPTTLVDEFILSPVVKRAFIQSIKVINAVINRFGL PEDIIIELAREKNSKDRRKFINKLQKQNEATRKKIEQLLAKYGNTNAKYMIEKI KLHDMQEGKCLYSLEAIPLEDLLSNPTHYEVDHIIPRSVSFDNSLNNKVLVKQ SENSKKGNRTPYQYLSSNESKISYNQFKQHILNLSKAKDRISKKKRDMLLEER DINKFEVQKEFINRNLVDTRYATRELSNLLKTYFSTHDYAVKVKTINGGFTNH LRKVWDFKKHRNHGYKHHAEDALVIANADFLFKTHKALRRTDKILEQPGLE VNDTTVKVDTEEKYQELFETPKQVKNIKQFRDFKYSHRVDKKPNRKLINDTL YSTREIDGETYVVQTLKDLYAKDNEKVKKLFTERPQKILMYQHDPKTFEKLM TILNQYAEAKNPLAAYYEDKGEYVTKYAKKGNGPAIHKIKYIDKKLGSYLDVS NKYPETQNKLVKLSLKSFRFDIYKCEQGYKMVSIGYLDVLKKDNYYYIPKDKYE AEKQKKKIKESDLFVGSFYKNDLIMYEDELFRVIGVNSDINNLVELNMVDITY KDFCEVNNVTGEKHIKKTIGKRVVLIEKYTTDILGNLYKTPLPKKPQLIFKRGEL	9,006	N588A	H565A	D15A
ScaCas9-Sc++	Streptococcus canis	MEKKYSIGLDIGTNSVGWAVITDDYKVPSKKFKVLGNTNRKSIKKNLMGALL FDSGETAEATRLKRTARRRYTRRKNRIRYLQEIFANEMAKLDDSFFQRLEESF LVEEDKKNERHPIFGNLADEVAYHRNYPTIYHLRKKLADSPEKADLRLIYLALA HIIKFRGHFLIEGKLNAENSDVAKLFYQLIQTYNQLFEESPLDEIEVDAKGILSA RLSKSKRLEKLIAVFPNEKKNGLFGNIIALALGLTPNFKSNFDLTEDAKLQLSKD TYDDDLDELLGQIGDQYADLFSAAKNLSDAILLSDILRSNSEVTKAPLSASMV KRYDEHHQDLALLKTLVRQQFPEKYAEIFKDDTKNGYAGYVGADKKLRKRS GKLATEEEFYKFIKPILEKMDGAEELLAKLNRDDLLRKQRTFDNGSIPHQIHLK ELHAILRRQEEFYPFLKENREKIEKILTFRIPYYVGPLARGNSRFAWLTRKSEEA ITPWNFEEVVDKGASAQSFIERMTNFDEQLPNKKVLPKHSLLYEYFTVYNEL TKVKYVTERMRKPEFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDS VEIIGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIE ERLKTYAHLFDDKVMKQLKRRHYTGWGRLSRKMINGIRDKQSGKTILDFLKS DGFSNRNFMQLIHDDSLTFKEEIEKAQVSGQGDSLHEQIADLAGSPAIKKGIL QTVKIVDELVKVMGHKPENIVIEMARENQTTTKGLQQSRERKKRIEEGIKELE SQILKENPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVP QSFIKDDSIDNKVLTRSVENRGKSDNVPSEEVVKKMKNYWRQLLNAKLITQ RKFDNLTKAERGGLSEADKAGFIKRQLVETRQITKHVARILDSRMNTKRDKN DKPIREVKVITLKSKLVSDFRKDFQLYKVRDINNYHHAHDAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKRFFYSNIMNFFKTEVKL ANGEIRKRPLIETNGETGEVVWNKEKDFATVRKVLAMPQVNIVKKTEVQTG GFSKESILSKRESAKLIPRKKGWDTRKYGGFGSPTVAYSILVVAKVEKGKAKKL KSVKVLVGITIMEKGSYEKDPIGFLEAKGYKDIKKELIFKLPKYSLFELENGRRR MLASAKELQKANELVLPQHLVRLLYYTQNISATTGSNNLGYIEQHREEFKEIF	9,007	N872A	H849A	D10A

		EKIIDFSEKYILKNKVNSNLKSSFDEQFAVSDSILLSNSFVSLLKYTSFGASGGFT FLDLDVKQGRLRYQTVTEVLDATLIYQSITGLYETRTDLSQLGGD				
SpyCas9	Streptococcus pyogenes	MDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLF DSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRLEESFL VEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAH MIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLS KDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSAS MIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEF YKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQ EDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFE EVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTE GMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVED RFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYA HLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANR NFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKV VDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQ ILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSF LKDDSIDNKVLTRSDKNRGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKF DNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLI REVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIKKYPK LESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEI RKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKE LLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASA GELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEII EQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAF KYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGD	9,008	N863A	H840A	D10A
SpyCas9-NG	Streptococcus pyogenes	MDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLF DSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRLEESFL VEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAH MIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLS KDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSAS MIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEF YKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQ EDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFE EVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTE GMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVED RFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYA HLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANR NFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKV VDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQ ILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSF LKDDSIDNKVLTRSDKNRGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKF DNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLI REVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIKKYPK LESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEI RKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES IRPKRNSDKLIARKKDWDPKKYGGFVSPTVAYSVLVVAKVEKGKSKKLKSVKE LLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASA RFLQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEII EQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPRAF KYFDTTIDRKVYRSTKEVLDATLIHQSITGLYETRIDLSQLGGD	9,009	N863A	H840A	D10A
SpyCas9-SpRY	Streptococcus pyogenes	MDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLF DSGETAERTRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRLEESFL VEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAH MIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS	9,010	N863A	H840A	D10A

		ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLS KDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSAS MIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEF YKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQ EDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFE EVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTE GMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVED RFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYA HLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANR NFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKV VDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQ ILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSF LKDDSIDNKVLTRSDKNRGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKF DNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLI REVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIKKYPK LESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEI RKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES IRPKRNSDKLIARKKDWDPKKYGGFLWPTVAYSVLVVAKVEKGKSKKLKSVK ELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLAS AKQLQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDE IIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTRLGAPRAF KYFDTTIDPKQYRSTKEVLDATLIHQSITGLYETRIDLSQLGGD				
St1Cas9	Streptococcus thermophilus	MSDLVLGLDIGIGSVGVGILNKVTGEIIHKNSRIFPAAQAENNLVRRTNRQG RRLARRKKHRRVRLNRLFEESGLITDFTKISINLNPYQLRVKGLTDELSNEELFI ALKNMVKHRGISYLDDASDDGNSSVGDYAQIVKENSKQLETKTPGQIQLER YQTYGQLRGDFTVEKDGKKHRLINVFPTSAYRSEALRILQTQQEFNPQITDEF INRYLEILTGKRKYYHGPGNEKSRTDYGRYRTSGETLDNIFGILIGKCTFYPDEF RAAKASYTAQEFNLLNDLNNLTVPTETKKLSKEQKNQIINYVKNEKAMGPAK LFKYIAKLLSCDVADIKGYRIDKSGKAEIHTFEAYRKMKTLETLDIEQMDRETL DKLAYVLTLNTEREGIQEALEHEFADGSFSQKQVDELVQFRKANSSIFGKGW HNFSVKLMMELIPELYETSEEQMTILTRLGKQKTTSSSNKTKYIDEKLLTEEIY NPVVAKSVRQAIKIVNAAIKEYGDFDNIVIEMARETNEDDEKKAIQKIQKAN KDEKDAAMLKAANQYNGKAELPHSVFHGHKQLATKIRLWHQQGERCLYT GKTISIHDLINNSNQFEVDHILPLSITFDDSLANKVLVYATANQEKGQRTPYQ ALDSMDDAWSFRELKAFVRESKTLSNKKKEYLLTEEDISKFDVRKKFIERNLV DTRYASRVVLNALQEHFRAHKIDTKVSVVRGQFTSQLRRHWGIEKTRDTYH HHAVDALIIAASSQLNLWKKQKNTLVSYSEDQLLDIETGELISDDEYKESVFK APYQHFVDTLKSKEFEDSILFSYQVDSKFNRKISDATIYATRQAKVGKDKADE TYVLGKIKDIYTQDGYDAFMKIYKKDKSKFLMYRHDPQTFEKVIEPILENYPN KQINEKGKEVPCNPFLKYKEEHGYIRKYSKKGNGPEIKSLKYYDSKLGNHIDIT PKDSNNKVVLQSVSPWRADVYFNKTTGKYEILGLKYADLQFEKGTGTYKISQ EKYNDIKKKEGVDSDSEFKFTLYKNDLLLVKDTETKEQQLFRFLSRTMPKQKH YVELKPYDKQKFEGGEALIKVLGNVANSGQCKKGLGKSNISIYKVRTDVLGN QHIIKNEGDKPKLDF	9,011	N622A	H599A	D9A
BlatCas9	Brevibacillus laterosporus	MAYTMGIDVGIASCGWAIVDLERQRIIDIGVRTFEKAENPKNGEALAVPRRE ARSSRRRLRRKKHRIERLKHMFVRNGLAVDIQHLEQTLRSQNEIDVWQLRV DGLDRMLTQKEWLRVLIHLAQRRGFQSNRKTDGSSEDGQVLVNVTENDRL MEEKDYRTVAEMMVKDEKFSDHKRNKNGNYHGVVSRSSLLVEIHTLFETQ RQHHNSLASKDFELEYVNIWSAQRPVATKDQIEKMIGTCTFLPKEKRAPKAS WHFQYFMLLQTINHIRITNVQGTRSLNKEEIEQVVNMALTKSKVSYHDTRKI LDLSEEYQFVGLDYGKEDEKKKVESKETIIKLDDYHKLNKIFNEVELAKGETWE ADDYDTVAYALTFFKDDEDIRDYLQNKYKDSKNRLVKNLANKEYTNELIGKV STLSFRKVGHLSLKALRKIIPFLEQGMTYDKACQAAGFDFQGISKKKRSVVLP VIDQISNPVVNRALTQTRKVINALIKKYGSPETIHIETARELSKTFDERKNITKD YKENRDKNEHAKKHLSELGIINPTGLDIVKYKLWCEQQGRCMYSNQPISFER LKESGYTEVDHIIPYSRSMNDSYNNRVLVMTRENREKGNQTPFEYMGNDT QRWYEFEQRVTTNPQIKKEKRQNLLLKGFTNRRELEMLERNLNDTRYITKYL SHFISTNLEFSPSDKKKKVVNTSGRITSHLRSRWGLEKNRGQNDLHHAMDAI VIAVTSDSFIQQVTNYYKRKERRELNGDDKFPLPWKFFREEVIARLSPNPKEQ	9,012	N607A	H584A	D8A

		IEALPNHFYSEDELADLQPIFVSRMPKRSITGEAHQAQFRRVVGKTKEGKNIT AKKTALVDISYDKNGDFNMYGRETDPATYEAIKERYLEFGGNVKKAFSTDLH KPKKDGTKGPLIKSVRIMENKTLVHPVNKGKGVVYNSSIVRTDVFQRKEKYY LLPVYVTDVTKGKLPNKVIVAKKGYHDWIEVDDSFTFLFSLYPNDLIFIRQNPK KKISLKKRIESHSISDSKEVQEIHAYYKGVDSSTAAIEFIIHDGSYYAKGVGVQN LDCFEKYQVDILGNYFKVKGEKRLELETSDSNHKGKDVNSIKSTSR				
cCas9-v16	Staphylococcus aureus	MKRNYILGLDIGITSVGYGIIDYETRDVIDAGVRLFKEANVENNEGRRSKRGA RRLKRRRRHRIQRVKKLLFDYNLLTDHSELSGINPYEARVKGLSQKLSEEEFSA ALLHLAKRRGVHNVNEVEEDTGNELSTKEQISRNSKALEEKYVAELQLERLKK DGEVRGSINRFKTSDYVKEAKQLLKVQKAYHQLDQSFIDTYIDLLETRRTYYE GPGEGSPFGWKDIKEWYEMLMGHCTYFPEELRSVKYAYNADLYNALNDLN NLVITRDENEKLEYYEKFQIIENVFKQKKKPTLKQIAKEILVNEEDIKGYRVTST GKPEFTNLKVYHDIKDITARKEIIENAELLDQIAKILTIYQSSEDIQEELTNLNSE LTQEEIEQISNLKGYTGTHNLSLKAINLILDELWHTNDNQIAIFNRLKLVPKKV DLSQQKEIPTTLVDDFILSPVVKRSFIQSIKVINAIIKKYGLPNDIIIELAREKNSK DAQKMINEMQKRNRQTNERIEEIIRTTGKENAKYLIEKIKLHDMQEGKCLYS LEAIPLEDLLNNPFNYEVDHIIPRSVSFDNSFNNKVLVKQEENSKKGNRTPFQ YLSSSDSKISYETFKKHILNLAKGKGRISKTKKEYLLEERDINRFSVQKDFINRNL VDTRYATRGLMNLLRSYFRVNNLDVKVKSINGGFTSFLRRKWKFKKERNKG YKHHAEDALIIANADFIFKEWKKLDKAKKVMENQMFEEKQAESMPEIETEQ EYKEIFITPHQIKHIKDFKDYKYSHRVDKKPNRKLINDTLYSTRKDDKGNTLIV NNLNGLYDKDNDKLKKLINKSPEKLLMYHHDPQTYQKLKLIMEQYGDEKNP LYKYYEETGNYLTKYSKKDNGPVIKKIKYYGNKLNAHLDITDDYPNSRNKVVK LSLKPYRFDVYLDNGVYKFVTVKNLDVIKKENYYEVNSKCYEEAKKLKKISNQ AEFIASFYKNDLIKINGELYRVIGVNSDKNNLIEVNMIDITYREYLENMNDKRP PHIIKTIASKTQSIKKYSTDILGNLYEVKSKKHPQIIKKG	9,013	N580A	H557A	D10A
cCas9-v17	Staphylococcus aureus	MKRNYILGLDIGITSVGYGIIDYETRDVIDAGVRLFKEANVENNEGRRSKRGA RRLKRRRRHRIQRVKKLLFDYNLLTDHSELSGINPYEARVKGLSQKLSEEEFSA ALLHLAKRRGVHNVNEVEEDTGNELSTKEQISRNSKALEEKYVAELQLERLKK DGEVRGSINRFKTSDYVKEAKQLLKVQKAYHQLDQSFIDTYIDLLETRRTYYE GPGEGSPFGWKDIKEWYEMLMGHCTYFPEELRSVKYAYNADLYNALNDLN NLVITRDENEKLEYYEKFQIIENVFKQKKKPTLKQIAKEILVNEEDIKGYRVTST GKPEFTNLKVYHDIKDITARKEIIENAELLDQIAKILTIYQSSEDIQEELTNLNSE LTQEEIEQISNLKGYTGTHNLSLKAINLILDELWHTNDNQIAIFNRLKLVPKKV DLSQQKEIPTTLVDDFILSPVVKRSFIQSIKVINAIIKKYGLPNDIIIELAREKNSK DAQKMINEMQKRNRQTNERIEEIIRTTGKENAKYLIEKIKLHDMQEGKCLYS LEAIPLEDLLNNPFNYEVDHIIPRSVSFDNSFNNKVLVKQEENSKKGNRTPFQ YLSSSDSKISYETFKKHILNLAKGKGRISKTKKEYLLEERDINRFSVQKDFINRNL VDTRYATRGLMNLLRSYFRVNNLDVKVKSINGGFTSFLRRKWKFKKERNKG YKHHAEDALIIANADFIFKEWKKLDKAKKVMENQMFEEKQAESMPEIETEQ EYKEIFITPHQIKHIKDFKDYKYSHRVDKKPNRKLINDTLYSTRKDDKGNTLIV NNLNGLYDKDNDKLKKLINKSPEKLLMYHHDPQTYQKLKLIMEQYGDEKNP LYKYYEETGNYLTKYSKKDNGPVIKKIKYYGNKLNAHLDITDDYPNSRNKVVK LSLKPYRFDVYLDNGVYKFVTVKNLDVIKKENYYEVNSKCYEEAKKLKKISNQ AEFIASFYKNDLIKINGELYRVIGVNNSTRNIVELNMIDITYREYLENMNDKRP PHIIKTIASKTQSIKKYSTDILGNLYEVKSKKHPQIIKKG	9,014	N580A	H557A	D10A
cCas9-v21	Staphylococcus aureus	MKRNYILGLDIGITSVGYGIIDYETRDVIDAGVRLFKEANVENNEGRRSKRGA RRLKRRRRHRIQRVKKLLFDYNLLTDHSELSGINPYEARVKGLSQKLSEEEFSA ALLHLAKRRGVHNVNEVEEDTGNELSTKEQISRNSKALEEKYVAELQLERLKK DGEVRGSINRFKTSDYVKEAKQLLKVQKAYHQLDQSFIDTYIDLLETRRTYYE GPGEGSPFGWKDIKEWYEMLMGHCTYFPEELRSVKYAYNADLYNALNDLN NLVITRDENEKLEYYEKFQIIENVFKQKKKPTLKQIAKEILVNEEDIKGYRVTST GKPEFTNLKVYHDIKDITARKEIIENAELLDQIAKILTIYQSSEDIQEELTNLNSE LTQEEIEQISNLKGYTGTHNLSLKAINLILDELWHTNDNQIAIFNRLKLVPKKV DLSQQKEIPTTLVDDFILSPVVKRSFIQSIKVINAIIKKYGLPNDIIIELAREKNSK DAQKMINEMQKRNRQTNERIEEIIRTTGKENAKYLIEKIKLHDMQEGKCLYS LEAIPLEDLLNNPFNYEVDHIIPRSVSFDNSFNNKVLVKQEENSKKGNRTPFQ YLSSSDSKISYETFKKHILNLAKGKGRISKTKKEYLLEERDINRFSVQKDFINRNL	9,015	N580A	H557A	D10A

		VDTRYATRGLMNLLRSYFRVNNLDVKVKSINGGFTSFLRRKWKFKKERNKG YKHHAEDALIIANADFIFKEWKKLDKAKKVMENQMFEEKQAESMPEIETEQ EYKEIFITPHQIKHIKDFKDYKYSHRVDKKPNRKLINDTLYSTRKDDKGNTLIV NNLNGLYDKDNDKLKKLINKSPEKLLMYHHDPQTYQKLKLIMEQYGDEKNP LYKYYEETGNYLTKYSKKDNGPVIKKIKYYGNKLNAHLDITDDYPNSRNKVVK LSLKPYRFDVYLDNGVYKFVTVKNLDVIKKENYYEVNSKCYEEAKKLKKISNQ AEFIASFYKNDLIKINGELYRVIGVNSDDRNIIELNMIDITYREYLENMNDKRP PHIIKTIASKTQSIKKYSTDILGNLYEVKSKKHPQIIKKG				
cCas9-v42	Staphylococcus aureus	MKRNYILGLDIGITSVGYGIIDYETRDVIDAGVRLFKEANVENNEGRRSKRGA RRLKRRRRHRIQRVKKLLFDYNLLTDHSELSGINPYEARVKGLSQKLSEEEFSA ALLHLAKRRGVHNVNEVEEDTGNELSTKEQISRNSKALEEKYVAELQLERLKK DGEVRGSINRFKTSDYVKEAKQLLKVQKAYHQLDQSFIDTYIDLLETRRTYYE GPGEGSPFGWKDIKEWYEMLMGHCTYFPEELRSVKYAYNADLYNALNDLN NLVITRDENEKLEYYEKFQIIENVFKQKKKPTLKQIAKEILVNEEDIKGYRVTST GKPEFTNLKVYHDIKDITARKEIIENAELLDQIAKILTIYQSSEDIQEELTNLNSE LTQEEIEQISNLKGYTGTHNLSLKAINLILDELWHTNDNQIAIFNRLKLVPKKV DLSQQKEIPTTLVDDFILSPVVKRSFIQSIKVINAIIKKYGLPNDIIIELAREKNSK DAQKMINEMQKRNRQTNERIEEIIRTTGKENAKYLIEKIKLHDMQEGKCLYS LEAIPLEDLLNNPFNYEVDHIIPRSVSFDNSFNNKVLVKQEENSKKGNRTPFQ YLSSSDSKISYETFKKHILNLAKGKGRISKTKKEYLLEERDINRFSVQKDFINRNL VDTRYATRGLMNLLRSYFRVNNLDVKVKSINGGFTSFLRRKWKFKKERNKG YKHHAEDALIIANADFIFKEWKKLDKAKKVMENQMFEEKQAESMPEIETEQ EYKEIFITPHQIKHIKDFKDYKYSHRVDKKPNRKLINDTLYSTRKDDKGNTLIV NNLNGLYDKDNDKLKKLINKSPEKLLMYHHDPQTYQKLKLIMEQYGDEKNP LYKYYEETGNYLTKYSKKDNGPVIKKIKYYGNKLNAHLDITDDYPNSRNKVVK LSLKPYRFDVYLDNGVYKFVTVKNLDVIKKENYYEVNSKCYEEAKKLKKISNQ AEFIASFYKNDLIKINGELYRVIGVNNNRLNKIELNMIDITYREYLENMNDKRP PHIIKTIASKTQSIKKYSTDILGNLYEVKSKKHPQIIKKG	9,016	N580A	H557A	D10A
CdiCas9	Corynebacterium diphtheriae	MKYHVGIDVGTFSVGLAAIEVDDAGMPIKTLSLVSHIHDSGLDPDEIKSAVT RLASSGIARRTRRLYRRKRRRLQQLDKFIQRQGWPVIELEDYSDPLYPWKVR AELAASYIADEKERGEKLSVALRHIARHRGWRNPYAKVSSLYLPDGPSDAFK AIREEIKRASGQPVPETATVGQMVTLCELGTLKLRGEGGVLSARLQQSDYAR EIQEICRMQEIGQELYRKIIDVVFAAESPKGSASSRVGKDPLQPGKNRALKAS DAFQRYRIAALIGNLRVRVDGEKRILSVEEKNLVFDHLVNLTPKKEPEWVTIA EILGIDRGQLIGTATMTDDGERAGARPPTHDTNRSIVNSRIAPLVDWWKTA SALEQHAMVKALSNAEVDDFDSPEGAKVQAFFADLDDDVHAKLDSLHLPV GRAAYSEDTLVRLTRRMLSDGVDLYTARLQEFGIEPSWTPPTPRIGEPVGNP AVDRVLKTVSRWLESATKTWGAPERVIIEHVREGFVTEKRAREMDGDMRR RAARNAKLFQEMQEKLNVQGKPSRADLWRYQSVQRQNCQCAYCGSPITF SNSEMDHIVPRAGQGSTNTRENLVAVCHRCNQSKGNTPFAIWAKNTSIEG VSVKEAVERTRHWVTDTGMRSTDFKKFTKAVVERFQRATMDEEIDARSME SVAWMANELRSRVAQHFASHGTTVRVYRGSLTAEARRASGISGKLKFFDGV GKSRLDRRHHAIDAAVIAFTSDYVAETLAVRSNLKQSQAHRQEAPQWREFT GKDAEHRAAWRVWCQKMEKLSALLTEDLRDDRVVVMSNVRLRLGNGSA HKETIGKLSKVKLSSQLSVSDIDKASSEALWCALTREPGFDPKEGLPANPERHI RVNGTHVYAGDNIGLFPVSAGSIALRGGYAELGSSFHHARVYKITSGKKPAF AMLRVYTIDLLPYRNQDLFSVELKPQTMSMRQAEKKLRDALATGNAEYLG WLVVDDELVVDTSKIATDQVKAVEAELGTIRRWRVDGFFSPSKLRLRPLQM SKEGIKKESAPELSKIIDRPGWLPAVNKLFSDGNVTVVRRDSLGRVRLESTAH LPVTWKVQ	9,017	N597A	H573A	D8A
CjeCas9	Campylobacter jejuni	MARILAFDIGISSIGWAFSENDELKDCGVRIFTKVENPKTGESLALPRRLARSA RKRLARRKARLNHLKHLIANEFKLNYEDYQSFDESLAKAYKGSLISPYELRFRA LNELLSKQDFARVILHIAKRRGYDDIKNSDDKEKGAILKAIKQNEEKLANYQS VGEYLYKEYFQKFKENSKEFTNVRNKKESYERCIAQSFLKDELKLIFKKQREFG FSFSKKFEEEVLSVAFYKRALKDFSHLVGNCSFFTDEKRAPKNSPLAFMFVAL TRIINLLNNLKNTEGILYTKDDLNALLNEVLKNGTLTYKQTKKLLGLSDDYEFK GEKGTYFIEFKKYKEFIKALGEHNLSQDDLNEIAKDITLIKDEIKLKKALAKYDLN QNQIDSLSKLEFKDHLNISFKALKLVTPLMLEGKKYDEACNELNLKVAINEDK	9,018	N582A	H559A	D8A

		KDFLPAFNETYYKDEVTNPVVLRAIKEYRKVLNALLKKYGKVHKINIELAREVG KNHSQRAKIEKEQNENYKAKKDAELECEKLGLKINSKNILKLRLFKEQKEFCAY SGEKIKISDLQDEKMLEIDHIYPYSRSFDDSYMNKVLVFTKQNQEKLNQTPFE AFGNDSAKWQKIEVLAKNLPTKKQKRILDKNYKDKEQKNFKDRNLNDTRYI ARLVLNYTKDYLDFLPLSDDENTKLNDTQKGSKVHVEAKSGMLTSALRHTW GFSAKDRNNHLHHAIDAVIIAYANNSIVKAFSDFKKEQESNSAELYAKKISELD YKNKRKFFEPFSGFRQKVLDKIDEIFVSKPERKKPSGALHEETFRKEEEFYQSY GGKEGVLKALELGKIRKVNGKIVKNGDMFRVDIFKHKKTNKFYAVPIYTMDF ALKVLPNKAVARSKKGEIKDWILMDENYEFCFSLYKDSLILIQTKDMQEPEFV YYNAFTSSTVSLIVSKHDNKFETLSKNQKILFKNANEKEVIAKSIGIQNLKVFEK YIVSALGEVTKAEFRQREDFKK				
GeoCas9	Geobacillus stearothermophilus	MRYKIGLDIGITSVGWAVMNLDIPRIEDLGVRIFDRAENPQTGESLALPRRLA RSARRRLRRRKHRLERIRRLVIREGILTKEELDKLFEEKHEIDVWQLRVEALDR KLNNDELARVLLHLAKRRGFKSNRKSERSNKENSTMLKHIEENRAILSSYRTV GEMIVKDPKFALHKRNKGENYTNTIARDDLEREIRLIFSKQREFGNMSCTEEF ENEYITIWASQRPVASKDDIEKKVGFCTFEPKEKRAPKATYTFQSFIAWEHIN KLRLISPSGARGLTDEERRLLYEQAFQKNKITYHDIRTLLHLPDDTYFKGIVYDR GESRKQNENIRFLELDAYHQIRKAVDKVYGKGKSSSFLPIDFDTFGYALTLFKD DADIHSYLRNEYEQNGKRMPNLANKVYDNELIEELLNLSFTKFGHLSLKALRS ILPYMEQGEVYSSACERAGYTFTGPKKKQKTMLLPNIPPIANPVVMRALTQA RKVVNAIIKKYGSPVSIHIELARDLSQTFDERRKTKKEQDENRKKNETAIRQL MEYGLTLNPTGHDIVKFKLWSEQNGRCAYSLQPIEIERLLEPGYVEVDHVIPY SRSLDDSYTNKVLVLTRENREKGNRIPAEYLGVGTERWQQFETFVLTNKQFS KKKRDRLLRLHYDENEETEFKNRNLNDTRYISRFFANFIREHLKFAESDDKQK VYTVNGRVTAHLRSRWEFNKNREESDLHHAVDAVIVACTTPSDIAKVTAFY QRREQNKELAKKTEPHFPQPWPHFADELRARLSKHPKESIKALNLGNYDDQ KLESLQPVFVSRMPKRSVTGAAHQETLRRYVGIDERSGKIQTVVKTKLSEIKL DASGHFPMYGKESDPRTYEAIRQRLLEHNNDPKKAFQEPLYKPKKNGEPGP VIRTVKIIDTKNQVIPLNDGKTVAYNSNIVRVDVFEKDGKYYCVPVYTMDIM KGILPNKAIEPNKPYSEWKEMTEDYTFRFSLYPNDLIRIELPREKTVKTAAGEE INVKDVFVYYKTIDSANGGLELISHDHRFSLRGVGSRTLKRFEKYQVDVLGNI YKVRGEKRVGLASSAHSKPGKTIRPLQSTRD	9,019	N605A	H582A	D8A
iSpyMacCas9	Streptococcus spp.	MDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLF DSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRLEESFL VEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAH MIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRKLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLS KDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSAS MIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEF YKFIKPILEKMDGTEELLVKLKREDLLRKQRTFDNGSIPHQIHLGELHAILRRQ EDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFE EVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTE GMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVED RFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYA HLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANR NFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKV VDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQ ILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSF LKDDSIDNKVLTRSDKNRGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKF DNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLI REVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIKKYPK LESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEI RKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEIQTVGQNGG LFDDNPKSPLEVTPSKLVPLKKELNPKKYGGYQKPTTAYPVLLITDTKQLIPISV MNKKQFEQNPVKFLRDRGYQQVGKNDFIKLPKYTLVDIGDGIKRLWASSKEI HKGNQLVVSKKSQILLYHAHHLDSDLSNDYLQNHNQQFDVLFNEIISFSKKC KLGKEHIQKIENVYSNKKNSASIEELAESFIKLLGFTQLGATSPFNFLGVKLNQ KQYKGKKDYILPCTEGTLIRQSITGLYETRVDLSKIGEDSGGSGGSKRTADGSE FES	9,020	N863A	H840A	D10A

NmeCas9	Neisseria meningitidis	MAAFKPNSINYILGLDIGIASVGWAMVEIDEEENPIRLIDLGVRVFERAEVPK TGDSLAMARRLARSVRRLTRRRAHRLLRTRRLLKREGVLQAANFDENGLIKS LPNTPWQLRAAALDRKLTPLEWSAVLLHLIKHRGYLSQRKNEGETADKELG ALLKGVAGNAHALQTGDFRTPAELALNKFEKESGHIRNQRSDYSHTFSRKDL QAELILLFEKQKEFGNPHVSGGLKEGIETLLMTQRPALSGDAVQKMLGHCTF EPAEPKAAKNTYTAERFIWLTKLNNLRILEQGSERPLTDTERATLMDEPYRKS KLTYAQARKLLGLEDTAFFKGLRYGKDNAEASTLMEMKAYHAISRALEKEGL KDKKSPLNLSPELQDEIGTAFSLFKTDEDITGRLKDRIQPEILEALLKHISFDKFV QISLKALRRIVPLMEQGKRYDEACAEIYGDHYGKKNTEEKIYLPPIPADEIRNP VVLRALSQARKVINGVVRRYGSPARIHIETAREVGKSFKDRKEIEKRQEENRK DREKAAAKFREYFPNFVGEPKSKDILKLRLYEQQHGKCLYSGKEINLGRLNEK GYVEIDHALPFSRTWDDSFNNKVLVLGSENQNKGNQTPYEYFNGKDNSRE WQEFKARVETSRFPRSKKQRILLQKFDEDGFKERNLNDTRYVNRFLCQFVA DRMRLTGKGKKRVFASNGQITNLLRGFWGLRKVRAENDRHHALDAVVVA CSTVAMQQKITRFVRYKEMNAFDGKTIDKETGEVLHQKTHFPQPWEFFAQ EVMIRVFGKPDGKPEFEEADTLEKLRTLLAEKLSSRPEAVHEYVTPLFVSRAP NRKMSGQGHMETVKSAKRLDEGVSVLRVPLTQLKLKDLEKMVNREREPKL YEALKARLEAHKDDPAKAFAEPFYKYDKAGNRTQQVKAVRVEQVQKTGVW VRNHNGIADNATMVRVDVFEKGDKYYLVPIYSWQVAKGILPDRAVVQGKD EEDWQLIDDSFNFKFSLHPNDLVEVITKKARMFGYFASCHRGTGNINIRIHD LDHKIGKNGILEGIGVKTALSFQKYQIDELGKEIRPCRLKKRPPVR	9,021	N611A	H588A	D16A
ScaCas9	Streptococcus canis	MEKKYSIGLDIGTNSVGWAVITDDYKVPSKKFKVLGNTNRKSIKKNLMGALL FDSGETAEATRLKRTARRYTRRKNRIRYLQEIFANEMAKLDDSFFQRLEESF LVEEDKKNERHPIFGNLADEVAYHRNYPTIYHLRKKLADSPEKADLRLIYLALA HIIKFRGHFLIEGKLNAENSDVAKLFYQLIQTYNQLFEESPLDEIEVDAKGILSA RLSKSKRLEKLIAVFPNEKKNGLFGNIIALALGLTPNFKSNFDLTEDAKLQLSKD TYDDDLDELLGQIGDQYADLFSAAKNLSDAILLSDILRSNSEVTKAPLSASMV KRYDEHHQDLALLKTLVRQQFPEKYAEIFKDDTKNGYAGYVGIGIKHRKRTT KLATQEEFYKFIKPILEKMDGAEELLAKLNRDDLLRKQRTFDNGSIPHQIHLKE LHAILRRQEEFYPFLKENREKIEKILTFRIPYYVGPLARGNSRFAWLTRKSEEAI TPWNFEEVVDKGASAQSFIERMTNFDEQLPNKKVLPKHSLLYEYFTVYNELT KVKYVTERMRKPEFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSV EIIGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEE RLKTYAHLFDDKVMKQLKRRHYTGWGRLSRKMINGIRDKQSGKTILDFLKS DGFSNRNFMQLIHDDSLTFKEEIEKAQVSGQGDSLHEQIADLAGSPAIKKGIL QTVKIVDELVKVMGHKPENIVIEMARENQTTTKGLQQSRERKKRIEEGIKELE SQILKENPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVP QSFIKDDSIDNKVLTRSVENRGKSDNVPSEEVVKKMKNYWRQLLNAKLITQ RKFDNLTKAERGGLSEADKAGFIKRQLVETRQITKHVARILDSRMNTKRDKN DKPIREVKVITLKSKLVSDFRKDFQLYKVRDINNYHHAHDAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKRFFYSNIMNFFKTEVKL ANGEIRKRPLIETNGETGEVVWNKEKDFATVRKVLAMPQVNIVKKTEVQTG GFSKESILSKRESAKLIPRKKGWDTRKYGGFGSPTVAYSILVVAKVEKGKAKKL KSVKVLVGITIMEKGSYEKDPIGFLEAKGYKDIKKELIFKLPKYSLFELENGRRR MLASATELQKANELVLPQHLVRLLYYTQNISATTGSNNLGYIEQHREEFKEIF EKIIDFSEKYILKNKVNSNLKSSFDEQFAVSDSILLSNSFVSLLKYTSFGASGGFT FLDLDVKQGRLRYQTVTEVLDATLIYQSITGLYETRTDLSQLGGD	9,022	N872A	H849A	D10A
ScaCas9-HiFi-Sc++	Streptococcus canis	MEKKYSIGLDIGTNSVGWAVITDDYKVPSKKFKVLGNTNRKSIKKNLMGALL FDSGETAEATRLKRTARRYTRRKNRIRYLQEIFANEMAKLDDSFFQRLEESF LVEEDKKNERHPIFGNLADEVAYHRNYPTIYHLRKKLADSPEKADLRLIYLALA HIIKFRGHFLIEGKLNAENSDVAKLFYQLIQTYNQLFEESPLDEIEVDAKGILSA RLSKSKRLEKLIAVFPNEKKNGLFGNIIALALGLTPNFKSNFDLTEDAKLQLSKD TYDDDLDELLGQIGDQYADLFSAAKNLSDAILLSDILRSNSEVTKAPLSASMV KRYDEHHQDLALLKTLVRQQFPEKYAEIFKDDTKNGYAGYVGADKKLRKRS GKLATEEEFYKFIKPILEKMDGAEELLAKLNRDDLLRKQRTFDNGSIPHQIHLK ELHAILRRQEEFYPFLKENREKIEKILTFRIPYYVGPLARGNSRFAWLTRKSEEA ITPWNFEEVVDKGASAQSFIERMTNFDEQLPNKKVLPKHSLLYEYFTVYNEL TKVKYVTERMRKPEFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDS VEIIGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIE	9,023	N872A	H849A	D10A

		ERLKTYAHLFDDKVMKQLKRRHYTGWGRLSRKMINGIRDKQSGKTILDFLKS DGFSNANFMQLIHDDSLTFKEEIEKAQVSGQGDSLHEQIADLAGSPAIKKGIL QTVKIVDELVKVMGHKPENIVIEMARENQTTTKGLQQSRERKKRIEEGIKELE SQILKENPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVP QSFIKDDSIDNKVLTRSVENRGKSDNVPSEEVVKKMKNYWRQLLNAKLITQ RKFDNLTKAERGGLSEADKAGFIKRQLVETRQITKHVARILDSRMNTKRDKN DKPIREVKVITLKSKLVSDFRKDFQLYKVRDINNYHHAHDAYLNAVVGTALIK KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKRFFYSNIMNFFKTEVKL ANGEIRKRPLIETNGETGEVVWNKEKDFATVRKVLAMPQVNIVKKTEVQTG GFSKESILSKRESAKLIPRKKGWDTRKYGGFGSPTVAYSILVVAKVEKGKAKKL KSVKVLVGITIMEKGSYEKDPIGFLEAKGYKDIKKELIFKLPKYSLFELENGRRR MLASAKELQKANELVLPQHLVRLLYYTQNISATTGSNNLGYIEQHREEFKEIF EKIIDFSEKYILKNKVNSNLKSSFDEQFAVSDSILLSNSFVSLLKYTSFGASGGFT FLDLDVKQGRLRYQTVTEVLDATLIYQSITGLYETRTDLSQLGGD				
SpyCas9-3var-NRRH	Streptococcus pyogenes	MDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLF DSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRLEESFL VEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAH MIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLS KDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSAS MVKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEE FYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGIIPHQIHLGELHAILRRQ GDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFE EVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTE GMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVED RFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYA HLFDDKVMKQLKRLRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRN FMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVV DELVKVMGGHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQI LKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSF LKDDSIDNKVLTRSDKNRGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKF DNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLI REVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIKKYPK LESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEI RKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKGNSDKLIARKKDWDPKKYGGFNSPTAAYSVLVVAKVEKGKSKKLKSVK ELLGITIMERSSFEKNPIGFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLAS AGVLHKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDE IIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGVPAA FKYFDTTIDKKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGD	9,024	N863A	H840A	D10A
SpyCas9-3var-NRTH	Streptococcus pyogenes	MDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLF DSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRLEESFL VEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAH MIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLS KDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSAS MVKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEE FYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGIIPHQIHLGELHAILRRQ GDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFE EVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTE GMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVED RFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYA HLFDDKVMKQLKRLRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRN FMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVV DELVKVMGGHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQI LKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSF LKDDSIDNKVLTRSDKNRGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKF DNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLI REVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIKKYPK	9,025	N863A	H840A	D10A

		LESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEI RKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKGNSDKLIARKKDWDPKKYGGFNSPTVAYSVLVVAKVEKGKSKKLKSVK ELLGITIMERSSFEKNPIGFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLAS ASVLHKGNELALPSKYVNFLYLASHYEKLKGSSEDNKQKQLFVEQHKHYLDEI IEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGASAAF KYFDTTIGRKLYTSTKEVLDATLIHQSITGLYETRIDLSQLGGD				
SpyCas9-3var-NRCH	Streptococcus pyogenes	MDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLF DSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRLEESFL VEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAH MIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLS KDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSAS MVKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEE FYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGIIPHQIHLGELHAILRRQ GDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFE EVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTE GMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVED RFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYA HLFDDKVMKQLKRLRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRN FMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVV DELVKVMGGHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQI LKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSF LKDDSIDNKVLTRSDKNRGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKF DNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLI REVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIKKYPK LESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEI RKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKGNSDKLIARKKDWDPKKYGGFNSPTVAYSVLVVAKVEKGKSKKLKSVK ELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLAS AGVLQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDE IIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAA FKYFDTTINRKQYNTTKEVLDATLIRQSITGLYETRIDLSQLGGD	9,026	N863A	H840A	D10A
SpyCas9-HF1	Streptococcus pyogenes	MDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLF DSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRLEESFL VEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAH MIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLS KDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSAS MIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEF YKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQ EDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFE EVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTE GMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVED RFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYA HLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANR NFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKV VDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQ ILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSF LKDDSIDNKVLTRSDKNRGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKF DNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLI REVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIKKYPK LESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEI RKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKE LLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASA GELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEII EQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAF KYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGD	9,027	N863A	H840A	D10A

SpyCas9-QQR1	Streptococcus pyogenes	MDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKNRGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASARELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKQYRSTKEVLDATLIHQSITGLYETRIDLSQLGGD	9,028	N863A	H840A	D10A
SpyCas9-SpG	Streptococcus pyogenes	MDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKNRGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFLWPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAKQLQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKQYRSTKEVLDATLIHQSITGLYETRIDLSQLGGD	9,029	N863A	H840A	D10A
SpyCas9-VQR	Streptococcus pyogenes	MDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEF	9,030	N863A	H840A	D10A

		YKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQ EDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFE EVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTE GMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVED RFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYA HLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANR NFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKV VDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQ ILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSF LKDDSIDNKVLTRSDKNRGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKF DNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLI REVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIKKYPK LESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEI RKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFVSPTVAYSVLVVAKVEKGKSKKLKSVKE LLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASA GELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEII EQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAF KYFDTTIDRKQYRSTKEVLDATLIHQSITGLYETRIDLSQLGGD				
SpyCas9-VRER	Streptococcus pyogenes	MDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLF DSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRLEESFL VEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAH MIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLS KDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSAS MIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEF YKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQ EDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFE EVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTE GMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVED RFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYA HLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANR NFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKV VDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQ ILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSF LKDDSIDNKVLTRSDKNRGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKF DNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLI REVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIKKYPK LESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEI RKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFVSPTVAYSVLVVAKVEKGKSKKLKSVKE LLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASA RELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEII EQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAF KYFDTTIDRKEYRSTKEVLDATLIHQSITGLYETRIDLSQLGGD	9,031	N863A	H840A	D10A
SpyCas9-xCas	Streptococcus pyogenes	MDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLF DSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRLEESFL VEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAH MIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDTKLQLS KDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSAS MIKLYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEF YKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGIIPHQIHLGELHAILRRQE DFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEK VVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTE GMRKPAFLSGDQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVED RFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYA HLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANR NFIQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVV	9,032	N863A	H840A	D10A

		DELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQI LKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSF LKDDSIDNKVLTRSDKNRGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKF DNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLI REVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIKKYPK LESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEI RKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES ILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKE LLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASA GVLQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEII EQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAF KYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGD				
SpyCas9-xCas-NG	Streptococcus pyogenes	MDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLF DSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRLEESFL VEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAH MIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILS ARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDTKLQLS KDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSAS MIKLYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEF YKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGIIPHQIHLGELHAILRRQE DFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEK VVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTE GMRKPAFLSGDQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVED RFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYA HLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANR NFIQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVV DELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQI LKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSF LKDDSIDNKVLTRSDKNRGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKF DNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLI REVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIKKYPK LESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEI RKRPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKES IRPKRNSDKLIARKKDWDPKKYGGFVSPTVAYSVLVVAKVEKGKSKKLKSVKE LLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASA RFLQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEII EQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPRAF KYFDTTIDRKVYRSTKEVLDATLIHQSITGLYETRIDLSQLGGD	9,033	N863A	H840A	D10A
St1Cas9-CNRZ1066	Streptococcus thermophilus	MSDLVLGLDIGIGSVGVGILNKVTGEIIHKNSRIFPAAQAENNLVRRTNRQG RRLARRKKHRRVRLNRLFEESGLITDFTKISINLNPYQLRVKGLTDELSNEELFI ALKNMVKHRGISYLDDASDDGNSSVGDYAQIVKENSKQLETKTPGQIQLER YQTYGQLRGDFTVEKDGKKHRLINVFPTSAYRSEALRILQTQQEFNPQITDEF INRYLEILTGKRKYYHGPGNEKSRTDYGRYRTSGETLDNIFGILIGKCTFYPDEF RAAKASYTAQEFNLLNDLNNLTVPTETKKLSKEQKNQIINYVKNEKAMGPAK LFKYIAKLLSCDVADIKGYRIDKSGKAEIHTFEAYRKMKTLETLDIEQMDRETL DKLAYVLTLNTEREGIQEALEHEFADGSFSQKQVDELVQFRKANSSIFGKGW HNFSVKLMMELIPELYETSEEQMTILTRLGKQKTTSSSNKTKYIDEKLLTEEIY NPVVAKSVRQAIKIVNAAIKEYGDFDNIVIEMARETNEDDEKKAIQKIQKAN KDEKDAAMLKAANQYNGKAELPHSVFHGHKQLATKIRLWHQQGERCLYT GKTISIHDLINNSNQFEVDHILPLSITFDDSLANKVLVYATANQEKGQRTPYQ ALDSMDDAWSFRELKAFVRESKTLSNKKKEYLLTEEDISKFDVRKKFIERNLV DTRYASRVVLNALQEHFRAHKIDTKVSVVRGQFTSQLRRHWGIEKTRDTYH HHAVDALIIAASSQLNLWKKQKNTLVSYSEEQLLDIETGELISDDEYKESVFKA PYQHFVDTLKSKEFEDSILFSYQVDSKFNRKISDATIYATRQAKVGKDKKDET YVLGKIKDIYTQDGYDAFMKIYKKDKSKFLMYRHDPQTFEKVIEPILENYPNK QMNEKGKEVPCNPFLKYKEEHGYIRKYSKKGNGPEIKSLKYYDSKLLGNPIDI TPENSKNKVVLQSLKPWRTDVYFNKATGKYEILGLKYADLQFEKGTGTYKIS QEKYNDIKKKEGVDSDSEFKFTLYKNDLLLVKDTETKEQQLFRFLSRTLPKQK	9,034	N622A	H599A	D9A

		HYVELKPYDKQKFEGGEALIKVLGNVANGGQCIKGLAKSNISIYKVRTDVLG NQHIIKNEGDKPKLDF				
St1Cas9-LMG1831	Streptococcus thermophilus	MSDLVLGLDIGIGSVGVGILNKVTGEIIHKNSRIFPAAQAENNLVRRTNRQG RRLARRKKHRRVRLNRLFEESGLITDFTKISINLNPYQLRVKGLTDELSNEELFI ALKNMVKHRGISYLDDASDDGNSSVGDYAQIVKENSKQLETKTPGQIQLER YQTYGQLRGDFTVEKDGKKHRLINVFPTSAYRSEALRILQTQQEFNPQITDEF INRYLEILTGKRKYYHGPGNEKSRTDYGRYRTSGETLDNIFGILIGKCTFYPDEF RAAKASYTAQEFNLLNDLNNLTVPTETKKLSKEQKNQIINYVKNEKAMGPAK LFKYIAKLLSCDVADIKGYRIDKSGKAEIHTFEAYRKMKTLETLDIEQMDRETL DKLAYVLTLNTEREGIQEALEHEFADGSFSQKQVDELVQFRKANSSIFGKGW HNFSVKLMMELIPELYETSEEQMTILTRLGKQKTTSSSNKTKYIDEKLLTEEIY NPVVAKSVRQAIKIVNAAIKEYGDFDNIVIEMARETNEDDEKKAIQKIQKAN KDEKDAAMLKAANQYNGKAELPHSVFHGHKQLATKIRLWHQQGERCLYT GKTISIHDLINNSNQFEVDHILPLSITFDDSLANKVLVYATANQEKGQRTPYQ ALDSMDDAWSFRELKAFVRESKTLSNKKKEYLLTEEDISKFDVRKKFIERNLV DTRYASRVVLNALQEHFRAHKIDTKVSVVRGQFTSQLRRHWGIEKTRDTYH HHAVDALIIAASSQLNLWKKQKNTLVSYSEEQLLDIETGELISDDEYKESVFKA PYQHFVDTLKSKEFEDSILFSYQVDSKFNRKISDATIYATRQAKVGKDKKDET YVLGKIKDIYTQDGYDAFMKIYKKDKSKFLMYRHDPQTFEKVIEPILENYPNK QMNEKGKEVPCNPFLKYKEEHGYIRKYSKKGNGPEIKSLKYYDSKLLGNPIDI TPENSKNKVVLQSLKPWRTDVYFNKNTGKYEILGLKYADLQFEKKTGTYKISQ EKYNGIMKEEGVDSDSEFKFTLYKNDLLLVKDTETKEQQLFRFLSRTMPNVK YYVELKPYSKDKFEKNESLIEILGSADKSGRCIKGLGKSNISIYKVRTDVLGNQH IIKNEGDKPKLDF	9,035	N622A	H599A	D9A
St1Cas9-MTH17CL396	Streptococcus thermophilus	MSDLVLGLDIGIGSVGVGILNKVTGEIIHKNSRIFPAAQAENNLVRRTNRQG RRLARRKKHRRVRLNRLFEESGLITDFTKISINLNPYQLRVKGLTDELSNEELFI ALKNMVKHRGISYLDDASDDGNSSVGDYAQIVKENSKQLETKTPGQIQLER YQTYGQLRGDFTVEKDGKKHRLINVFPTSAYRSEALRILQTQQEFNPQITDEF INRYLEILTGKRKYYHGPGNEKSRTDYGRYRTSGETLDNIFGILIGKCTFYPDEF RAAKASYTAQEFNLLNDLNNLTVPTETKKLSKEQKNQIINYVKNEKAMGPAK LFKYIAKLLSCDVADIKGYRIDKSGKAEIHTFEAYRKMKTLETLDIEQMDRETL DKLAYVLTLNTEREGIQEALEHEFADGSFSQKQVDELVQFRKANSSIFGKGW HNFSVKLMMELIPELYETSEEQMTILTRLGKQKTTSSSNKTKYIDEKLLTEEIY NPVVAKSVRQAIKIVNAAIKEYGDFDNIVIEMARETNEDDEKKAIQKIQKAN KDEKDAAMLKAANQYNGKAELPHSVFHGHKQLATKIRLWHQQGERCLYT GKTISIHDLINNSNQFEVDHILPLSITFDDSLANKVLVYATANQEKGQRTPYQ ALDSMDDAWSFRELKAFVRESKTLSNKKKEYLLTEEDISKFDVRKKFIERNLV DTRYASRVVLNALQEHFRAHKIDTKVSVVRGQFTSQLRRHWGIEKTRDTYH HHAVDALIIAASSQLNLWKKQKNTLVSYSEDQLLDIETGELISDDEYKESVFK APYQHFVDTLKSKEFEDSILFSYQVDSKFNRKISDATIYATRQAKVGKDKADE TYVLGKIKDIYTQDGYDAFMKIYKKDKSKFLMYRHDPQTFEKVIEPILENYPN KQINEKGKEVPCNPFLKYKEEHGYIRKYSKKGNGPEIKSLKYYDSKLGNHIDIT PKDSNNKVVLQSLKPWRTDVYFNKNTGKYEILGLKYSDMQFEKGTGKYSISK EQYENIKVREGVDENSEFKFTLYKNDLLLLKDSENGEQILLRFTSRNDTSKHYV ELKPYNRQKFEGSEYLIKSLGTVAKGGQCIKGLGKSNISIYKVRTDVLGNQHII KNEGDKPKLDF	9,036	N622A	H599A	D9A
St1Cas9-TH1477	Streptococcus thermophilus	MSDLVLGLDIGIGSVGVGILNKVTGEIIHKNSRIFPAAQAENNLVRRTNRQG RRLARRKKHRRVRLNRLFEESGLITDFTKISINLNPYQLRVKGLTDELSNEELFI ALKNMVKHRGISYLDDASDDGNSSVGDYAQIVKENSKQLETKTPGQIQLER YQTYGQLRGDFTVEKDGKKHRLINVFPTSAYRSEALRILQTQQEFNPQITDEF INRYLEILTGKRKYYHGPGNEKSRTDYGRYRTSGETLDNIFGILIGKCTFYPDEF RAAKASYTAQEFNLLNDLNNLTVPTETKKLSKEQKNQIINYVKNEKAMGPAK LFKYIAKLLSCDVADIKGYRIDKSGKAEIHTFEAYRKMKTLETLDIEQMDRETL DKLAYVLTLNTEREGIQEALEHEFADGSFSQKQVDELVQFRKANSSIFGKGW HNFSVKLMMELIPELYETSEEQMTILTRLGKQKTTSSSNKTKYIDEKLLTEEIY NPVVAKSVRQAIKIVNAAIKEYGDFDNIVIEMARETNEDDEKKAIQKIQKAN KDEKDAAMLKAANQYNGKAELPHSVFHGHKQLATKIRLWHQQGERCLYT GKTISIHDLINNSNQFEVDHILPLSITFDDSLANKVLVYATANQEKGQRTPYQ	9,037	N622A	H599A	D9A

		ALDSMDDAWSFRELKAFVRESKTLSNKKKEYLLTEEDISKFDVRKKFIERNLV DTRYASRVVLNALQEHFRAHKIDTKVSVVRGQFTSQLRRHWGIEKTRDTYH HHAVDALIIAASSQLNLWKKQKNTLVSYSEDQLLDIETGELISDDEYKESVFK APYQHFVDTLKSKEFEDSILFSYQVDSKFNRKISDATIYATRQAKVGKDKADE TYVLGKIKDIYTQDGYDAFMKIYKKDKSKFLMYRHDPQTFEKVIEPILENYPN KQINEKGKEVPCNPFLKYKEEHGYIRKYSKKGNGPEIKSLKYYDSKLGNHIDIT PKDSNNKVVLQSLKPWRTDVYFNKNTGKYEILGLKYSDMQFEKGTGKYSISK EQYENIKVREGVDENSEFKFTLYKNDLLLLKDSENGEQILLRFTSRNDTSKHYV ELKPYNRQKFEGSEYLIKSLGTVVKGGRCIKGLGKSNISIYKVRTDVLGNQHIIK NEGDKPKLDF				
sRGN3.1	Staphylococcus spp.	MNQKFILGLDIGITSVGYGLIDYETKNIIDAGVRLFPEANVENNEGRRSKRGS RRLKRRRIHRLERVKLLLTEYDLINKEQIPTSNNPYQIRVKGLSEILSKDELAIAL LHLAKRRGIHNVDVAADKEETASDSLSTKDQINKNAKFLESRYVCELQKERLE NEGHVRGVENRFLTKDIVREAKKIIDTQMQYYPEIDETFKEKYISLVETRREYF EGPGQGSPFGWNGDLKKWYEMLMGHCTYFPQELRSVKYAYSADLFNALN DLNNLIIQRDNSEKLEYHEKYHIIENVFKQKKKPTLKQIAKEIGVNPEDIKGYRI TKSGTPEFTSFKLFHDLKKVVKDHAILDDIDLLNQIAEILTIYQDKDSIVAELGQ LEYLMSEADKQSISELTGYTGTHSLSLKCMNMIIDELWHSSMNQMEVFTYL NMRPKKYELKGYQRIPTDMIDDAILSPVVKRTFIQSINVINKVIEKYGIPEDIIIE LARENNSDDRKKFINNLQKKNEATRKRINEIIGQTGNQNAKRIVEKIRLHDQ QEGKCLYSLESIPLEDLLNNPNHYEVDHIIPRSVSFDNSYHNKVLVKQSENSK KSNLTPYQYFNSGKSKLSYNQFKQHILNLSKSQDRISKKKKEYLLEERDINKFE VQKEFINRNLVDTRYATRELTNYLKAYFSANNMNVKVKTINGSFTDYLRKV WKFKKERNHGYKHHAEDALIIANADFLFKENKKLKAVNSVLEKPEIETKQLDI QVDSEDNYSEMFIIPKQVQDIKDFRNFKYSHRVDKKPNRQLINDTLYSTRKK DNSTYIVQTIKDIYAKDNTTLKKQFDKSPEKFLMYQHDPRTFEKLEVIMKQYA NEKNPLAKYHEETGEYLTKYSKKNNGPIVKSLKYIGNKLGSHLDVTHQFKSST KKLVKLSIKNYRFDVYLTEKGYKFVTIAYLNVFKKDNYYYIPKDKYQELKEKKKI KDTDQFIASFYKNDLIKLNGDLYKIIGVNSDDRNIIELDYYDIKYKDYCEINNIK GEPRIKKTIGKKTESIEKFTTDVLGNLYLHSTEKAPQLIFKRGL	9,038	N585A	H562A	D10A
sRGN3.3	Staphylococcus spp.	MNQKFILGLDIGITSVGYGLIDYETKNIIDAGVRLFPEANVENNEGRRSKRGS RRLKRRRIHRLERVKLLLTEYDLINKEQIPTSNNPYQIRVKGLSEILSKDELAIAL LHLAKRRGIHNVDVAADKEETASDSLSTKDQINKNAKFLESRYVCELQKERLE NEGHVRGVENRFLTKDIVREAKKIIDTQMQYYPEIDETFKEKYISLVETRREYF EGPGQGSPFGWNGDLKKWYEMLMGHCTYFPQELRSVKYAYSADLFNALN DLNNLIIQRDNSEKLEYHEKYHIIENVFKQKKKPTLKQIAKEIGVNPEDIKGYRI TKSGTPEFTSFKLFHDLKKVVKDHAILDDIDLLNQIAEILTIYQDKDSIVAELGQ LEYLMSEADKQSISELTGYTGTHSLSLKCMNMIIDELWHSSMNQMEVFTYL NMRPKKYELKGYQRIPTDMIDDAILSPVVKRTFIQSINVINKVIEKYGIPEDIIIE LARENNSDDRKKFINNLQKKNEATRKRINEIIGQTGNQNAKRIVEKIRLHDQ QEGKCLYSLESIPLEDLLNNPNHYEVDHIIPRSVSFDNSYHNKVLVKQSENSK KSNLTPYQYFNSGKSKLSYNQFKQHILNLSKSQDRISKKKKEYLLEERDINKFE VQKEFINRNLVDTRYATRELTSYLKAYFSANNMDVKVKTINGSFTNHLRKV WRFDKYRNHGYKHHAEDALIIANADFLFKENKKLQNTNKILEKPTIENNTKK VTVEKEEDYNNVFETPKLVEDIKQYRDYKFSHRVDKKPNRQLINDTLYSTRM KDEHDYIVQTITDIYGKDNTNLKKQFNKNPEKFLMYQNDPKTFEKLSIIMKQ YSDEKNPLAKYYEETGEYLTKYSKKNNGPIVKKIKLLGNKVGNHLDVTNKYEN STKKLVKLSIKNYRFDVYLTEKGYKFVTIAYLNVFKKDNYYYIPKDKYQELKEKK KIKDTDQFIASFYKNDLIKLNGDLYKIIGVNSDDRNIIELDYYDIKYKDYCEINNI KGEPRIKKTIGKKTESIEKFTTDVLGNLYLHSTEKAPQLIFKRGL	9,039	N585A	H562A	D10A

In some embodiments, a Cas protein requires a protospacer adjacent motif (PAM) to be present in or adjacent to a target DNA sequence for the Cas protein to bind and/or function. In some embodiments, the PAM is or comprises, from 5′ to 3′, NGG, YG, NNGRRT, NNNRRT,

NGA, TYCV, TATV, NTTN, or NNNGATT, where N stands for any nucleotide, Y stands for C or T, R stands for A or G, and V stands for A or C or G.In some embodiments, a Cas protein is a protein listed in Table 7 or 8. In some embodiments, a Cas protein comprises one or more mutations altering its PAM. In some embodiments, a Cas protein comprises E1369R, E1449H, and R1556A mutations or analogous substitutions to the amino acids corresponding to said positions. In some embodiments, a Cas protein comprises E782K, N968K, and R1015H mutations or analogous substitutions to the amino acids corresponding to said positions. In some embodiments, a Cas protein comprises D1135V, R1335Q, and T1337R mutations or analogous substitutions to the amino acids corresponding to said positions. In some embodiments, a Cas protein comprises S542R and K607R mutations or analogous substitutions to the amino acids corresponding to said positions. In some embodiments, a Cas protein comprises S542R, K548V, and N552R mutations or analogous substitutions to the amino acids corresponding to said positions. Exemplary advances in the engineering of Cas enzymes to recognize altered PAM sequences are reviewed in Collias et al Nature Communications 12:555 (2021), incorporated herein by reference in its entirety.

In some embodiments, the Cas protein is catalytically active and cuts one or both strands of the target DNA site. In some embodiments, cutting the target DNA site is followed by formation of an alteration, e.g., an insertion or deletion, e.g., by the cellular repair machinery.

In some embodiments, the Cas protein is modified to deactivate or partially deactivate the nuclease, e.g., nuclease-deficient Cas9. Whereas wild-type Cas9 generates double-strand breaks (DSBs) at specific DNA sequences targeted by a gRNA, a number of CRISPR endonucleases having modified functionalities are available, for example: a “nickase” version of Cas9 that has been partially deactivated generates only a single-strand break; a catalytically inactive Cas9 (“dCas9”) does not cut target DNA. In some embodiments, dCas9 binding to a DNA sequence may interfere with transcription at that site by steric hindrance. In some embodiments, dCas9 binding to an anchor sequence may interfere with (e.g., decrease or prevent) genomic complex (e.g., ASMC) formation and/or maintenance. In some embodiments, a DNA-binding domain comprises a catalytically inactive Cas9, e.g., dCas9. Many catalytically inactive Cas9 proteins are known in the art. In some embodiments, dCas9 comprises mutations in each endonuclease domain of the Cas protein, e.g., D10A and H840A or N863A mutations. In some embodiments, a catalytically inactive or partially inactive CRISPR/Cas domain comprises a Cas protein

comprising one or more mutations, e.g., one or more of the mutations listed in Table 7. In some embodiments, a Cas protein described on a given row of Table 7 comprises one, two, three, or all of the mutations listed in the same row of Table 7. In some embodiments, a Cas protein, e.g., not described in Table 7, comprises one, two, three, or all of the mutations listed in a row of Table 7 or a corresponding mutation at a corresponding site in that Cas protein.

In some embodiments, a catalytically inactive, e.g., dCas9, or partially deactivated Cas9 protein comprises a D11 mutation (e.g., D11A mutation) or an analogous substitution to the amino acid corresponding to said position. In some embodiments, a catalytically inactive Cas9 protein, e.g., dCas9, or partially deactivated Cas9 protein comprises a H969 mutation (e.g., H969A mutation) or an analogous substitution to the amino acid corresponding to said position. In some embodiments, a catalytically inactive Cas9 protein, e.g., dCas9, or partially deactivated Cas9 protein comprises a N995 mutation (e.g., N995A mutation) or an analogous substitution to the amino acid corresponding to said position. In some embodiments, a catalytically inactive Cas9 protein, e.g., dCas9, comprises mutations at one, two, or three of positions D11, H969, and N995 (e.g., D11A, H969A, and N995A mutations) or analogous substitutions to the amino acids corresponding to said positions.

In some embodiments, a catalytically inactive Cas9 protein, e.g., dCas9, or partially deactivated Cas9 protein comprises a D10 mutation (e.g., a D10A mutation) or an analogous substitution to the amino acid corresponding to said position. In some embodiments, a catalytically inactive Cas9 protein, e.g., dCas9, or partially deactivated Cas9 protein comprises a H557 mutation (e.g., a H557A mutation) or an analogous substitution to the amino acid corresponding to said position. In some embodiments, a catalytically inactive Cas9 protein, e.g., dCas9, comprises a D10 mutation (e.g., a D10A mutation) and a H557 mutation (e.g., a H557A mutation) or analogous substitutions to the amino acids corresponding to said positions.

In some embodiments, a catalytically inactive Cas9 protein, e.g., dCas9, or partially deactivated Cas9 protein comprises a D839 mutation (e.g., a D839A mutation) or an analogous substitution to the amino acid corresponding to said position. In some embodiments, a catalytically inactive Cas9 protein, e.g., dCas9, or partially deactivated Cas9 protein comprises a H840 mutation (e.g., a H840A mutation) or an analogous substitution to the amino acid corresponding to said position. In some embodiments, a catalytically inactive Cas9 protein, e.g., dCas9, or partially deactivated Cas9 protein comprises a N863 mutation (e.g., a N863A

mutation) or an analogous substitution to the amino acid corresponding to said position. In some embodiments, a catalytically inactive Cas9 protein, e.g., dCas9, comprises a D10 mutation (e.g., D10A), a D839 mutation (e.g., D839A), a H840 mutation (e.g., H840A), and a N863 mutation (e.g., N863A) or analogous substitutions to the amino acids corresponding to said positions.

In some embodiments, a catalytically inactive Cas9 protein, e.g., dCas9, or partially deactivated Cas9 protein comprises a E993 mutation (e.g., a E993A mutation) or an analogous substitution to the amino acid corresponding to said position.

In some embodiments, a catalytically inactive Cas9 protein, e.g., dCas9, or partially deactivated Cas9 protein comprises a D917 mutation (e.g., a D917A mutation) or an analogous substitution to the amino acid corresponding to said position. In some embodiments, a catalytically inactive Cas9 protein, e.g., dCas9, or partially deactivated Cas9 protein comprises a a E1006 mutation (e.g., a E1006A mutation) or an analogous substitution to the amino acid corresponding to said position. In some embodiments, a catalytically inactive Cas9 protein, e.g., dCas9, or partially deactivated Cas9 protein comprises a D1255 mutation (e.g., a D1255A mutation) or an analogous substitution to the amino acid corresponding to said position. In some embodiments, a catalytically inactive Cas9 protein, e.g., dCas9, comprises a D917 mutation (e.g., D917A), a E1006 mutation (e.g., E1006A), and a D1255 mutation (e.g., D1255A) or analogous substitutions to the amino acids corresponding to said positions.

In some embodiments, a catalytically inactive Cas9 protein, e.g., dCas9, or partially deactivated Cas9 protein comprises a D16 mutation (e.g., a D16A mutation) or an analogous substitution to the amino acid corresponding to said position. In some embodiments, a catalytically inactive Cas9 protein, e.g., dCas9, or partially deactivated Cas9 protein comprises a D587 mutation (e.g., a D587A mutation) or an analogous substitution to the amino acid corresponding to said position. In some embodiments, a partially deactivated Cas domain has nickase activity. In some embodiments, a partially deactivated Cas9 domain is a Cas9 nickase domain. In some embodiments, the catalytically inactive Cas domain or dead Cas domain produces no detectable double strand break formation. In some embodiments, a catalytically inactive Cas9 protein, e.g., dCas9, or partially deactivated Cas9 protein comprises a H588 mutation (e.g., a H588A mutation) or an analogous substitution to the amino acid corresponding to said position. In some embodiments, a catalytically inactive Cas9 protein, e.g., dCas9, or partially deactivated Cas9 protein comprises a N611 mutation (e.g., a N611A mutation) or an

analogous substitution to the amino acid corresponding to said position. In some embodiments, a catalytically inactive Cas9 protein, e.g., dCas9, comprises a D16 mutation (e.g., D16A), a D587 mutation (e.g., D587A), a H588 mutation (e.g., H588A), and a N611 mutation (e.g., N611A) or analogous substitutions to the amino acids corresponding to said positions.

In some embodiments, a DNA-binding domain or endonuclease domain may comprise a Cas molecule comprising or linked (e.g., covalently) to a gRNA (e.g., a template nucleic acid, e.g., template RNA, comprising a gRNA).

In some embodiments, an endonuclease domain or DNA binding domain comprises a *Streptococcus pyogenes* Cas9 (SpCas9) or a functional fragment or variant thereof. In some embodiments, the endonuclease domain or DNA binding domain comprises a modified SpCas9. In embodiments, the modified SpCas9 comprises a modification that alters protospacer-adjacent motif (PAM) specificity. In embodiments, the PAM has specificity for the nucleic acid sequence 5′-NGT-3′. In embodiments, the modified SpCas9 comprises one or more amino acid substitutions, e.g., at one or more of positions L1111, D1135, G1218, E1219, A1322, of R1335, e.g., selected from L1111R, D1135V, G1218R, E1219F, A1322R, R1335V. In embodiments, the modified SpCas9 comprises the amino acid substitution T1337R and one or more additional amino acid substitutions, e.g., selected from L1111, D1135L, S1136R, G1218S, E1219V, D1332A, D1332S, D1332T, D1332V, D1332L, D1332K, D1332R, R1335Q, T1337, T1337L, T1337Q, T1337I, T1337V, T1337F, T1337S, T1337N, T1337K, T1337H, T1337Q, and T1337M, or corresponding amino acid substitutions thereto. In embodiments, the modified SpCas9 comprises: (i) one or more amino acid substitutions selected from D1135L, S1136R, G1218S, E1219V, A1322R, R1335Q, and T1337; and (ii) one or more amino acid substitutions selected from L1111R, G1218R, E1219F, D1332A, D1332S, D1332T, D1332V, D1332L, D1332K, D1332R, T1337L, T1337I, T1337V, T1337F, T1337S, T1337N, T1337K, T1337R, T1337H, T1337Q, and T1337M, or corresponding amino acid substitutions thereto.

In some embodiments, the endonuclease domain or DNA binding domain comprises a Cas domain, e.g., a Cas9 domain. In embodiments, the endonuclease domain or DNA binding domain comprises a nuclease-active Cas domain, a Cas nickase (nCas) domain, or a nuclease-inactive Cas (dCas) domain. In embodiments, the endonuclease domain or DNA binding domain comprises a nuclease-active Cas9 domain, a Cas9 nickase (nCas9) domain, or a nuclease-inactive Cas9 (dCas9) domain. In some embodiments, the endonuclease domain or DNA binding domain

comprises a Cas9 domain of Cas9 (e.g., dCas9 and nCas9), Cas12a/Cpfl, Cas12b/C2cl, Cas12c/C2c3, Cas12d/CasY, Cas12e/CasX, Cas12g, Cas12h, or Cas12i. In some embodiments, the endonuclease domain or DNA binding domain comprises a Cas9 (e.g., dCas9 and nCas9), Cas12a/Cpfl, Cas12b/C2cl, Cas12c/C2c3, Cas12d/CasY, Cas12e/CasX, Cas12g, Cas12h, or Cas12i. In some embodiments, the endonuclease domain or DNA binding domain comprises an S. pyogenes or an S. thermophilus Cas9, or a functional fragment thereof. In some embodiments, the endonuclease domain or DNA binding domain comprises a Cas9 sequence, e.g., as described in Chylinski, Rhun, and Charpentier (2013) RNA Biology 10:5, 726-737; incorporated herein by reference. In some embodiments, the endonuclease domain or DNA binding domain comprises the HNH nuclease subdomain and/or the RuvC1 subdomain of a Cas, e.g., Cas9, e.g., as described herein, or a variant thereof. In some embodiments, the endonuclease domain or DNA binding domain comprises Cas12a/Cpfl, Cas12b/C2cl, Cas12c/C2c3, Cas12d/CasY, Cas12e/CasX, Cas12g, Cas12h, or Cas12i. In some embodiments, the endonuclease domain or DNA binding domain comprises a Cas polypeptide (e.g., enzyme), or a functional fragment thereof. In embodiments, the Cas polypeptide (e.g., enzyme) is selected from Cas1, Cas1B, Cas2, Cas3, Cas4, Cas5, Cas5d, Cas5t, Cas5h, Cas5a, Cas6, Cas7, Cas8, Cas8a, Cas8b, Cas8c, Cas9 (e.g., Csn1 or Csx12), Cas10, Cas10d, Cas12a/Cpfl, Cas12b/C2cl, Cas12c/C2c3, Cas12d/CasY, Cas12e/CasX, Cas12g, Cas12h, Cas12i, Csy1 , Csy2, Csy3, Csy4, Cse1, Cse2, Cse3, Cse4, Cse5e, Csc1, Csc2, Csa5, Csn1, Csn2, Csm1, Csm2, Csm3, Csm4, Csm5, Csm6, Cmr1, Cmr3, Cmr4, Cmr5, Cmr6, Csb1, Csb2, Csb3, Csx17, Csx14, Csx10, Csx16, CsaX, Csx3, Csx1, Csx1S, Csx11, Csf1, Csf2, CsO, Csf4, Csd1, Csd2, Cst1, Cst2, Csh1, Csh2, Csa1, Csa2, Csa3, Csa4, Csa5, Type II Cas effector proteins, Type V Cas effector proteins, Type VI Cas effector proteins, CARF, DinG, Cpf1, Cas12b/C2c1, Cas12c/C2c3, Cas12b/C2c1, Cas12c/C2c3, SpCas9(K855A), eSpCas9(1.1), SpCas9-HF1, hyper accurate Cas9 variant (HypaCas9), homologues thereof, modified or engineered versions thereof, and/or functional fragments thereof. In embodiments, the Cas9 comprises one or more substitutions, e.g., selected from H840A, D10A, P475A, W476A, N477A, D1125A, W1126A, and D1127A. In embodiments, the Cas9 comprises one or more mutations at positions selected from: D10, G12, G17, E762, H840, N854, N863, H982, H983, A984, D986, and/or A987, e.g., one or more substitutions selected from D10A, G12A, G17A, E762A, H840A, N854A, N863A, H982A, H983A, A984A, and/or D986A. In some embodiments, the endonuclease domain or DNA

binding domain comprises a Cas (e.g., Cas9) sequence from Corynebacterium ulcerans, Corynebacterium diphtheria, Spiroplasma syrphidicola, Prevotella intermedia, Spiroplasma taiwanense, Streptococcus iniae, Belliella baltica, Psychroflexus torquis, Streptococcus thermophilus, Listeria innocua, Campylobacter jejuni, Neisseria meningitidis, Streptococcus pyogenes, or Staphylococcus aureus, or a fragment or variant thereof.

In some embodiments, the endonuclease domain or DNA binding domain comprises a Cpf1 domain, e.g., comprising one or more substitutions, e.g., at position D917, E1006A, D1255 or any combination thereof, e.g., selected from D917A, E1006A, D1255A, D917A/E1006A, D917A/D1255A, E1006A/D1255A, and D917A/E1006A/D1255A.

In some embodiments, the endonuclease domain or DNA binding domain comprises spCas9, spCas9-VRQR, spCas9- VRER, xCas9 (sp), saCas9, saCas9-KKH, spCas9-MQKSER, spCas9-LRKIQK, or spCas9- LRVSQL.

In some embodiments, a gene modifying polypeptide has an endonuclease domain comprising a Cas9 nickase, e.g., Cas9 H840A. In embodiments, the Cas9 H840A has the following amino acid sequence:

Cas9 nickase (H840A):

DKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEA
TRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRLEESFLVEEDKKHERHPIFGN
IVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDV
DKLFIQLVQTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLI
ALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAIL
LSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAG
YIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAI
LRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVV
DKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLS
GEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKII
KDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWG
RLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDSL
HEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRE
RMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDV

DAIVPQSFLKDDSIDNKVLTRSDKNRGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRK
FDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVI
TLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIKKYPKLESEFVYGDYK
VYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWD
KGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGG
FDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKK
DLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPED
NEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHL
FTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGD (SEQ
ID NO: 11,001)

In some embodiments, a gene modifying polypeptide comprises a dCas9 sequence comprising a D10A and/or H840A mutation, e.g., the following sequence:

SMDKKYSIGLAIGTNSVGWAVITDDYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGET
AEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRLEESFLVEEDKKHERHPI
FGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDN
SDVDKLFIQLVQTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLF
GNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLS
DAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNG
YAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGE
LHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFE
EVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKP
AFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDL
LKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYT
GWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKEDIQKAQVSGQ
GDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQK
NSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLS
DYDVDAIVPQSFLKDDSIDNKVLTRSDKNRGKSDNVPSEEVVKKMKNYWRQLLNAKLI
TQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIR
EVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIKKYPKLESEFVY
GDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETG
EIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPK
KYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYK
EVKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKG
SPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAE
NIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGD
(SEQ ID NO: 5007)

TAL Effectors and Zinc Finger Nucleases

In some embodiments, an endonuclease domain or DNA-binding domain comprises a TAL effector molecule. A TAL effector molecule, e.g., a TAL effector molecule that specifically binds a DNA sequence, typically comprises a plurality of TAL effector domains or fragments thereof, and optionally one or more additional portions of naturally occurring TAL effectors (e.g., N- and/or C-terminal of the plurality of TAL effector domains). Many TAL effectors are known to those of skill in the art and are commercially available, e.g., from Thermo Fisher Scientific.

Naturally occurring TALEs are natural effector proteins secreted by numerous species of bacterial pathogens including the plant pathogen *Xanthomonas* which modulates gene expression in host plants and facilitates bacterial colonization and survival. The specific binding of TAL effectors is based on a central repeat domain of tandemly arranged nearly identical repeats of typically 33 or 34 amino acids (the repeat-variable di-residues, RVD domain).

Members of the TAL effectors family differ mainly in the number and order of their repeats. The number of repeats typically ranges from 1.5 to 33.5 repeats and the C-terminal repeat is usually shorter in length (e.g., about 20 amino acids) and is generally referred to as a "half-repeat." Each repeat of the TAL effector generally features a one-repeat-to-one-base-pair correlation with different repeat types exhibiting different base-pair specificity (one repeat recognizes one base-pair on the target gene sequence). Generally, the smaller the number of repeats, the weaker the protein-DNA interactions. A number of 6.5 repeats has been shown to be sufficient to activate transcription of a reporter gene (Scholze et al., 2010).

Repeat to repeat variations occur predominantly at amino acid positions 12 and 13, which have therefore been termed "hypervariable" and which are responsible for the specificity of the interaction with the target DNA promoter sequence, as shown in Table 9 listing exemplary repeat variable diresidues (RVD) and their correspondence to nucleic acid base targets.

Table 9 – RVDs and Nucleic Acid Base Specificity

Target	Possible RVD Amino Acid Combinations												
A	NI	NN	CI	HI	KI								

G	N N	GN	SN	VN	LN	DN	QN	EN	HN	RH	NK	AN	FN
C	H D	RD	KD	ND	AD								
T	N G	HG	VG	IG	EG	MG	YG	AA	EP	VA	QG	KG	RG

Accordingly, it is possible to modify the repeats of a TAL effector to target specific DNA sequences. Further studies have shown that the RVD NK can target G. Target sites of TAL effectors also tend to include a T flanking the 5′ base targeted by the first repeat, but the exact mechanism of this recognition is not known. More than 113 TAL effector sequences are known to date. Non-limiting examples of TAL effectors from *Xanthomonas* include, Hax2, Hax3, Hax4, AvrXa7, AvrXa10 and AvrBs3.

Accordingly, the TAL effector domain of a TAL effector molecule described herein may be derived from a TAL effector from any bacterial species (e.g., *Xanthomonas* species such as the African strain of *Xanthomonas oryzae* pv. *Oryzae* (Yu et al. 2011), *Xanthomonas campestris* pv. *raphani* strain 756C and *Xanthomonas oryzae* pv. *oryzicola*strain BLS256 (Bogdanove et al. 2011). In some embodiments, the TAL effector domain comprises an RVD domain as well as flanking sequence(s) (sequences on the N-terminal and/or C-terminal side of the RVD domain) also from the naturally occurring TAL effector. It may comprise more or fewer repeats than the RVD of the naturally occurring TAL effector. The TAL effector molecule can be designed to target a given DNA sequence based on the above code and others known in the art. The number of TAL effector domains (e.g., repeats (monomers or modules)) and their specific sequence can beselected based on the desired DNA target sequence. For example, TAL effector domains, e.g., repeats, may be removed or added in order to suit a specific target sequence. In an embodiment, the TAL effector molecule of the present invention comprises between 6.5 and 33.5 TAL effector domains, e.g., repeats. In an embodiment, TAL effector molecule of the present invention comprises between 8 and 33.5 TAL effector domains, e.g., repeats, e.g., between 10 and 25 TAL effector domains, e.g., repeats, e.g., between 10 and 14 TAL effector domains, e.g., repeats.

In some embodiments, the TAL effector molecule comprises TAL effector domains that correspond to a perfect match to the DNA target sequence. In some embodiments, a mismatch between a repeat and a target base-pair on the DNA target sequence is permitted as along as it allows for the function of the polypeptide comprising the TAL effector molecule. In general, TALE binding is inversely correlated with the number of mismatches. In some embodiments, the TAL effector molecule of a polypeptide of the present invention comprises no more than 7 mismatches, 6 mismatches, 5 mismatches, 4 mismatches, 3 mismatches, 2 mismatches, or 1 mismatch, and optionally no mismatch, with the target DNA sequence. Without wishing to be bound by theory, in general the smaller the number of TAL effector domains in the TAL effector molecule, the smaller the number of mismatches will be tolerated and still allow for the function of the polypeptide comprising the TAL effector molecule. The binding affinity is thought to depend on the sum of matching repeat-DNA combinations. For example, TAL effector molecules having 25 TAL effector domains or more may be able to tolerate up to 7 mismatches.

In addition to the TAL effector domains, the TAL effector molecule of the present invention may comprise additional sequences derived from a naturally occurring TAL effector. The length of the C-terminal and/or N-terminal sequence(s) included on each side of the TAL effector domain portion of the TAL effector molecule can vary and be selected by one skilled in the art, for example based on the studies of Zhang et al. (2011). Zhang et al., have characterized a number of C-terminal and N-terminal truncation mutants in Hax3 derived TAL-effector based proteins and have identified key elements, which contribute to optimal binding to the target sequence and thus activation of transcription. Generally, it was found that transcriptional activity is inversely correlated with the length of N-terminus. Regarding the C-terminus, an important element for DNA binding residues within the first 68 amino acids of the Hax 3 sequence was identified. Accordingly, in some embodiments, the first 68 amino acids on the C-terminal side of the TAL effector domains of the naturally occurring TAL effector is included in the TAL effector molecule. Accordingly, in an embodiment, a TAL effector molecule comprises 1) one or more TAL effector domains derived from a naturally occurring TAL effector; 2) at least 70, 80, 90, 100, 110, 120, 130, 140, 150, 170, 180, 190, 200, 220, 230, 240, 250, 260, 270, 280 or more amino acids from the naturally occurring TAL effector on the N-terminal side of the TAL effector domains; and/or 3) at least 68, 80, 90, 100, 110, 120, 130, 140, 150, 170, 180, 190,

200, 220, 230, 240, 250, 260 or more amino acids from the naturally occurring TAL effector on the C-terminal side of the TAL effector domains.

In some embodiments, an endonuclease domain or DNA-binding domain is or comprises a Zn finger molecule. A Zn finger molecule comprises a Zn finger protein, e.g., a naturally occurring Zn finger protein or engineered Zn finger protein, or fragment thereof. Many Zn finger proteins are known to those of skill in the art and are commercially available, e.g., from Sigma-Aldrich.

In some embodiments, a Zn finger molecule comprises a non-naturally occurring Zn finger protein that is engineered to bind to a target DNA sequence of choice. See, for example, Beerli, et al. (2002) Nature Biotechnol. 20:135-141; Pabo, et al. (2001) Ann. Rev. Biochem. 70:313-340; Isalan, et al. (2001) Nature Biotechnol. 19:656-660; Segal, et al. (2001) Curr. Opin. Biotechnol. 12:632-637; Choo, et al. (2000) Curr. Opin. Struct. Biol. 10:411-416; U.S. Pat. Nos. 6,453,242; 6,534,261; 6,599,692; 6,503,717; 6,689,558; 7,030,215; 6,794,136; 7,067,317; 7,262,054; 7,070,934; 7,361,635; 7,253,273; and U.S. Patent Publication Nos. 2005/0064474; 2007/0218528; 2005/0267061, all incorporated herein by reference in their entireties.

An engineered Zn finger protein may have a novel binding specificity, compared to a naturally-occurring Zn finger protein. Engineering methods include, but are not limited to, rational design and various types of selection. Rational design includes, for example, using databases comprising triplet (or quadruplet) nucleotide sequences and individual Zn finger amino acid sequences, in which each triplet or quadruplet nucleotide sequence is associated with one or more amino acid sequences of zinc fingers which bind the particular triplet or quadruplet sequence. See, for example, U.S. Pat. Nos. 6,453,242 and 6,534,261, incorporated by reference herein in their entireties.

Exemplary selection methods, including phage display and two-hybrid systems, are disclosed in U.S. Pat. Nos. 5,789,538; 5,925,523; 6,007,988; 6,013,453; 6,410,248; 6,140,466; 6,200,759; and 6,242,568; as well as International Patent Publication Nos. WO 98/37186; WO 98/53057; WO 00/27878; and WO 01/88197 and GB 2,338,237. In addition, enhancement of binding specificity for zinc finger proteins has been described, for example, in International Patent Publication No. WO 02/077227.

In addition, as disclosed in these and other references, zinc finger domains and/or multi-fingered zinc finger proteins may be linked together using any suitable linker sequences, including for example, linkers of 5 or more amino acids in length. See, also, U.S. Pat. Nos. 6,479,626; 6,903,185; and 7,153,949 for exemplary linker sequences 6 or more amino acids in length. The proteins described herein may include any combination of suitable linkers between the individual zinc fingers of the protein. In addition, enhancement of binding specificity for zinc finger binding domains has been described, for example, in co-owned International Patent Publication No. WO 02/077227.

Zn finger proteins and methods for design and construction of fusion proteins (and polynucleotides encoding same) are known to those of skill in the art and described in detail in U.S. Pat. Nos. 6,140,0815; 789,538; 6,453,242; 6,534,261; 5,925,523; 6,007,988; 6,013,453; and 6,200,759; International Patent Publication Nos. WO 95/19431; WO 96/06166; WO 98/53057; WO 98/54311; WO 00/27878; WO 01/60970; WO 01/88197; WO 02/099084; WO 98/53058; WO 98/53059; WO 98/53060; WO 02/016536; and WO 03/016496.

In addition, as disclosed in these and other references, Zn finger proteins and/or multi-fingered Zn finger proteins may be linked together, e.g., as a fusion protein, using any suitable linker sequences, including for example, linkers of 5 or more amino acids in length. See, also, U.S. Pat. Nos. 6,479,626; 6,903,185; and 7,153,949 for exemplary linker sequences 6 or more amino acids in length. The Zn finger molecules described herein may include any combination of suitable linkers between the individual zinc finger proteins and/or multi-fingered Zn finger proteins of the Zn finger molecule.

In certain embodiments, the DNA-binding domain or endonuclease domain comprises a Zn finger molecule comprising an engineered zinc finger protein that binds (in a sequence-specific manner) to a target DNA sequence. In some embodiments, the Zn finger molecule comprises one Zn finger protein or fragment thereof. In other embodiments, the Zn finger molecule comprises a plurality of Zn finger proteins (or fragments thereof), e.g., 2, 3, 4, 5, 6 or more Zn finger proteins (and optionally no more than 12, 11, 10, 9, 8, 7, 6, 5, 4, 3, or 2 Zn finger proteins). In some embodiments, the Zn finger molecule comprises at least three Zn finger proteins. In some embodiments, the Zn finger molecule comprises four, five or six fingers. In some embodiments, the Zn finger molecule comprises 8, 9, 10, 11 or 12 fingers. In some embodiments, a Zn finger molecule comprising three Zn finger proteins recognizes a target DNA

sequence comprising 9 or 10 nucleotides. In some embodiments, a Zn finger molecule comprising four Zn finger proteins recognizes a target DNA sequence comprising 12 to 14 nucleotides. In some embodiments, a Zn finger molecule comprising six Zn finger proteins recognizes a target DNA sequence comprising 18 to 21 nucleotides.

In some embodiments, a Zn finger molecule comprises a two-handed Zn finger protein. Two handed zinc finger proteins are those proteins in which two clusters of zinc finger proteins are separated by intervening amino acids so that the two zinc finger domains bind to two discontinuous target DNA sequences. An example of a two handed type of zinc finger binding protein is SIP1, where a cluster of four zinc finger proteins is located at the amino terminus of the protein and a cluster of three Zn finger proteins is located at the carboxyl terminus (see Remade, et al. (1999) EMBO Journal 18(18):5073-5084). Each cluster of zinc fingers in these proteins is able to bind to a unique target sequence and the spacing between the two target sequences can comprise many nucleotides.

Linkers

In some embodiments, a gene modifying polypeptide may comprise a linker, e.g., a peptide linker, e.g., a linker as described in Table 10. In some embodiments, a gene modifying polypeptide comprises, in an N-terminal to C-terminal direction, a Cas domain (e.g., a Cas domain of Table 8), a linker of Table 10 (or a sequence having at least 70%, 80%, 85%, 90%, 95%, or 99% identity thereto), and an RT domain (e.g., an RT domain of Table 6). In some embodiments, a gene modifying polypeptide comprises a flexible linker between the endonuclease and the RT domain, e.g., a linker comprising the amino acid sequence SGGSSGGSSGSETPGTSESATPESSGGSSGGSS (SEQ ID NO: 11,002). In some embodiments, an RT domain of a gene modifying polypeptide may be located C-terminal to the endonuclease domain. In some embodiments, an RT domain of a gene modifying polypeptide may be located N-terminal to the endonuclease domain.

Table 10 Exemplary linker sequences

Amino Acid Sequence	SEQ ID NO
GGS	
GGSGGS	5102
GGSGGSGGS	5103

Amino Acid Sequence	SEQ ID NO
GGSGGSGGSGGS	5104
GGSGGSGGSGGSGGS	5105
GGSGGSGGSGGSGGSGGS	5106
GGGGS	5107
GGGGSGGGGS	5108
GGGGSGGGGSGGGGS	5109
GGGGSGGGGSGGGGSGGGGS	5110
GGGGSGGGGSGGGGSGGGGSGGGGS	5111
GGGGSGGGGSGGGGSGGGGSGGGGSGGGGS	5112
GGG	
GGGG	5114
GGGGG	5115
GGGGGG	5116
GGGGGGG	5117
GGGGGGGG	5118
GSS	
GSSGSS	5120
GSSGSSGSS	5121
GSSGSSGSSGSS	5122
GSSGSSGSSGSSGSS	5123
GSSGSSGSSGSSGSSGSS	5124
EAAAK	5125
EAAAKEAAAK	5126
EAAAKEAAAKEAAAK	5127
EAAAKEAAAKEAAAKEAAAK	5128
EAAAKEAAAKEAAAKEAAAKEAAAK	5129
EAAAKEAAAKEAAAKEAAAKEAAAKEAAAK	5130
PAP	
PAPAP	5132
PAPAPAP	5133
PAPAPAPAP	5134
PAPAPAPAPAP	5135
PAPAPAPAPAPAP	5136
GGSGGG	5137
GGGGGS	5138
GGSGSS	5139
GSSGGS	5140
GGSEAAAK	5141

Amino Acid Sequence	SEQ ID NO
EAAAKGGS	5142
GGSPAP	5143
PAPGGS	5144
GGGGSS	5145
GSSGGG	5146
GGGEAAAK	5147
EAAAKGGG	5148
GGGPAP	5149
PAPGGG	5150
GSSEAAAK	5151
EAAAKGSS	5152
GSSPAP	5153
PAPGSS	5154
EAAAKPAP	5155
PAPEAAAK	5156
GGSGGGGSS	5157
GGSGSSGGG	5158
GGGGGSGSS	5159
GGGGSSGGS	5160
GSSGGSGGG	5161
GSSGGGGGS	5162
GGSGGGEAAAK	5163
GGSEAAAKGGG	5164
GGGGGSEAAAK	5165
GGGEAAAKGGS	5166
EAAAKGGSGGG	5167
EAAAKGGGGGS	5168
GGSGGGPAP	5169
GGSPAPGGG	5170
GGGGGSPAP	5171
GGGPAPGGS	5172
PAPGGSGGG	5173
PAPGGGGGS	5174
GGSGSSEAAAK	5175
GGSEAAAKGSS	5176
GSSGGSEAAAK	5177
GSSEAAAKGGS	5178
EAAAKGGSGSS	5179

Amino Acid Sequence	SEQ ID NO
EAAAKGSSGGS	5180
GGSGSSPAP	5181
GGSPAPGSS	5182
GSSGGSPAP	5183
GSSPAPGGS	5184
PAPGGSGSS	5185
PAPGSSGGS	5186
GGSEAAAKPAP	5187
GGSPAPEAAAK	5188
EAAAKGGSPAP	5189
EAAAKPAPGGS	5190
PAPGGSEAAAK	5191
PAPEAAAKGGS	5192
GGGGSSEAAAK	5193
GGGEAAAKGSS	5194
GSSGGGEAAAK	5195
GSSEAAAKGGG	5196
EAAAKGGGGSS	5197
EAAAKGSSGGG	5198
GGGGSSPAP	5199
GGGPAPGSS	5200
GSSGGGPAP	5201
GSSPAPGGG	5202
PAPGGGGSS	5203
PAPGSSGGG	5204
GGGEAAAKPAP	5205
GGGPAPEAAAK	5206
EAAAKGGGPAP	5207
EAAAKPAPGGG	5208
PAPGGGEAAAK	5209
PAPEAAAKGGG	5210
GSSEAAAKPAP	5211
GSSPAPEAAAK	5212
EAAAKGSSPAP	5213
EAAAKPAPGSS	5214
PAPGSSEAAAK	5215
PAPEAAAKGSS	5216
AEAAAKEAAAKEAAAKEAAAKALEAEAAAKEAAAKEAAAKEAAAKA	5217

Amino Acid Sequence	SEQ ID NO
GGGGSEAAAKGGGGS	5218
EAAAKGGGGSEAAAK	5219
SGSETPGTSESATPES	5220
GSAGSAAGSGEF	5221
SGGSSGGSSGSETPGTSESATPESSGGSSGGSS	5222

In some embodiments, a linker of a gene modifying polypeptide comprises a motif chosen from: $(SGGS)_n$ (SEQ ID NO: 5025), $(GGGS)_n$ (SEQ ID NO: 5026), $(GGGGS)_n$ (SEQ ID NO: 5027), $(G)_n$, $(EAAAK)_n$ (SEQ ID NO: 5028), $(GGS)_n$, or $(XP)_n$.

Gene modifying polypeptide selection by pooled screening

Candidate gene modifying polypeptides may be screened to evaluate a candidate's gene editing ability. For example, an RNA gene modifying system designed for the targeted editing of a coding sequence in the human genome may be used. In certain embodiments, such a gene modifying system may be used in conjunction with a pooled screening approach.

For example, a library of gene modifying polypeptide candidates and a template guide RNA (tgRNA) may be introduced into mammalian cells to test the candidates' gene editing abilities by a pooled screening approach. In specific embodiments, a library of gene modifying polypeptide candidates is introduced into mammalian cells followed by introduction of the tgRNA into the cells.

Representative, non-limiting examples of mammalian cells that may be used in screening include HEK293T cells, U2OS cells, HeLa cells, HepG2 cells, Huh7 cells, K562 cells, or iPS cells.

A gene modifying polypeptide candidate may comprise 1) a Cas-nuclease, for example a wild-type Cas nuclease, e.g., a wild-type Cas9 nuclease, a mutant Cas nuclease, e.g., a Cas nickase, for example, a Cas9 nickase such as a Cas9 N863A nickase, or a Cas nuclease selected from **Table 7 or Table 8**, 2) a peptide linker, e.g., a sequence from **Table D or Table 10,** that may exhibit varying degrees of length, flexibility, hydrophobicity, and/or secondary structure; and 3) a reverse transcriptase (RT), e.g. an RT domain from **Table D or Table 6**. A gene modifying polypeptide candidate library comprises: a plurality of different gene modifying polypeptide candidates that differ from each other with respect to one, two or all three of the Cas nuclease, peptide linker or

RT domain components, or a plurality of nucleic acid expression vectors that encode such gene modifying polypeptide candidates.

For screening of gene modifying polypeptide candidates, a two-component system may be used that comprises a gene modifying polypeptide component and a tgRNA component. A gene modifying component may comprise, for example, an expression vector, e.g., an expression plasmid or lentiviral vector, that encodes a gene modifying polypeptide candidate, for example, comprises a human codon-optimized nucleic acid that encodes a gene modifying polypeptide candidate, e.g., a Cas-linker-RT fusion as described above. In a particular embodiment, a lentiviral cassette is utilized that comprises: (i) a promoter for expression in mammalian cells, e.g., a CMV promoter; (ii) a gene modifying library candidate, e.g. a Cas-linker-RT fusion comprising a Cas nuclease of **Table 7 or Table 8**, a peptide linker of **Table 10**, and an RT of **Table 6**, for example a Cas-linker-RT fusion as in **Table D**; (iii) a self-cleaving polypeptide, e.g., a T2A peptide; (iv) a marker enabling selection in mammalian cells, e.g., a puromycin resistance gene; and (v) a termination signal, e.g., a poly A tail.

The tgRNA component may comprise a tgRNA or expression vector, e.g., an expression plasmid, that produces the tgRNA, for example, utilizes a U6 promoter to drive expression of the tgRNA, wherein the tgRNA is a non-coding RNA sequence that is recognized by Cas and localizes it to the genomic locus of interest, and that also templates reverse transcription of the desired edit into the genome by the RT domain.

To prepare a pool of cells expressing gene modifying polypeptide library candidates, mammalian cells, e.g., HEK293T or U2OS cells, may be transduced with pooled gene modifying polypeptide candidate expression vector preparations, e.g., lentiviral preparations, of the gene modifying candidate polypeptide library. In a particular embodiment, lentiviral plasmids are utilized, and HEK293 Lenti-X cells are seeded in 15 cm plates (~$12x10^6$ cells) prior to lentiviral plasmid transfection. In such an embodiment, lentiviral plasmid transfection may be performed using the Lentiviral Packaging Mix (Biosettia) and transfection of the plasmid DNA for the gene modifying candidate library is performed the following day using Lipofectamine 2000 and Opti-MEM media according to the manufacturer's protocol. In such an embodiment, extracellular DNA may be removed by a full media change the next day and virus-containing media may be harvested 48 hours after. Lentiviral media may be concentrated using Lenti-X Concentrator (TaKaRa

Biosciences) and 5 mL lentiviral aliquots may be made and stored at -80°C. Lentiviral titering is performed by enumerating colony forming units post-selection, e.g., post Puromycin selection.

For monitoring gene editing of a target DNA, mammalian cells, e.g., HEK293T or U2OS cells, carrying a target DNA may be utilized. In other embodiments for monitoring gene editing of a target DNA, mammalian cells, e.g., HEK293T or U2OS cells, carrying a target DNA genomic landing pad may be utilized. In particular embodiments, the target DNA genomic landing pad may comprise a gene to be edited for treatment of a disease or disorder of interest. In other particular embodiments, the target DNA is a gene sequence that expresses a protein that exhibits detectable characteristics that may be monitored to determine whether gene editing has occurred. For example, in certain embodiments, a blue fluorescence protein (BFP)- or green fluorescence protein (GFP)-expressing genomic landing pad is utilized. In certain embodiments, mammalian cells, e.g., HEK293T or U2OS cells, comprising a target DNA, e.g., a target DNA genomic landing pad, are seeded in culture plates at 500x-3000x cells per gene modifying library candidate and transduced at a 0.2-0.3 multiplicity of infection (MOI) to minimize multiple infections per cell. Puromycin (2.5 ug/mL) may be added 48 hours post infection to allow for selection of infected cells. In such an embodiment, cells may be kept under puromycin selection for at least 7 days and then scaled up for tgRNA introduction, e.g., tgRNA electroporation.

To ascertain whether gene editing occurs, mammalian cells containing a target DNA to be edited may be infected with gene modifying polypeptide library candidates then transfected with tgRNA designed for use in editing of the target DNA. Subsequently, the cells may be analyzed to determine whether editing of the target locus has occurred according to the designed outcome, or whether no editing or imperfect editing has occurred, e.g., by using cell sorting and sequence analysis.

In a particular embodiment, to ascertain whether genome editing occurs, BFP- or GFP-expressing mammalian cells, e.g., HEK293T or U2OS cells, may be infected with gene modifying library candidates and then transfected or electroporated with tgRNA plasmid or RNA, e.g., by electroporation of 250,000 cells/well with 200 ng of a tgRNA plasmid designed to convert BFP-to-GFP or GFP-to-BFP, at a cell count ensuring >250x-1000x coverage per library candidate. In such an embodiment, the genome-editing capacity of the various constructs in this assay may be assessed by sorting the cells by Fluorescence-Activated Cell Sorting (FACS) for expression of the color-converted fluorescent protein (FP) at 4-10 days post-electroporation. Cells are sorted and

harvested as distinct populations of unedited cells (exhibiting original florescence protein signal), edited cells (exhibiting converted fluorescence protein signal), and imperfect edit (exhibiting no florescence protein signal) cells. A sample of unsorted cells may also be harvested as the input population to determine candidate enrichment during analysis.

To determine which gene modifying library candidates exhibit genome-editing capacity in an assay, genomic DNA (gDNA) is harvested from the sorted cell populations, and analyzed by sequencing the gene modifying library candidates in each population. Briefly, gene modifying candidates may be amplified from the genome using primers specific to the gene modifying polypeptide expression vector, e.g., the lentiviral cassette, amplified in a second round of PCR to dilute genomic DNA, and then sequenced, for example, sequenced by a next-generation sequencing platform. After quality control of sequencing reads, reads of at least about 1500 nucleotides and generally no more than about 3200 nucleotides are mapped to the gene modifying polypeptide library sequences and those containing a minimum of about an 80% match to a library sequence are considered to be successfully aligned to a given candidate for purposes of this pooled screen. In order to identify candidates capable of performing gene editing in the assay, e.g., the BFP-to-GFP or GFP-to-BFP edit, the read count of each library candidate in the edited population is compared to its read count in the initial, unsorted population.

For purposes of pooled screening, gene modifying candidates with genome-editing capacity are identified based on enrichment in the edited (converted FP) population relative to unsorted (input) cells. In some embodiments, an enrichment of at least 1.0, 1.5, 2.0, 2.5, 3.0, 4.0, 5.0, 6.0, 7.0, 8.0, 9.0, 10, 15, 20, 25, 30, 40, 50, 60, 70, 80, 90, or at least 100-fold over the input indicates potentially useful gene editing activity, e.g., at least 2-fold enrichment. In some embodiments, the enrichment is converted to a log-value by taking the log base 2 of the enrichment ratio. In some embodiments, a log2 enrichment score of at least 0, 1, 2, 3, 4, 5, 5.5, 6.0, 6.2, 6.3, 6.4, 6.5, or at least 6.6 indicates potentially useful gene editing activity, e.g., a log2 enrichment score of at least 1.0. In particular embodiments, enrichment values observed for gene modifying candidates may be compared to enrichment values observed under similar conditions utilizing a reference, e.g., Element ID No: 17380.

In some embodiments, multiple tgRNAs may be used to screen the gene modifying candidate library. In particular embodiments, a plurality of tgRNAs may be utilized to optimize template/Cas-linker-RT fusion pairs, e.g., for gene editing of particular target genes, for example,

gene targets for the treatment of disease. In specific embodiments, a pooled approach to screening gene modifying candidates may be performed using a multiplicity of different tgRNAs in an arrayed format.

In some embodiments, multiple types of edits, e.g., insertions, substitutions, and/or deletions of different lengths, may be used to screen the gene modifying candidate library.

In some embodiments, multiple target sequences, e.g., different fluorescent proteins, may be used to screen the gene modifying candidate library. In some embodiments, multiple target sequences, e.g., different fluorescent proteins, may be used to screen the gene modifying candidate library. In some embodiments, multiple cell types, e.g., HEK293T or U2OS, may be used to screen the gene modifying candidate library. The person of ordinary skill in the art will appreciate that a given candidate may exhibit altered editing capacity or even the gain or loss of any observable or useful activity across different conditions, including tgRNA sequence (e.g., nucleotide modifications, PBS length, RT template length), target sequence, target location, type of edit, location of mutation relative to the first-strand nick of the gene modifying polypeptide, or cell type. Thus, in some embodiments, gene modifying library candidates are screened across multiple parameters, e.g., with at least two distinct tgRNAs in at least two cell types, and gene editing activity is identified by enrichment in any single condition. In other embodiments, a candidate with more robust activity across different tgRNA and cell types is identified by enrichment in at least two conditions, e.g., in all conditions screened. For clarity, candidates found to exhibit little to no enrichment under any given condition are not assumed to be inactive across all conditions and may be screened with different parameters or reconfigured at the polypeptide level, e.g., by swapping, shuffling, or evolving domains (e.g., RT domain), linkers, or other signals (e.g., NLS).

Sequences of exemplary Cas9-linker-RT fusions

In some embodiments, a gene modifying polypeptide comprises a linker sequence and an RT sequence. In some embodiments, a gene modifying polypeptide comprises a linker sequence as listed in Table D, or an amino acid sequence having at least 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, or 99% identity thereto. In some embodiments, a gene modifying polypeptide comprises the amino acid sequence of an RT domain as listed in Table D, or an amino acid sequence having at least 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, or 99% identity thereto. In some embodiments, a gene modifying polypeptide comprises a linker sequence as listed in

Table D, or an amino acid sequence having at least 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, or 99% identity thereto; and the amino acid sequence of an RT domain as listed in Table D, or an amino acid sequence having at least 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, or 99% identity thereto. In some embodiments, a gene modifying polypeptide comprises: (i) a linker sequence as listed in a row of Table D, or an amino acid sequence having at least 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, or 99% identity thereto; and (ii) the amino acid sequence of an RT domain as listed in the same row of Table D, or an amino acid sequence having at least 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, or 99% identity thereto.

Exemplary Gene Modifying Polypeptides

In some embodiments, a gene modifying polypeptide (e.g., a gene modifying polypeptide that is part of a system described herein) comprises an amino acid sequence of any one of SEQ ID NOs: 1-7743, or an amino acid sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, or 99% identity thereto. In some embodiments, a gene modifying polypeptide comprises an amino acid sequence of any one of SEQ ID NOs: 1-7743, or an amino acid sequence having at least 80% identity thereto. In some embodiments, a gene modifying polypeptide comprises an amino acid sequence of any one of SEQ ID NOs: 1-7743, or an amino acid sequence having at least 90% identity thereto. In some embodiments, a gene modifying polypeptide comprises an amino acid sequence of any one of SEQ ID NOs: 1-7743, or an amino acid sequence having at least 95% identity thereto. In some embodiments, a gene modifying polypeptide comprises an amino acid sequence of any one of SEQ ID NOs: 1-7743, or an amino acid sequence having at least 99% identity thereto. In some embodiments, a gene modifying polypeptide comprises an amino acid sequence of any one of SEQ ID NOs: 1-7743. In some embodiments, a gene modifying polypeptide comprises an amino acid sequence of any one of SEQ ID NOs: 6001-7743, or an amino acid sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, or 99% identity thereto. In some embodiments, a gene modifying polypeptide comprises an amino acid sequence of any one of SEQ ID NOs: 4501-4541, or an amino acid sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, or 99% identity thereto.

In some embodiments, a gene modifying polypeptide comprises an amino acid sequence as listed in Table A1, or an amino acid sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, or 99% identity thereto.

In some embodiments, a gene modifying polypeptide comprises an amino acid sequence as listed in Table T1, or an amino acid sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, or 99% identity thereto. In some embodiments, a gene modifying polypeptide comprises a linker comprising a linker sequence as listed in Table T1, or an amino acid sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, or 99% identity thereto. In some embodiments, a gene modifying polypeptide comprises an RT domain comprising an RT domain sequence as listed in Table T1, or an amino acid sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, or 99% identity thereto. In some embodiments, a gene modifying polypeptide comprises: (i) a linker comprising a linker sequence as listed in a row of Table T1, or an amino acid sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, or 99% identity thereto; and (ii) an RT domain comprising an RT domain sequence as listed in the same row of Table T1, or an amino acid sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, or 99% identity thereto.

Table T1. Selection of exemplary gene modifying polypeptides

SEQ ID NO: for Full Polypeptide Sequence	Linker Sequence	SEQ ID NO: of linker	RT name
1372	AEAAAKEAAAKEAAAKEAAAKALEAEAAAKEAAAKEAAAKEAAAKA	15,401	AVIRE_P03360_3mutA
1197	AEAAAKEAAAKEAAAKEAAAKALEAEAAAKEAAAKEAAAKEAAAKA	15,402	FLV_P10273_3mutA
2784	AEAAAKEAAAKEAAAKEAAAKALEAEAAAKEAAAKEAAAKEAAAKA	15,403	MLVMS_P03355_3mutA_WS
647	AEAAAKEAAAKEAAAKEAAAKALEAEAAAKEAAAKEAAAKEAAAKA	15,404	SFV3L_P27401_2mutA

In some embodiments, a gene modifying polypeptide comprises an amino acid sequence as listed in Table T2, or an amino acid sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, or 99% identity thereto. In some embodiments, a gene modifying polypeptide comprises a linker comprising a linker sequence as listed in Table T2, or an amino acid sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, or 99% identity thereto. In some embodiments, a gene modifying polypeptide comprises an RT domain comprising an RT domain sequence as listed in Table T2, or an amino acid sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, or 99% identity thereto. In some embodiments, a gene modifying polypeptide comprises: (i) a linker

comprising a linker sequence as listed in a row of Table T2, or an amino acid sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, or 99% identity thereto; and (ii) an RT domain comprising an RT domain sequence as listed in the same row of Table T2, or an amino acid sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, or 99% identity thereto.

Table T2. Selection of exemplary gene modifying polypeptides

SEQ ID NO: for Full Polypeptide Sequence	Linker Sequence	SEQ ID NO: of linker	RT name
2311	GGGGSGGGGSGGGGSGGGGS	15,405	MLVCB_P08361_3mutA
1373	GGGGSGGGGSGGGGSGGGGSGGGGSGGGGS	15,406	AVIRE_P03360_3mutA
2644	GGGGSGGGGSGGGGSGGGGSGGGGSGGGGS	15,407	MLVMS_P03355_PLV919
2304	GSSGSSGSSGSSGSSGSS	15,408	MLVCB_P08361_3mutA
2325	EAAAKEAAAKEAAAKEAAAK	15,409	MLVCB_P08361_3mutA
2322	EAAAKEAAAKEAAAKEAAAKEAAAKEAAAK	15,410	MLVCB_P08361_3mutA
2187	PAPAPAPAPAP	15,411	MLVBM_Q7SVK7_3mut
2309	PAPAPAPAPAPAP	15,412	MLVCB_P08361_3mutA
2534	PAPAPAPAPAPAP	15,413	MLVFF_P26809_3mutA
2797	PAPAPAPAPAPAP	15,414	MLVMS_P03355_3mutA_WS
3084	PAPAPAPAPAPAP	15,415	MLVMS_P03355_3mutA_WS
2868	PAPAPAPAPAPAP	15,416	MLVMS_P03355_PLV919
126	EAAAKGGG	15,417	PERV_Q4VFZ2_3mut
306	EAAAKGGG	15,418	PERV_Q4VFZ2_3mut
1410	PAPGGG	15,419	AVIRE_P03360_3mutA
804	GGGGSSGGS	15,420	WMSV_P03359_3mut
1937	GGGGGSEAAAK	15,421	BAEVM_P10272_3mutA
2721	GGGEAAAKGGS	15,422	MLVMS_P03355_3mut
3018	GGGEAAAKGGS	15,423	MLVMS_P03355_3mut
1018	GGGEAAAKGGS	15,424	XMRV6_A1Z651_3mutA
2317	GGSGGGPAP	15,425	MLVCB_P08361_3mutA
2649	PAPGGSGGG	15,426	MLVMS_P03355_PLV919
2878	PAPGGSGGG	15,427	MLVMS_P03355_PLV919
912	GGSEAAAKPAP	15,428	WMSV_P03359_3mutA
2338	GGSPAPEAAAK	15,429	MLVCB_P08361_3mutA
2527	GGSPAPEAAAK	15,430	MLVFF_P26809_3mutA
141	EAAAKGGSPAP	15,431	PERV_Q4VFZ2_3mut
341	EAAAKGGSPAP	15,432	PERV_Q4VFZ2_3mut

2315	EAAAKPAPGGS	15,433	MLVCB_P08361_3mutA
3080	EAAAKPAPGGS	15,434	MLVMS_P03355_3mutA_WS
2688	GGGGSSEAAAK	15,435	MLVMS_P03355_PLV919
2885	GGGGSSEAAAK	15,436	MLVMS_P03355_PLV919
2810	GSSGGGEAAAK	15,437	MLVMS_P03355_3mutA_WS
3057	GSSGGGEAAAK	15,438	MLVMS_P03355_3mutA_WS
1861	GSSEAAAKGGG	15,439	MLVAV_P03356_3mutA
3056	GSSGGGPAP	15,440	MLVMS_P03355_3mutA_WS
1038	GSSPAPGGG	15,441	XMRV6_A1Z651_3mutA
2308	PAPGGGGSS	15,442	MLVCB_P08361_3mutA
1672	GGGEAAAKPAP	15,443	KORV_Q9TTC1-Pro_3mutA
2526	GGGEAAAKPAP	15,444	MLVFF_P26809_3mutA
1938	GGGPAPEAAAK	15,445	BAEVM_P10272_3mutA
2641	GSSEAAAKPAP	15,446	MLVMS_P03355_PLV919
2891	GSSEAAAKPAP	15,447	MLVMS_P03355_PLV919
1225	GSSPAPEAAAK	15,448	FLV_P10273_3mutA
2839	GSSPAPEAAAK	15,449	MLVMS_P03355_3mutA_WS
3127	GSSPAPEAAAK	15,450	MLVMS_P03355_3mutA_WS
2798	PAPGSSEAAAK	15,451	MLVMS_P03355_3mutA_WS
3091	PAPGSSEAAAK	15,452	MLVMS_P03355_3mutA_WS
1372	AEAAAKEAAAKEAAAKEAAAKALEAEAAAKEAAAKEAAAKEAAAKA	15,453	AVIRE_P03360_3mutA
1197	AEAAAKEAAAKEAAAKEAAAKALEAEAAAKEAAAKEAAAKEAAAKA	15,454	FLV_P10273_3mutA
2611	AEAAAKEAAAKEAAAKEAAAKALEAEAAAKEAAAKEAAAKEAAAKA	15,455	MLVMS_P03355_PLV919
2784	AEAAAKEAAAKEAAAKEAAAKALEAEAAAKEAAAKEAAAKEAAAKA	15,456	MLVMS_P03355_3mutA_WS
480	AEAAAKEAAAKEAAAKEAAAKALEAEAAAKEAAAKEAAAKEAAAKA	15,457	SFV1_P23074_2mutA
647	AEAAAKEAAAKEAAAKEAAAKALEAEAAAKEAAAKEAAAKEAAAKA	15,458	SFV3L_P27401_2mutA
1006	AEAAAKEAAAKEAAAKEAAAKALEAEAAAKEAAAKEAAAKEAAAKA	15,459	XMRV6_A1Z651_3mutA
2518	SGSETPGTSESATPES	15,460	MLVFF_P26809_3mutA

Subsequences of Exemplary Gene Modifying Polypeptides

In some embodiments, the gene modifying polypeptide comprises, in N-terminal to C-terminal order, one or more (e.g., 1, 2, 3, 4, 5, or all 6) of an N-terminal methionine residue, a first nuclear localization signal (NLS), a DNA binding domain, a linker, an RT domain, and/or a second NLS. In some embodiments, a gene modifying polypeptide comprises, in N-terminal to C-terminal order, a NLS (e.g., a first NLS), a DNA binding domain, a linker, and an RT domain, wherein the linker and RT domain are the linker and RT domain of a gene modifying polypeptide of any one of SEQ ID NOs: 1-7743, or an amino acid sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, or 99% identity to said linker and RT domain. In some embodiments, a gene modifying polypeptide comprises, in N-terminal to C-terminal order, a DNA binding domain, a linker, an RT domain, and an NLS (e.g., a second NLS) wherein the linker and RT domain are the linker and RT domain of a gene modifying polypeptide of any one of SEQ ID NOs: 1-7743, or an amino acid sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, or 99% identity to said linker and RT domain. In some embodiments, a gene modifying polypeptide comprises, in N-terminal to C-terminal order, a first NLS, a DNA binding domain, a linker, an RT domain, and a second NLS, wherein the linker and RT domain are the linker and RT domain of a gene modifying polypeptide of any one of SEQ ID NOs: 1-7743, or an amino acid sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, or 99% identity to said linker and RT domain. In some embodimetns, the gene modifying polypeptide further comprises an N-terminal methionine residue.

In some embodiments, the gene modifying polypeptide comprises, in N-terminal to C-terminal order, one or more (e.g., 1, 2, 3, 4, 5, or all 6) of an N-terminal methionine residue, a first nuclear localization signal (NLS) (e.g., of a gene modifying polypeptide of any one of SEQ ID NOs: 1-7743 and/or as listed in any of Tables A1, T1, or T2, or an amino acid sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, or 99% identity thereto), a DNA binding domain (e.g., a Cas domain, e.g., a SpyCas9 domain, e.g., as listed in Table 8, or an amino acid sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, or 99% identity thereto; or a DNA binding domain of a gene modifying polypeptide of any one of SEQ ID NOs: 1-7743 and/or as listed in any of Tables A1, T1, or T2, or an amino acid sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, or 99% identity thereto), a linker (e.g., of a gene modifying polypeptide of any one of SEQ ID NOs: 1-7743 and/or as listed in any of Tables A1, T1, or T2, or an amino acid

sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, or 99% identity thereto), an RT domain (e.g., of a gene modifying polypeptide of any one of SEQ ID NOs: 1-7743 and/or as listed in any of Tables A1, T1, or T2, or an amino acid sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, or 99% identity thereto), and a second NLS (e.g., of a gene modifying polypeptide of any one of SEQ ID NOs: 1-7743 and/or as listed in any of Tables A1, T1, or T2, or an amino acid sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, or 99% identity thereto). In some embodiments, the gene modifying polypeptide further comprises (e.g., C-terminal to the second NLS) a T2A sequence and/or a puromycin sequence (e.g., of a gene modifying polypeptide of any one of SEQ ID NOs: 1-7743 and/or as listed in any of Tables A1, T1, or T2, or an amino acid sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, or 99% identity thereto). In some embodiments, a nucleic acid encoding a gene modifying polypeptide (e.g., as described herein) encodes a T2A sequence, e.g., wherein the T2A sequence is situated between a region encoding the gene modifying polypeptide and a second region, wherein the second region optionally encodes a selectable marker, e.g., puromycin.

In certain embodiments, the first NLS comprises a first NLS sequence of a gene modifying polypeptide having an amino acid sequence of any one of SEQ ID NOs: 1-7743, or an amino acid sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, or 99% identity thereto. In certain embodiments, the first NLS comprises a first NLS sequence of a gene modifying polypeptide as listed in any of Tables A1, T1, or T2, or an amino acid sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, or 99% identity thereto. In certain embodiments, the first NLS sequence comprises a C-myc NLS. In certain embodiments, the first NLS comprises the amino acid sequence PAAKRVKLD (SEQ ID NO: 11,095) , or an amino acid sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, or 99% identity thereto.

In certain embodiments, the gene modifying polypeptide further comprises a spacer sequence between the first NLS and the DNA binding domain. In certain embodiments, the spacer sequence between the first NLS and the DNA binding domain comprises 1, 2, 3, 4, 5, 6, 7, 8, 9, or 10 amino acids. In certain embodiments, the spacer sequence between the first NLS and the DNA binding domain comprises the amino acid sequence GG.

In certain embodiments, the DNA binding domain comprises a DNA binding domain of a gene modifying polypeptide of any one of SEQ ID NOs: 1-7743, or an amino acid sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, or 99% identity thereto. In certain

embodiments, the DNA binding domain comprises a DNA binding domain of a gene modifying polypeptide as listed in any of Tables A1, T1, or T2, or an amino acid sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, or 99% identity thereto. In certain embodiments, the DNA binding domain comprises a Cas domain (e.g., as listed in Table 8). In certain embodiments, the DNA binding domain comprises the amino acid sequence of a SpyCas9 polypeptide (e.g., as listed in Table 8, e.g., a Cas9 N863A polypeptide), or an amino acid sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, or 99% identity thereto. In certain embodiments, the DNA binding domain comprises the amino acid sequence:

DKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLK
RTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYH
EKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYN
QLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFD
LAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASM
IKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDG
TEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIP
YYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSL
LYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDS
VEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAH
LFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFK
EDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQT
TQKGQKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRL
SDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKF
DNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSK
LVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKS
EQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM
PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGK
SKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASA
GELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVI
LADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDA
TLIHQSITGLYETRIDLSQLGGD (SEQ ID NO: 11,096),

or an amino acid sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, or 99% identity thereto.

In certain embodiments, the gene modifying polypeptide further comprises a spacer sequence between the DNA binding domain and the linker. In certain embodiments, the spacer sequence between the DNA binding domain and the linker comprises 1, 2, 3, 4, 5, 6, 7, 8, 9, or 10 amino acids. In certain embodiments, the spacer sequence between the DNA binding domain and the linker comprises the amino acid sequence GG.

In certain embodiments, the linker comprises a linker sequence of a gene modifying polypeptide of any one of SEQ ID NOs: 1-7743, or an amino acid sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, or 99% identity thereto. In certain embodiments, the linker comprises a linker sequence of a gene modifying polypeptide as listed in any of Tables A1, T1, or T2, or an amino acid sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, or 99% identity thereto. In certain embodiments, the linker comprises an amino acid sequence as listed in Table D or 10, or an amino acid sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, or 99% identity thereto.

In certain embodiments, the gene modifying polypeptide further comprises a spacer sequence between the linker and the RT domain. In certain embodiments, the spacer sequence between the linker and the RT domain comprises 1, 2, 3, 4, 5, 6, 7, 8, 9, or 10 amino acids. In certain embodiments, the spacer sequence between the linker and the RT domain comprises the amino acid sequence GG.

In certain embodiments, the RT domain comprises a RT domain sequence of a gene modifying polypeptide of any one of SEQ ID NOs: 1-7743, or an amino acid sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, or 99% identity thereto. In certain embodiments, the RT domain comprises a RT domain sequence of a gene modifying polypeptide as listed in any of Tables A1, T1, or T2, or an amino acid sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, or 99% identity thereto. In certain embodiments, the RT domain comprises an amino acid sequence as listed in Table D or 6, or an amino acid sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, or 99% identity thereto. In some embodiments, the RT domain has a length of about 400-500, 500-600, 600-700, 700-800, 800-900, or 900-1000 amino acids.

In certain embodiments, the gene modifying polypeptide further comprises a spacer sequence between the RT domain and the second NLS. In certain embodiments, the spacer

sequence between the RT domain and the second NLS comprises 1, 2, 3, 4, 5, 6, 7, 8, 9, or 10 amino acids. In certain embodiments, the spacer sequence between the RT domain and the second NLS comprises the amino acid sequence AG.

In certain embodiments, the second NLS comprises a second NLS sequence of a gene modifying polypeptide of any one of SEQ ID NOs: 1-7743. In certain embodiments, the second NLS comprises a second NLS sequence of a gene modifying polypeptide as listed in any of Tables A1, T1, or T2. In certain embodiments, the second NLS sequence comprises a plurality of partial NLS sequences. In embodiments, the NLS sequence, e.g., the second NLS sequence, comprises a first partial NLS sequence, e.g., comprising the amino acid sequence KRTADGSEFE (SEQ ID NO: 11,097), or an amino acid sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, or 99% identity thereto. In embodiments, the NLS sequence, e.g., the second NLS sequence, comprises a second partial NLS sequence. In embodiments, the NLS sequence, e.g., the second NLS sequence, comprises an SV40A5 NLS, e.g., a bipartite SV40A5 NLS, e.g., comprising the amino acid sequence KRTADGSEFESPKKKAKVE (SEQ ID NO: 11,098), or an amino acid sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, or 99% identity thereto. In certain embodiments, the NLS sequence, e.g., the second NLS sequence, comprises the amino acid sequence KRTADGSEFEKRTADGSEFESPKKKAKVE (SEQ ID NO: 11,099), or an amino acid sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, or 99% identity thereto.

In certain embodiments, the gene modifying polypeptide further comprises a spacer sequence between the second NLS and the T2A sequence and/or puromycin sequence. In certain embodiments, the spacer sequence between the second NLS and the T2A sequence and/or puromycin sequence comprises 1, 2, 3, 4, 5, 6, 7, 8, 9, or 10 amino acids. In certain embodiments, the spacer sequence between the second NLS and the T2A sequence and/or puromycin sequence comprises the amino acid sequence GSG.

Linkers and RT domains

In some embodiments, the gene modifying polypeptide comprises a linker (e.g., as described herein) and an RT domain (e.g., as described herein). In certain embodiments, the gene modifying polypeptide comprises, in N-terminal to C-terminal order, a linker (e.g., as described herein) and an RT domain (e.g., as described herein).

In certain embodiments, the linker comprises a linker sequence as listed in Table 10, or an amino acid sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, or 99% identity thereto. In certain embodiments, the linker comprises a linker sequence of any one of SEQ ID NOs: 1-7743, or an amino acid sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, or 99% identity thereto. In certain embodiments, the linker comprises a linker sequence of any one of SEQ ID NOs: 6001-7743, or an amino acid sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, or 99% identity thereto. In certain embodiments, the linker comprises a linker sequence of any one of SEQ ID NOs: 4501-4541, or an amino acid sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, or 99% identity thereto. In certain embodiments, the linker comprises a linker sequence of an exemplary gene modifying polypeptide listed in any of Tables A1, T1, or T2, or an amino acid sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, or 99% identity thereto. In certain embodiments, the RT domain comprises an RT domain sequence as listed in Table 6, or an amino acid sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, or 99% identity thereto. In certain embodiments, the RT domain comprises an RT domain sequence of an exemplary gene modifying polypeptide listed in any of Tables A1, T1, or T2, or an amino acid sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, or 99% identity thereto.

In some embodiments, a gene modifying polypeptide comprises a portion of a gene modifying polypeptide of any one of SEQ ID NOs: 1-7743, wherein the portion comprises a linker and RT domain, or an amino acid sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, or 99% identity to said portion.

In some embodiments, a gene modifying polypeptide comprises a linker of a gene modifying polypeptide of any one of SEQ ID NOs: 1-7743, or an amino acid sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, or 99% identity to said linker. In some embodiments, a gene modifying polypeptide comprises a linker of a gene modifying polypeptide of any one of SEQ ID NOs: 6001-7743, or an amino acid sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, or 99% identity to said linker. In some embodiments, a gene modifying polypeptide comprises a linker of a gene modifying polypeptide of any one of SEQ ID NOs: 4501-4541, or an amino acid sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, or 99% identity to said linker. In some embodiments, a gene modifying polypeptide comprises a linker of a gene

modifying polypeptide as listed in any of Tables A1, T1, or T2, or a linker comprising an amino acid sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, or 99% identity thereto.

In some embodiments, a gene modifying polypeptide comprises an RT domain of a gene modifying polypeptide of any one of SEQ ID NOs: 1-7743, or an amino acid sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, or 99% identity to said RT domain. In some embodiments, a gene modifying polypeptide comprises an RT domain of a gene modifying polypeptide of any one of SEQ ID NOs: 6001-7743, or an amino acid sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, or 99% identity said RT domain. In some embodiments, a gene modifying polypeptide comprises an RT domain of a gene modifying polypeptide of any one of SEQ ID NOs: 4501-4541, or an amino acid sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, or 99% identity said RT domain. In some embodiments, a gene modifying polypeptide comprises an RT domain of a gene modifying polypeptide as listed in any of Tables A1, T1, or T2, or an RT domain comprising an amino acid sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, or 99% identity thereto.

In certain embodiments, the linker and the RT domain of a gene modifying polypeptide comprise the amino acid sequences of a linker and RT domain (or amino acid sequences having at least 70%, 75%, 80%, 85%, 90%, 95%, or 99% identity thereto) of a gene modifying polypeptide having the amino acid sequence of any one of SEQ ID NOs: 1-7743. In certain embodiments, the linker and the RT domain of a gene modifying polypeptide comprise amino acid sequences of a linker and RT domain having at least 80% identity to the linker and RT domains of any one of SEQ ID NOs: 1-7743. In certain embodiments, the linker and the RT domain of a gene modifying polypeptide comprise amino acid sequences of a linker and RT domain having at least 90% identity to the linker and RT domains of any one of SEQ ID NOs: 1-7743. In certain embodiments, the linker and the RT domain of a gene modifying polypeptide comprise amino acid sequences of a linker and RT domain having at least 95% identity to the linker and RT domains of any one of SEQ ID NOs: 1-7743. In certain embodiments, the linker and the RT domain of a gene modifying polypeptide comprise amino acid sequences of a linker and RT domain having at least 99% identity to the linker and RT domains of any one of SEQ ID NOs: 1-7743. In certain embodiments, the linker and the RT domain of a gene modifying polypeptide comprise the amino acid sequences of a linker and RT domain (or amino acid sequences having at least 70%, 75%, 80%, 85%, 90%, 95%, or 99% identity thereto) of a gene

modifying polypeptide having the amino acid sequence of any one of SEQ ID NOs: 6001-7743. In certain embodiments, the linker and the RT domain of a gene modifying polypeptide comprise the amino acid sequences of a linker and RT domain (or amino acid sequences having at least 70%, 75%, 80%, 85%, 90%, 95%, or 99% identity thereto) of a gene modifying polypeptide having the amino acid sequence of any one of SEQ ID NOs: 4501-4541. In certain embodiments, the linker and the RT domain of a gene modifying polypeptide comprise the amino acid sequences of a linker and RT domain (or amino acid sequences having at least 70%, 75%, 80%, 85%, 90%, 95%, or 99% identity thereto) from a single row of any of Tables A1, T1, or T2 (e.g., from a single exemplary gene modifying polypeptide as listed in any of Tables A1, T1, or T2).

In certain embodiments, the linker and the RT domain of a gene modifying polypeptide comprise the amino acid sequences of a linker and RT domain (or amino acid sequences having at least 70%, 75%, 80%, 85%, 90%, 95%, or 99% identity thereto) from two different amino acid sequences selected from SEQ ID NOs: 1-7743. In certain embodiments, the linker and the RT domain of a gene modifying polypeptide comprise the amino acid sequences of a linker and RT domain (or amino acid sequences having at least 70%, 75%, 80%, 85%, 90%, 95%, or 99% identity thereto) from different rows of any of Tables A1, T1, or T2.

In certain embodiments, the gene modifying polypeptide further comprises a first NLS (e.g., a 5’ NLS), e.g., as described herein. In certain embodiments, the gene modifying polypeptide further comprises a second NLS (e.g., a 3’ NLS), e.g., as described herein. In certain embodiments, the gene modifying polypeptide further comprises an N-terminal methionine residue.

RT Families and Mutants

In certain embodiments, a gene modifying polypeptide comprises comprises the amino acid sequence of an RT domain sequence from a family selected from: AVIRE, BAEVM, FFV, FLV, FOAMV, GALV, KORV, MLVAV, MLVBM, MLVCB, MLVFF, MLVMS, PERV, SFV1, SFV3L, WMSV, XMRV6, BLVAU, BLVJ, HTL1A, HTL1C, HTL1L, HTL32, HTL3P, HTLV2, JSRV, MLVF5, MLVRD, MMTVB, MPMV, SFVCP, SMRVH, SRV1, SRV2, and WDSV. In certain embodiments, a gene modifying polypeptide comprises comprises the amino acid sequence of an RT domain sequence from a family selected from: AVIRE, BAEVM, FFV,

FLV, FOAMV, GALV, KORV, MLVAV, MLVBM, MLVCB, MLVFF, MLVMS, PERV, SFV1, SFV3L, WMSV, and XMRV6.

In certain embodiments, a gene modifying polypeptide comprises comprises the amino acid sequence of an RT domain sequence from an MLVMS RT domain. In embodiments, the amino acid sequence of an RT domain sequence comprises one or more point mutations as listed in column 1 of Table M1, or a point mutation corresponding thereto. In embodiments, the amino acid sequence of an RT domain sequence comprises one or more point mutations as listed in column 3 of Table M1 (Gen1 MLVMS), or a point mutation corresponding thereto. In embodiments, the amino acid sequence of an RT domain sequence comprises one or more point mutations at an amino acid position of the RT domain as listed in columns 1 and 2 of Table M2, or an amino acid position corresponding thereto.

In certain embodiments, a gene modifying polypeptide comprises comprises the amino acid sequence of an RT domain sequence from an AVIRE RT domain. In embodiments, the amino acid sequence of an RT domain sequence comprises one or more point mutations as listed in column 2 of Table M1, or a point mutation corresponding thereto. In embodiments, the amino acid sequence of an RT domain sequence comprises one or more point mutations as listed in column 4 of Table M1 (Gen2 AVIRE), or a point mutation corresponding thereto. In embodiments, the amino acid sequence of an RT domain sequence comprises one or more point mutations at an amino acid position of the RT domain as listed in columns 3 and 4 of Table M2, or an amino acid position corresponding thereto. In certain embodiments, the RT domain comprises an IENSSP (SEQ ID NO: 37639) (e.g., at the C-terminus).

Table M1. Exemplary point mutations in MLVMS and AVIRE RT domains

RT-linker filing (MLVMS)	Corresponding AVIRE	Gen1 MLVMS (PLV4921)	Gen2 AVIRE (PLV10990)
		H8Y	
P51L	Q51L		
S67R	T67R		
E67K	E67K		
E69K	E69K		
T197A	T197A		
D200N	D200N	D200N	D200N
H204R	N204R		

E302K	E302K		
		T306K	T306K
F309N	Y309N		
W313F	W313F	W313F	W313F
T330P	G330P	T330P	G330P
L435G	T436G		
N454K	N455K		
D524G	D526G		
E562Q	E564Q		
D583N	D585N		
H594Q	H596Q		
L603W	L605W	L603W	L605W
D653N	D655N		
L671P	L673P		
		IENSSP (SEQ ID NO: 37639) at C-term	

Table M2. Positions that can be mutated in exemplary MLVMS and AVIRE RT domains

WT residue & position			
MLVMS aa	**MLVMS position # ***	**AVIRE aa**	**AVIRE position # ***
H	8	Y	8
P	51	Q	51
S	67	T	67
E	69	E	69
T	197	T	197
D	200	D	200
H	204	N	204
E	302	E	302
T	306	T	306
F	309	Y	309
W	313	W	313
T	330	G	330
L	435	T	436
N	454	N	455
D	524	D	526

E	562	E	564
D	583	D	585
H	594	H	596
L	603	L	605
D	653	D	655
L	671	S	673

In certain embodiments, a gene modifying polypeptide comprises a gamma retrovirus derived RT domain. In certain embodiments, the gamma retrovirus-derived RT domain of a gene modifying polypeptide comprises the amino acid sequence of an RT domain sequence from a family selected from: AVIRE, BAEVM, FFV, FLV, FOAMV, GALV, KORV, MLVAV, MLVBM, MLVCB, MLVFF, MLVMS, PERV, SFV1, SFV3L, WMSV, and XMRV6. In some embodiments, the gamma retrovirus-derived RT domain of a gene modifying polypeptide is not derived from PERV. In some embodiments, said RT includes one, two, three, four, five, six or more mutations shown in Table 2 and corresponding to mutations D200N, L603W, T330P, D524G, E562Q, D583N, P51L, S67R, E67K, T197A, H204R, E302K, F309N, W313F, L435G, N454K, H594Q, L671P, E69K, or D653N in the RT domain of murine leukemia virus reverse transcriptase. In some embodiments, the gene modifying polypeptide further comprises a linker having at least 99% identity to a linker domains of any one of SEQ ID NOs: 1-7743. In some embodiments, the gene modifying polypeptide further comprises a linker having at least 99% or 100% identity to SEQ ID NO: 5217 or SEQ ID NO:11,041.

In embodiments, the RT domain comprises the amino acid sequence of an RT domain of an AVIRE RT (e.g., an AVIRE_P03360 sequence, e.g., SEQ ID NO: 8001), or an amino acid sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, or 99% identity thereto. In some embodiments, the RT domain comprises the amino acid sequence of an AVIRE RT further comprising one, two, three, four, or five mutations selected from the group consisting of D200N, G330P, L605W, T306K, and W313F, or a corresponding position in a homologous RT domain. In some embodiments, the RT domain comprises the amino acid sequence of an AVIRE RT further comprising one, two, or three mutations selected from the group consisting of D200N, G330P, and L605W, or a corresponding position in a homologous RT domain.

In embodiments, the RT domain comprises the amino acid sequence of an RT domain of a BAEVM RT (e.g., an BAEVM_P10272 sequence, e.g., SEQ ID NO: 8004), or an amino acid

sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, or 99% identity thereto. In some embodiments, the RT domain comprises the amino acid sequence of a BAEVM RT further comprising one, two, three, four, or five mutations selected from the group consisting of D198N, E328P, L602W, T304K, and W311F, or a corresponding position in a homologous RT domain. In some embodiments, the RT domain comprises the amino acid sequence of a BAEVM RT further comprising one, two, or three mutations selected from the group consisting of D198N, E328P, and L602W, or a corresponding position in a homologous RT domain.

In embodiments, the RT domain comprises the amino acid sequence of an RT domain of an FFV RT (e.g., an FFV_O93209 sequence, e.g., SEQ ID NO: 8012), or an amino acid sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, or 99% identity thereto. In some embodiments, the RT domain comprises the amino acid sequence of an FFV RT further comprising one, two, three, or four mutations selected from the group consisting of D21N, T293N, T419P, and L393K, or a corresponding position in a homologous RT domain. In some embodiments, the RT domain comprises the amino acid sequence of an FFV RT further comprising one, two, or three mutations selected from the group consisting of D21N, T293N, and T419P, or a corresponding position in a homologous RT domain. In some embodiments, the RT domain comprises the amino acid sequence of an FFV RT further comprising the mutation D21N. In some embodiments, the RT domain comprises the amino acid sequence of an FFV RT further comprising one, two, or three mutations selected from the group consisting of T207N, T333P, and L307K, or a corresponding position in a homologous RT domain. In some embodiments, the RT domain comprises the amino acid sequence of an FFV RT further comprising one or two mutations selected from the group consisting of T207N and T333P, or a corresponding position in a homologous RT domain.

In embodiments, the RT domain comprises the amino acid sequence of an RT domain of an FLV RT (e.g., an FLV_P10273 sequence, e.g., SEQ ID NO: 8019), or an amino acid sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, or 99% identity thereto. In some embodiments, the RT domain comprises the amino acid sequence of an FLV RT further comprising one, two, three, or four mutations selected from the group consisting of D199N, L602W, T305K, and W312F, or a corresponding position in a homologous RT domain. In some embodiments, the RT domain comprises the amino acid sequence of an FLV RT further comprising one or two

mutations selected from the group consisting of D199N and L602W, or a corresponding position in a homologous RT domain.

In embodiments, the RT domain comprises the amino acid sequence of an RT domain of a FOAMV RT (e.g., an FOAMV_P14350 sequence, e.g., SEQ ID NO: 8021), or an amino acid sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, or 99% identity thereto. In some embodiments, the RT domain comprises the amino acid sequence of an FOAMV RT further comprising one, two, three, or four mutations selected from the group consisting of D24N, T296N, S420P, and L396K, or a corresponding position in a homologous RT domain. In some embodiments, the RT domain comprises the amino acid sequence of an FOAMV RT further comprising one, two, or three mutations selected from the group consisting of D24N, T296N, and S420P, or a corresponding position in a homologous RT domain. In some embodiments, the RT domain comprises the amino acid sequence of an FOAMV RT further comprising the mutation D24N, or a corresponding position in a homologous RT domain. In some embodiments, the RT domain comprises the amino acid sequence of an FOAMV RT further comprising one, two, or three mutations selected from the group consisting of T207N, S331P, and L307K, or a corresponding position in a homologous RT domain. In some embodiments, the RT domain comprises the amino acid sequence of an FOAMV RT further comprising one or two mutations selected from the group consisting of T207N and S331P, or a corresponding position in a homologous RT domain.

In embodiments, the RT domain comprises the amino acid sequence of an RT domain of a GALV RT (e.g., an GALV_P21414 sequence, e.g., SEQ ID NO: 8027), or an amino acid sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, or 99% identity thereto. In some embodiments, the RT domain comprises the amino acid sequence of a GALV RT further comprising one, two, three, four, or five mutations selected from the group consisting of D198N, E328P, L600W, T304K, and W311F, or a corresponding position in a homologous RT domain. In some embodiments, the RT domain comprises the amino acid sequence of a GALV RT further comprising one, two, or three mutations selected from the group consisting of D198N, E328P, and L600W, or a corresponding position in a homologous RT domain.

In embodiments, the RT domain comprises the amino acid sequence of an RT domain of a KORV RT (e.g., an KORV_Q9TTC1 sequence, e.g., SEQ ID NO: 8047), or an amino acid sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, or 99% identity thereto. In some

embodiments, the RT domain comprises the amino acid sequence of a GALV RT further comprising one, two, three, four, five, or six mutations selected from the group consisting of D32N, D322N, E452P, L274W, T428K, and W435F, or a corresponding position in a homologous RT domain. In some embodiments, the RT domain comprises the amino acid sequence of a GALV RT further comprising one, two, three, or four mutations selected from the group consisting of D32N, D322N, E452P, and L274W, or a corresponding position in a homologous RT domain. In some embodiments, the RT domain comprises the amino acid sequence of a GALV RT further comprising the mutation D32N. In some embodiments, the RT domain comprises the amino acid sequence of a KORV RT further comprising one, two, three, four, or five mutations selected from the group consisting of D231N, E361P, L633W, T337K, and W344F, or a corresponding position in a homologous RT domain. In some embodiments, the RT domain comprises the amino acid sequence of a KORV RT further comprising one, two, or three mutations selected from the group consisting of D231N, E361P, and L633W, or a corresponding position in a homologous RT domain.

In embodiments, the RT domain comprises the amino acid sequence of an RT domain of a MLVAV RT (e.g., an MLVAV_P03356 sequence, e.g., SEQ ID NO: 8053), or an amino acid sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, or 99% identity thereto. In some embodiments, the RT domain comprises the amino acid sequence of a MLVAV RT further comprising one, two, three, four, or five mutations selected from the group consisting of D200N, T330P, L603W, T306K, and W313F, or a corresponding position in a homologous RT domain. In some embodiments, the RT domain comprises the amino acid sequence of a MLVAV RT further comprising one, two, or three mutations selected from the group consisting of D200N, T330P, and L603W, or a corresponding position in a homologous RT domain.

In embodiments, the RT domain comprises the amino acid sequence of an RT domain of a MLVBM RT (e.g., an MLVBM_Q7SVK7 sequence, e.g., SEQ ID NO: 8056), or an amino acid sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, or 99% identity thereto. In some embodiments, the RT domain comprises the amino acid sequence of a MLVBM RT further comprising one, two, three, four, or five mutations selected from the group consisting of D199N, T329P, L602W, T305K, and W312F, or a corresponding position in a homologous RT domain. In some embodiments, the RT domain comprises the amino acid sequence of a MLVBM RT

further comprising one, two, and three mutations selected from the group consisting of D200N, T330P, and L603W, or a corresponding position in a homologous RT domain.

In embodiments, the RT domain comprises the amino acid sequence of an RT domain of a MLVCB RT (e.g., an MLVCB_P08361 sequence, e.g., SEQ ID NO: 8062), or an amino acid sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, or 99% identity thereto. In some embodiments, the RT domain comprises the amino acid sequence of a MLVCB RT further comprising one, two, three, four, or five mutations selected from the group consisting of D200N, T330P, L603W, T306K, and W313F, or a corresponding position in a homologous RT domain. In some embodiments, the RT domain comprises the amino acid sequence of a MLVCB RT further comprising one, two, and three mutations selected from the group consisting of D200N, T330P, and L603W, or a corresponding position in a homologous RT domain.

In embodiments, the RT domain comprises the amino acid sequence of an RT domain of a MLVFF RT, or an amino acid sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, or 99% identity thereto. In some embodiments, the RT domain comprises the amino acid sequence of a MLVFF RT further comprising one, two, three, four, or five mutations selected from the group consisting of D200N, T330P, L603W, T306K, and W313F, or a corresponding position in a homologous RT domain. In some embodiments, the RT domain comprises the amino acid sequence of a MLVFF RT further comprising one, two, and three mutations selected from the group consisting of D200N, T330P, and L603W, or a corresponding position in a homologous RT domain.

In embodiments, the RT domain comprises the amino acid sequence of an RT domain of a MLVMS RT (e.g., an MLVMS_reference sequence, e.g., SEQ ID NO: 8137; or an MLVMS_P03355 sequence, e.g., SEQ ID NO: 8070), or an amino acid sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, or 99% identity thereto. In some embodiments, the RT domain comprises the amino acid sequence of a MLVMS RT further comprising one, two, three, four, five, or six mutations selected from the group consisting of D200N, T330P, L603W, T306K, W313F, and H8Y, or a corresponding position in a homologous RT domain. In some embodiments, the RT domain comprises the amino acid sequence of a MLVMS RT further comprising one, two, three, four, or five mutations selected from the group consisting of D200N, T330P, L603W, T306K, and W313F, or a corresponding position in a homologous RT domain. In some embodiments, the RT domain comprises the amino acid sequence of a MLVMS RT

further comprising one, two, or three mutations selected from the group consisting of D200N, T330P, and L603W, or a corresponding position in a homologous RT domain.

In embodiments, the RT domain comprises the amino acid sequence of an RT domain of a PERV RT (e.g., an PERV_Q4VFZ2 sequence, e.g., SEQ ID NO: 8099), or an amino acid sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, or 99% identity thereto. In some embodiments, the RT domain comprises the amino acid sequence of a PERV RT further comprising one, two, three, four, or five mutations selected from the group consisting of D196N, E326P, L599W, T302K, and W309F, or a corresponding position in a homologous RT domain. In some embodiments, the RT domain comprises the amino acid sequence of a PERV RT further comprising one, two, or three mutations selected from the group consisting of D196N, E326P, and L599W, or a corresponding position in a homologous RT domain.

In embodiments, the RT domain comprises the amino acid sequence of an RT domain of a SFV1 RT (e.g., an SFV1_P23074 sequence, e.g., SEQ ID NO: 8105), or an amino acid sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, or 99% identity thereto. In some embodiments, the RT domain comprises the amino acid sequence of a SFV1 RT further comprising one, two, three, or four mutations selected from the group consisting of D24N, T296N, N420P, and L396K, or a corresponding position in a homologous RT domain. In some embodiments, the RT domain comprises the amino acid sequence of a SFV1 RT further comprising one, two, or three mutations selected from the group consisting of D24N, T296N, and N420P, or a corresponding position in a homologous RT domain. In some embodiments, the RT domain comprises the amino acid sequence of a SFV1 RT further comprising the D24N, or a corresponding position in a homologous RT domain.

In embodiments, the RT domain comprises the amino acid sequence of an RT domain of a SFV3L RT (e.g., an SFV3L_P27401 sequence, e.g., SEQ ID NO: 8111), or an amino acid sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, or 99% identity thereto. In some embodiments, the RT domain comprises the amino acid sequence of a SFV3L RT further comprising one, two, three, or four mutations selected from the group consisting of D24N, T296N, N422P, and L396K, or a corresponding position in a homologous RT domain. In some embodiments, the RT domain comprises the amino acid sequence of a SFV3L RT further comprising one, two, or three mutations selected from the group consisting of D24N, T296N, and N422P, or a corresponding position in a homologous RT domain. In some embodiments, the

RT domain comprises the amino acid sequence of a SFV3L RT further comprising the mutation D24N, or a corresponding position in a homologous RT domain. In some embodiments, the RT domain comprises the amino acid sequence of a SFV3L RT further comprising one, two, or three mutations selected from the group consisting of T307N, N333P, and L307K, or a corresponding position in a homologous RT domain. In some embodiments, the RT domain comprises the amino acid sequence of a SFV3L RT further comprising one or two mutations selected from the group consisting of T307N and N333P, or a corresponding position in a homologous RT domain.

In embodiments, the RT domain comprises the amino acid sequence of an RT domain of a WMSV RT (e.g., an WMSV_P03359 sequence, e.g., SEQ ID NO: 8131), or an amino acid sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, or 99% identity thereto. In some embodiments, the RT domain comprises the amino acid sequence of a WMSV RT further comprising one, two, three, four, or five mutations selected from the group consisting of D198N, E328P, L600W, T304K, and W311F, or a corresponding position in a homologous RT domain. In some embodiments, the RT domain comprises the amino acid sequence of a WMSV RT further comprising one, two, or three mutations selected from the group consisting of D198N, E328P, and L600W, or a corresponding position in a homologous RT domain.

In embodiments, the RT domain comprises the amino acid sequence of an RT domain of a XMRV6 RT (e.g., an XMRV6_A1Z651 sequence, e.g., SEQ ID NO: 8134), or an amino acid sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, or 99% identity thereto. In some embodiments, the RT domain comprises the amino acid sequence of a XMRV6 RT further comprising one, two, three, four, or five mutations selected from the group consisting of D200N, T330P, L603W, T306K, and W313F, or a corresponding position in a homologous RT domain. In some embodiments, the RT domain comprises the amino acid sequence of a XMRV6 RT further comprising one, two, or three mutations selected from the group consisting of D200N, T330P, and L603W, or a corresponding position in a homologous RT domain.

In certain embodiments, the RT domain of a gene modifying polypeptide comprises the amino acid sequence of an RT domain of an AVIRE RT, or an amino acid sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, or 99% identity thereto. In embodiments, the RT domain comprises the amino acid sequence of an RT domain comprised in a sequence listed in column 1 of Table A5, or an amino acid sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, or 99% identity thereto. In some embodiments, the gene modifying polypeptide further

comprises a linker having at least 99% or 100% identity to SEQ ID NO: 5217 or SEQ ID NO:11,041.

In certain embodiments, the RT domain of a gene modifying polypeptide comprises the amino acid sequence of an RT domain of an MLVMS RT, or an amino acid sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, or 99% identity thereto. In embodiments, the RT domain comprises the amino acid sequence of an RT domain comprised in a sequence listed in any of columns 2-6 of Table A5, or an amino acid sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, or 99% identity thereto. In some embodiments, the gene modifying polypeptide further comprises a linker having at least 99% or 100% identity to SEQ ID NO: 5217 or SEQ ID NO:11,041.

Table A5. Exemplary gene modifying polypeptides comprising an AVIRE RT domain or an MLVMS RT domain.

AVIRE SEQ ID NOs:	MLVMS SEQ ID NOs:				
1	2704	3007	3038	2638	2930
2	2706	3007	3038	2639	2930
3	2708	3008	3039	2639	2931
4	2709	3008	3039	2640	2931
5	2709	3009	3040	2640	2932
6	2710	3010	3040	2641	2932
7	2957	3010	3041	2641	2933
9	2957	3011	3041	2642	2933
10	2958	3012	3042	2642	2934
12	2959	3012	3042	2643	2934
13	2960	3013	3043	2643	2935
14	2962	3013	3043	2644	2935
6076	6042	3014	3044	2644	2936
6143	6068	3014	3044	2645	2936
6200	6097	3015	3045	2645	2937
6254	6136	3015	3045	2646	2937
6274	6156	3016	3046	2646	2938
6315	6215	3016	3046	2647	2938
6328	6216	3017	3047	2647	2939
6337	6301	3018	3047	2648	2939
6403	6352	3018	3048	2648	2940
6420	6365	3019	3048	2649	2940
6440	6411	3019	3049	2649	2941

6513	6436	3020	3049	2650	2941
6552	6458	3020	3050	2650	2942
6613	6459	3021	3051	2651	2942
6671	6524	3021	3051	2651	2943
6822	6562	3022	3052	2652	2943
6840	6563	3023	3052	2652	2944
6884	6699	3023	3053	2653	2945
6907	6865	3024	3053	2653	2945
6970	7022	3024	3054	2654	2946
7025	7037	3025	3054	2655	2946
7052	7088	3025	3055	2655	2947
7078	7116	3026	3055	2656	2947
7243	7175	3026	3056	2656	2948
7253	7200	3027	3056	2657	2948
7318	7206	3027	3057	2657	2949
7379	7277	3028	3057	2658	2949
7486	7294	3028	3058	2658	2950
7524	7330	3029	3058	2659	2950
7668	7411	3030	3059	2659	2951
7680	7455	3030	3059	2660	2951
7720	7477	3031	3060	2660	2952
1137	7511	3031	3060	2661	2952
1138	7538	3032	3061	2661	2953
1139	7559	3032	3061	2662	2953
1140	7560	3033	3062	2662	2954
1141	7593	3033	3062	2663	2954
1142	7594	3034	3063	2663	2955
1143	7607	3034	3063	2664	2955
1144	7623	6025	3064	2664	6485
1145	7638	6041	3064	2665	6486
1146	7717	6043	3065	2665	6504
1147	7731	6098	3065	2666	6505
1148	7732	6099	3066	2666	6595
1149	2711	6180	3066	2667	6596
1150	2711	6182	3067	2667	6751
1151	2712	6237	3067	2668	6752
1152	2712	6238	3068	2668	6777
1153	2713	6311	3068	2669	6778
1154	2713	6312	3069	2669	7172
1155	2714	6578	3069	2670	7174
1156	2714	6579	3070	2670	7313

1157	2715	6663	3070	2671	7314
1158	2715	6664	3071	2671	
1159	2716	6708	3071	2672	
1160	2716	6709	3072	2672	
1161	2717	6809	3072	2673	
1162	2717	6831	3073	2673	
1163	2718	6832	3073	2674	
1164	2718	6864	3074	2674	
1165	2719	6866	3074	2675	
1166	2719	7089	3075	2675	
1167	2720	7157	3075	2676	
6015	2720	7159	3076	2676	
6029	2721	7173	3076	2677	
6045	2721	7176	3077	2677	
6077	2722	7293	3077	2678	
6129	2722	7295	3078	2678	
6144	2723	7343	3078	2679	
6164	2723	7393	3079	2680	
6201	2724	7394	3079	2680	
6227	2724	7425	3080	2681	
6244	2725	7426	3080	2681	
6250	2725	7444	3081	2682	
6264	2726	7445	3081	2682	
6289	2726	7476	3082	2683	
6304	2727	7478	3082	2683	
6316	2727	7496	3083	2684	
6384	2728	7497	3083	2684	
6421	2728	7537	3084	2685	
6441	2729	7539	3084	2685	
6492	2729	2780	3085	2686	
6514	2730	2780	3085	2686	
6530	2730	2781	3086	2687	
6569	2731	2781	3086	2687	
6584	2731	2782	3087	2688	
6621	2732	2782	3087	2688	
6651	2732	2783	3088	2689	
6659	2733	2783	3088	2689	
6683	2734	2784	3089	2690	
6703	2734	2784	3089	2690	
6727	2735	2785	3090	2691	
6732	2735	2785	3090	2692	

6745	2736	2786	3091	2692	
6755	2736	2786	3091	2693	
6784	2737	2787	3092	2693	
6817	2737	2787	3092	2694	
6823	2738	2788	3093	2694	
6841	2739	2788	3093	2695	
6871	2740	2789	3094	2695	
6885	2740	2789	3095	2696	
6898	2741	2790	3095	2696	
6908	2741	2790	3096	2697	
6933	2742	2791	3096	2697	
6971	2742	2791	3097	2698	
7009	2743	2792	3097	2698	
7018	2743	2792	3098	2699	
7045	2744	2793	3098	2699	
7053	2744	2793	3099	2700	
7068	2745	2794	3099	2700	
7079	2745	2794	3100	2701	
7096	2746	2795	3100	2701	
7104	2746	2795	3101	2702	
7122	2747	2796	3101	2702	
7151	2747	2796	3102	2703	
7163	2748	2797	3102	2703	
7181	2748	2797	3103	2862	
7244	2749	2798	3103	2862	
7273	2750	2798	3104	2863	
7319	2750	2799	3104	2863	
7336	2751	2799	3105	2864	
7380	2751	2800	3105	2864	
7402	2752	2800	3106	2865	
7462	2752	2801	3106	2865	
7487	2753	2801	3107	2866	
7525	2753	2802	3107	2866	
7569	2754	2802	3108	2867	
7626	2754	2803	3108	2867	
7689	2755	2803	3109	2868	
7707	2755	2804	3109	2868	
7721	2756	2804	3110	2869	
1371	2756	2805	3110	2869	
1372	2757	2805	3111	2870	
1373	2758	2806	3111	2870	

1374	2758	2806	3112	2871	
1375	2759	2807	3112	2871	
1376	2759	2807	3113	2872	
1377	2760	2808	3113	2872	
1378	2760	2808	3114	2873	
1379	2761	2809	3114	2873	
1380	2761	2809	3115	2874	
1381	2762	2810	3115	2874	
1382	2762	2810	3116	2875	
1383	2763	2811	3116	2875	
1384	2763	2811	3117	2876	
1385	2764	2812	3117	2876	
1386	2764	2812	3118	2877	
1387	2765	2813	3118	2877	
1388	2765	2813	3119	2878	
1389	2766	2814	3119	2878	
1390	2766	2814	3120	2879	
1391	2767	2815	3120	2879	
1392	2767	2815	3121	2880	
1393	2768	2816	3121	2880	
1394	2768	2816	3122	2881	
1395	2769	2817	3122	2881	
1396	2769	2817	3123	2882	
1397	2770	2818	3123	2882	
1398	2770	2818	3124	2883	
1399	2771	2819	3124	2883	
1400	2771	2819	3125	2884	
1401	2772	2820	3125	2884	
1402	2773	2820	3126	2885	
1403	2773	2821	3126	2885	
1404	2774	2821	3127	2886	
1405	2774	2822	3127	2886	
1406	2775	2822	3128	2887	
1407	2775	2823	3128	2887	
1408	2776	2823	3129	2888	
1409	2776	2824	3129	2888	
1410	2777	2824	3130	2889	
1411	2777	2825	3130	2889	
1412	2778	2825	3131	2890	
1413	2779	2826	3131	2890	
1414	2779	2826	3132	2891	

1415	2965	2827	3133	2891	
1416	2965	2827	3133	2892	
1417	2966	2828	3134	2893	
1418	2966	2828	3134	2893	
1419	2967	2829	3135	2894	
1420	2968	2829	3135	2894	
1421	2968	2830	3136	2895	
1422	2969	2830	3136	2895	
1423	2969	2831	6181	2896	
1424	2970	2831	6183	2896	
1425	2970	2832	6284	2897	
1426	2971	2832	6285	2897	
1427	2971	2833	6760	2898	
1428	2972	2833	6761	2898	
1429	2972	2834	7036	2899	
1430	2973	2834	7038	2899	
1431	2974	2835	7158	2900	
1432	2974	2835	7160	2900	
1433	2975	2836	2610	2901	
1434	2976	2836	2610	2901	
1435	2976	2837	2611	2902	
1436	2977	2837	2611	2902	
1437	2977	2838	2612	2903	
1439	2978	2838	2612	2903	
1440	2978	2839	2613	2904	
1441	2979	2839	2613	2904	
1442	2979	2840	2614	2905	
1443	2980	2840	2614	2905	
1444	2980	2841	2615	2906	
1445	2981	2841	2615	2906	
1446	2981	2842	2616	2907	
1447	2982	2842	2616	2907	
6001	2982	2843	2617	2908	
6030	2983	2843	2617	2908	
6078	2983	2844	2618	2909	
6108	2984	2844	2618	2909	
6130	2985	2845	2619	2910	
6165	2985	2845	2619	2910	
6265	2986	2846	2620	2911	
6275	2987	2846	2620	2911	
6305	2987	2847	2621	2912	

6329	2988	2847	2621	2912	
6370	2988	2848	2622	2913	
6385	2989	2848	2622	2913	
6404	2989	2849	2623	2914	
6531	2990	2849	2623	2914	
6585	2990	2850	2624	2915	
6622	2991	2850	2624	2915	
6652	2991	2851	2625	2916	
6733	2992	2851	2625	2916	
6756	2992	2852	2626	2917	
6765	2993	2852	2626	2917	
6798	2993	2853	2627	2918	
6824	2994	2853	2627	2919	
6972	2994	2854	2628	2919	
7046	2995	2854	2628	2920	
7054	2995	2855	2629	2920	
7069	2996	2855	2629	2921	
7080	2996	2856	2630	2921	
7105	2997	2856	2630	2922	
7123	2998	2857	2631	2922	
7143	2998	2857	2631	2923	
7152	2999	2858	2632	2923	
7204	2999	2858	2632	2924	
7320	3001	2859	2633	2924	
7351	3001	2859	2633	2925	
7381	3002	2860	2634	2925	
7403	3002	2860	2634	2926	
7438	3003	2861	2635	2926	
7488	3003	2861	2635	2927	
7500	3004	3035	2636	2927	
7526	3004	3036	2636	2928	
7588	3005	3036	2637	2928	
7612	3005	3037	2637	2929	
7627	3006	3037	2638	2929	

Systems

In an aspect, the disclosure relates to a system comprising nucleic acid molecule encoding a gene modifying polypeptide (e.g., as described herein) and a template nucleic acid (e.g., a template RNA, e.g., as described herein). In certain embodiments, the nucleic acid molecule encoding the gene modifying polypeptide comprises one or more silent mutations in

the coding region (e.g., in the sequence encoding the RT domain) relative to a nucleic acid molecule as described herein. In certain embodiments, the system further comprises a gRNA (e.g., a gRNA that binds to a polypeptide that induces a nick, e.g., in the opposite strand of the target DNA bound by the gene modifying polypeptide).

In certain embodiments, the nucleic acid molecule encoding the gene modifying polypeptide encodes a polypeptide having an amino acid sequence selected from SEQ ID NOs: 1-7743, or an amino acid sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, or 99% identity thereto. In certain embodiments, the nucleic acid molecule encoding the gene modifying polypeptide encodes a polypeptide having an amino acid sequence selected from SEQ ID NOs: 6001-7743, or an amino acid sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, or 99% identity thereto. In certain embodiments, the nucleic acid molecule encoding the gene modifying polypeptide encodes a polypeptide having an amino acid sequence selected from SEQ ID NOs: 4501-4541, or an amino acid sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, or 99% identity thereto. In certain embodiments, the nucleic acid molecule encoding the gene modifying polypeptide encodes a polypeptide as listed in any of Tables A1, T1, or T2, or an amino acid sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, or 99% identity thereto.

In certain embodiments, the nucleic acid molecule encoding the gene modifying polypeptide comprises a sequence encoding a portion of an amino acid sequence selected from SEQ ID NOs: 1-7743, wherein the portion comprises a linker and RT domain, or an amino acid sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, or 99% identity to said portion. In certain embodiments, the nucleic acid molecule encoding the gene modifying polypeptide comprises a sequence encoding a portion of an amino acid sequence selected from SEQ ID NOs: 6001-7743, wherein the portion comprises a linker and RT domain, or an amino acid sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, or 99% identity to said portion. In certain embodiments, the nucleic acid molecule encoding the gene modifying polypeptide comprises a sequence encoding a portion of an amino acid sequence selected from SEQ ID NOs: 4501-4541, wherein the portion comprises a linker and RT domain, or an amino acid sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, or 99% identity to said portion. In certain embodiments, the nucleic acid molecule encoding the gene modifying polypeptide comprises a sequence encoding a portion of a polypeptide listed in any of Tables A1, T1, or T2, wherein the portion

comprises a linker and RT domain, or an amino acid sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, or 99% identity to said portion.

In certain embodiments, the nucleic acid molecule encoding the gene modifying polypeptide comprises a sequence encoding the linker of an amino acid sequence selected from SEQ ID NOs: 1-7743, or an amino acid sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, or 99% identity thereto. In certain embodiments, the nucleic acid molecule encoding the gene modifying polypeptide comprises a sequence encoding the linker of a polypeptide having an amino acid sequence selected from SEQ ID NOs: 6001-7743, or an amino acid sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, or 99% identity thereto. In certain embodiments, the nucleic acid molecule encoding the gene modifying polypeptide comprises a sequence encoding the linker of a polypeptide having an amino acid sequence selected from SEQ ID NOs: 4501-4541, or an amino acid sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, or 99% identity thereto. In certain embodiments, the nucleic acid molecule encoding the gene modifying polypeptide comprises a sequence encoding the linker of a polypeptide as listed in any of Tables A1, T1, or T2, or an amino acid sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, or 99% identity thereto.

In certain embodiments, the nucleic acid molecule encoding the gene modifying polypeptide comprises a sequence encoding the RT domain of an amino acid sequence selected from SEQ ID NOs: 1-7743, or an amino acid sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, or 99% identity thereto. In certain embodiments, the nucleic acid molecule encoding the gene modifying polypeptide comprises a sequence encoding the RT domain of a polypeptide having an amino acid sequence selected from SEQ ID NOs: 6001-7743, or an amino acid sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, or 99% identity thereto. In certain embodiments, the nucleic acid molecule encoding the gene modifying polypeptide comprises a sequence encoding the RT domain of a polypeptide having an amino acid sequence selected from SEQ ID NOs: 4501-4541, or an amino acid sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, or 99% identity thereto. In certain embodiments, the nucleic acid molecule encoding the gene modifying polypeptide comprises a sequence encoding the RT domain of a polypeptide as listed in any of Tables A1, T1, or T2, or an amino acid sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, or 99% identity thereto.

In an aspect, the disclosure relates to a system comprising a gene modifying polypeptide (e.g., as described herein) and a template nucleic acid (e.g., a template RNA, e.g., as described herein).

In certain embodiments, the gene modifying polypeptide comprises a polypeptide having an amino acid sequence selected from SEQ ID NOs: 1-7743, or an amino acid sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, or 99% identity thereto. In certain embodiments, the gene modifying polypeptide comprises a polypeptide having an amino acid sequence selected from SEQ ID NOs: 6001-7743, or an amino acid sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, or 99% identity thereto. In certain embodiments, the gene modifying polypeptide comprises a polypeptide having an amino acid sequence selected from SEQ ID NOs: 4501-4541, or an amino acid sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, or 99% identity thereto. In certain embodiments, the gene modifying polypeptide comprises a polypeptide as listed in any of Tables A1, T1, or T2, or an amino acid sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, or 99% identity thereto.

In certain embodiments, the gene modifying polypeptide comprises a portion of an amino acid sequence selected from SEQ ID NOs: 1-7743, wherein the portion comprises a linker and RT domain, or an amino acid sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, or 99% identity to said portion. In certain embodiments, the gene modifying polypeptide comprises a portion of an amino acid sequence selected from SEQ ID NOs: 6001-7743, wherein the portion comprises a linker and RT domain, or an amino acid sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, or 99% identity to said portion. In certain embodiments, the gene modifying polypeptide comprises a portion of an amino acid sequence selected from SEQ ID NOs: 4501-4541, wherein the portion comprises a linker and RT domain, or an amino acid sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, or 99% identity to said portion. In certain embodiments, the gene modifying polypeptide comprises a portion of a polypeptide listed in any of Tables A1, T1, or T2, wherein the portion comprises a linker and RT domain, or an amino acid sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, or 99% identity to said portion.

In certain embodiments, the gene modifying polypeptide comprises the linker of an amino acid sequence selected from SEQ ID NOs: 1-7743, or an amino acid sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, or 99% identity thereto. In certain embodiments, the gene modifying polypeptide comprises a sequence encoding the linker of a polypeptide having

an amino acid sequence selected from SEQ ID NOs: 6001-7743, or an amino acid sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, or 99% identity thereto. In certain embodiments, the gene modifying polypeptide comprises a sequence encoding the linker of a polypeptide having an amino acid sequence selected from SEQ ID NOs: 4501-4541, or an amino acid sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, or 99% identity thereto. In certain embodiments, the gene modifying polypeptide comprises the linker of a polypeptide as listed in any of Tables A1, T1, or T2, or an amino acid sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, or 99% identity thereto.

In certain embodiments, the gene modifying polypeptide comprises the RT domain of an amino acid sequence selected from SEQ ID NOs: 1-7743, or an amino acid sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, or 99% identity thereto. In certain embodiments, the gene modifying polypeptide comprises a sequence encoding the RT domain of a polypeptide having an amino acid sequence selected from SEQ ID NOs: 6001-7743, or an amino acid sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, or 99% identity thereto. In certain embodiments, the gene modifying polypeptide comprises a sequence encoding the RT domain of a polypeptide having an amino acid sequence selected from SEQ ID NOs: 4501-4541, or an amino acid sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, or 99% identity thereto. In certain embodiments, the gene modifying polypeptide comprises the RT domain of a polypeptide as listed in any of Tables A1, T1, or T2, or an amino acid sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, or 99% identity thereto.

Table A1. Exemplary amino acid sequences for gene modifying polypeptides comprising an RT domain and a linker sequence

SEQ ID NO:	Amino Acid Sequence
34	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKGSSGGLDDEYRLYS PLVKPDQNIQFWLEQFPQAWAETAGMGLAKQVPPQVIQLKASATPVSVRQYPLSKEAQEGIRPHVQRLIQQGILVPVQSPWNTPLLPVRKPGTNDYRPVQ DLREVNKRVQDIHPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGTGRTGQLTWTRLPQGFKNSPTIFNEALHRDLANFRIQ HPQVTLLQYVDDLLLAGATKQDCLEGTKALLLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWLTEARKKTVVQIPAPTTAKQVREFLGKAGFCRLF IPGFATLAAPLYPLTKPKGEFSWAPEHQKAFDAIKKALLSAPALALPDVTKPFTLYVDERKGVARGVLTQTLGPWRRPVAYLSKKLDPVASGWPVCLKAI AAVAILVKDADKLTLGQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNPATLLPEETDEPVTHDCHQLLIEETGVRKDLTDIP LTGEVLTWFTDGSSYVVEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSINIYTDSRYAFATAHVHGAIYKQRGWLTSAGREIKN KEEILSLLEALHLPKRLAIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLPAGKRTADGSEFEKRTADGSEFESPKKKAKVE
35	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK

	VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKGGSPAPGGLDDEYR LYSPLVKPDQNIQFWLEQFPQAWAETAGMGLAKQVPPQVIQLKASATPVSVRQYPLSKEAQEGIRPHVQRLIQQGILVPVQSPWNTPLLPVRKPGTNDYR PVQDLREVNKRVQDIHPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGTGRTGQLTWTRLPQGFKNSPTIFNEALHRDLANF RIQHPQVTLLQYVDDLLLAGATKQDCLEGTKALLLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWLTEARKKTVVQIPAPTTAKQVREFLGKAGFC RLFIPGFATLAAPLYPLTKPKGEFSWAPEHQKAFDAIKKALLSAPALALPDVTKPFTLYVDERKGVARGVLTQTLGPWRRPVAYLSKKLDPVASGWPVCL KAIAAVAILVKDADKLTLGQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNPATLLPEETDEPVTHDCHQLLIEETGVRKDLT DIPLTGEVLTWFTDGSSYVVEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSINIYTDSRYAFATAHVHGAIYKQRGWLTSAGRE IKNKEEILSLLEALHLPKRLAIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLPAGKRTADGSEFEKRTADGSEFESPKKKAKVE
35	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKGGSPAPGGLDDEYR LYSPLVKPDQNIQFWLEQFPQAWAETAGMGLAKQVPPQVIQLKASATPVSVRQYPLSKEAQEGIRPHVQRLIQQGILVPVQSPWNTPLLPVRKPGTNDYR PVQDLREVNKRVQDIHPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGTGRTGQLTWTRLPQGFKNSPTIFNEALHRDLANF RIQHPQVTLLQYVDDLLLAGATKQDCLEGTKALLLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWLTEARKKTVVQIPAPTTAKQVREFLGKAGFC RLFIPGFATLAAPLYPLTKPKGEFSWAPEHQKAFDAIKKALLSAPALALPDVTKPFTLYVDERKGVARGVLTQTLGPWRRPVAYLSKKLDPVASGWPVCL KAIAAVAILVKDADKLTLGQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNPATLLPEETDEPVTHDCHQLLIEETGVRKDLT DIPLTGEVLTWFTDGSSYVVEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSINIYTDSRYAFATAHVHGAIYKQRGWLTSAGRE IKNKEEILSLLEALHLPKRLAIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLPAGKRTADGSEFEKRTADGSEFESPKKKAKVE
36	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE

	VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGAEAAAKEAAAKEAAAKEAA AKALEAEAAAKEAAAKEAAAKEAAAKAGGLDDEYRLYSPLVKPDQNIQFWLEQFPQAWAETAGMGLAKQVPPQVIQLKASATPVSVRQYPLSKEAQEGIR PHVQRLIQQGILVPVQSPWNTPLLPVRKPGTNDYRPVQDLREVNKRVQDIHPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDP GTGRTGQLTWTRLPQGFKNSPTIFNEALHRDLANFRIQHPQVTLLQYVDDLLLAGATKQDCLEGTKALLLELSDLGYRASAKKAQICRREVTYLGYSLRD GQRWLTEARKKTVVQIPAPTTAKQVREFLGKAGFCRLFIPGFATLAAPLYPLTKPKGEFSWAPEHQKAFDAIKKALLSAPALALPDVTKPFTLYVDERKG VARGVLTQTLGPWRRPVAYLSKKLDPVASGWPVCLKAIAAVAILVKDADKLTLGQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPA ALNPATLLPEETDEPVTHDCHQLLIEETGVRKDLTDIPLTGEVLTWFTDGSSYVVEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEG KSINIYTDSRYAFATAHVHGAIYKQRGWLTSAGREIKNKEEILSLLEALHLPKRLAIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLPAGKRTADG SEFEKRTADGSEFESPKKKAKVE
36	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGAEAAAKEAAAKEAAAKEAA AKALEAEAAAKEAAAKEAAAKEAAAKAGGLDDEYRLYSPLVKPDQNIQFWLEQFPQAWAETAGMGLAKQVPPQVIQLKASATPVSVRQYPLSKEAQEGIR PHVQRLIQQGILVPVQSPWNTPLLPVRKPGTNDYRPVQDLREVNKRVQDIHPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDP GTGRTGQLTWTRLPQGFKNSPTIFNEALHRDLANFRIQHPQVTLLQYVDDLLLAGATKQDCLEGTKALLLELSDLGYRASAKKAQICRREVTYLGYSLRD GQRWLTEARKKTVVQIPAPTTAKQVREFLGKAGFCRLFIPGFATLAAPLYPLTKPKGEFSWAPEHQKAFDAIKKALLSAPALALPDVTKPFTLYVDERKG VARGVLTQTLGPWRRPVAYLSKKLDPVASGWPVCLKAIAAVAILVKDADKLTLGQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPA ALNPATLLPEETDEPVTHDCHQLLIEETGVRKDLTDIPLTGEVLTWFTDGSSYVVEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEG KSINIYTDSRYAFATAHVHGAIYKQRGWLTSAGREIKNKEEILSLLEALHLPKRLAIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLPAGKRTADG SEFEKRTADGSEFESPKKKAKVE
37	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA

	KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKEAAAKEAAAKGGLD DEYRLYSPLVKPDQNIQFWLEQFPQAWAETAGMGLAKQVPPQVIQLKASATPVSVRQYPLSKEAQEGIRPHVQRLIQQGILVPVQSPWNTPLLPVRKPGT NDYRPVQDLREVNKRVQDIHPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGTGRTGQLTWTRLPQGFKNSPTIFNEALHRD LANFRIQHPQVTLLQYVDDLLLAGATKQDCLEGTKALLLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWLTEARKKTVVQIPAPTTAKQVREFLGK AGFCRLFIPGFATLAAPLYPLTKPKGEFSWAPEHQKAFDAIKKALLSAPALALPDVTKPFTLYVDERKGVARGVLTQTLGPWRRPVAYLSKKLDPVASGW PVCLKAIAAVAILVKDADKLTLGQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNPATLLPEETDEPVTHDCHQLLIEETGVR KDLTDIPLTGEVLTWFTDGSSYVVEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSINIYTDSRYAFATAHVHGAIYKQRGWLTS AGREIKNKEEILSLLEALHLPKRLAIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLPAGKRTADGSEFEKRTADGSEFESPKKKAKVE
38	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSGSSPAPGGLDDEYRLY SPLVKPDQNIQFWLEQFPQAWAETAGMGLAKQVPPQVIQLKASATPVSVRQYPLSKEAQEGIRPHVQRLIQQGILVPVQSPWNTPLLPVRKPGTNDYRPV QDLREVNKRVQDIHPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGTGRTGQLTWTRLPQGFKNSPTIFNEALHRDLANFRI QHPQVTLLQYVDDLLLAGATKQDCLEGTKALLLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWLTEARKKTVVQIPAPTTAKQVREFLGKAGFCRL FIPGFATLAAPLYPLTKPKGEFSWAPEHQKAFDAIKKALLSAPALALPDVTKPFTLYVDERKGVARGVLTQTLGPWRRPVAYLSKKLDPVASGWPVCLKA IAAVAILVKDADKLTLGQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNPATLLPEETDEPVTHDCHQLLIEETGVRKDLTDI PLTGEVLTWFTDGSSYVVEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSINIYTDSRYAFATAHVHGAIYKQRGWLTSAGREIK NKEEILSLLEALHLPKRLAIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLPAGKRTADGSEFEKRTADGSEFESPKKKAKVE
39	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK

	ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKEAAAKEAAAKEAAA KEAAAKGGLDDEYRLYSPLVKPDQNIQFWLEQFPQAWAETAGMGLAKQVPPQVIQLKASATPVSVRQYPLSKEAQEGIRPHVQRLIQQGILVPVQSPWNT PLLPVRKPGTNDYRPVQDLREVNKRVQDIHPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGTGRTGQLTWTRLPQGFKNSP TIFNEALHRDLANFRIQHPQVTLLQYVDDLLLAGATKQDCLEGTKALLLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWLTEARKKTVVQIPAPTT AKQVREFLGKAGFCRLFIPGFATLAAPLYPLTKPKGEFSWAPEHQKAFDAIKKALLSAPALALPDVTKPFTLYVDERKGVARGVLTQTLGPWRRPVAYLS KKLDPVASGWPVCLKAIAAVAILVKDADKLTLGQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNPATLLPEETDEPVTHDCH QLLIEETGVRKDLTDIPLTGEVLTWFTDGSSYVVEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSINIYTDSRYAFATAHVHGA IYKQRGWLTSAGREIKNKEEILSLLEALHLPKRLAIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLPAGKRTADGSEFEKRTADGSEFESPKKKAK VE
40	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSSGGGEAAAKGGLDDEYR LYSPLVKPDQNIQFWLEQFPQAWAETAGMGLAKQVPPQVIQLKASATPVSVRQYPLSKEAQEGIRPHVQRLIQQGILVPVQSPWNTPLLPVRKPGTNDYR PVQDLREVNKRVQDIHPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGTGRTGQLTWTRLPQGFKNSPTIFNEALHRDLANF RIQHPQVTLLQYVDDLLLAGATKQDCLEGTKALLLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWLTEARKKTVVQIPAPTTAKQVREFLGKAGFC RLFIPGFATLAAPLYPLTKPKGEFSWAPEHQKAFDAIKKALLSAPALALPDVTKPFTLYVDERKGVARGVLTQTLGPWRRPVAYLSKKLDPVASGWPVCL KAIAAVAILVKDADKLTLGQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNPATLLPEETDEPVTHDCHQLLIEETGVRKDLT DIPLTGEVLTWFTDGSSYVVEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSINIYTDSRYAFATAHVHGAIYKQRGWLTSAGRE IKNKEEILSLLEALHLPKRLAIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLPAGKRTADGSEFEKRTADGSEFESPKKKAKVE
40	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA

	SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSSGGGEAAAKGGLDDEYR LYSPLVKPDQNIQFWLEQFPQAWAETAGMGLAKQVPPQVIQLKASATPVSVRQYPLSKEAQEGIRPHVQRLIQQGILVPVQSPWNTPLLPVRKPGTNDYR PVQDLREVNKRVQDIHPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGTGRTGQLTWTRLPQGFKNSPTIFNEALHRDLANF RIQHPQVTLLQYVDDLLLAGATKQDCLEGTKALLLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWLTEARKKTVVQIPAPTTAKQVREFLGKAGFC RLFIPGFATLAAPLYPLTKPKGEFSWAPEHQKAFDAIKKALLSAPALALPDVTKPFTLYVDERKGVARGVLTQTLGPWRRPVAYLSKKLDPVASGWPVCL KAIAAVAILVKDADKLTLGQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNPATLLPEETDEPVTHDCHQLLIEETGVRKDLT DIPLTGEVLTWFTDGSSYVVEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSINIYTDSRYAFATAHVHGAIYKQRGWLTSAGRE IKNKEEILSLLEALHLPKRLAIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLPAGKRTADGSEFEKRTADGSEFESPKKKAKVE
41	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSSGSSGSSGSSGGLDDEY RLYSPLVKPDQNIQFWLEQFPQAWAETAGMGLAKQVPPQVIQLKASATPVSVRQYPLSKEAQEGIRPHVQRLIQQGILVPVQSPWNTPLLPVRKPGTNDY RPVQDLREVNKRVQDIHPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGTGRTGQLTWTRLPQGFKNSPTIFNEALHRDLAN FRIQHPQVTLLQYVDDLLLAGATKQDCLEGTKALLLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWLTEARKKTVVQIPAPTTAKQVREFLGKAGF CRLFIPGFATLAAPLYPLTKPKGEFSWAPEHQKAFDAIKKALLSAPALALPDVTKPFTLYVDERKGVARGVLTQTLGPWRRPVAYLSKKLDPVASGWPVC LKAIAAVAILVKDADKLTLGQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNPATLLPEETDEPVTHDCHQLLIEETGVRKDL TDIPLTGEVLTWFTDGSSYVVEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSINIYTDSRYAFATAHVHGAIYKQRGWLTSAGR EIKNKEEILSLLEALHLPKRLAIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLPAGKRTADGSEFEKRTADGSEFESPKKKAKVE
41	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ

	SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSSGSSGSSGSSGGLDDEY RLYSPLVKPDQNIQFWLEQFPQAWAETAGMGLAKQVPPQVIQLKASATPVSVRQYPLSKEAQEGIRPHVQRLIQQGILVPVQSPWNTPLLPVRKPGTNDY RPVQDLREVNKRVQDIHPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGTGRTGQLTWTRLPQGFKNSPTIFNEALHRDLAN FRIQHPQVTLLQYVDDLLLAGATKQDCLEGTKALLLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWLTEARKKTVVQIPAPTTAKQVREFLGKAGF CRLFIPGFATLAAPLYPLTKPKGEFSWAPEHQKAFDAIKKALLSAPALALPDVTKPFTLYVDERKGVARGVLTQTLGPWRRPVAYLSKKLDPVASGWPVC LKAIAAVAILVKDADKLTLGQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNPATLLPEETDEPVTHDCHQLLIEETGVRKDL TDIPLTGEVLTWFTDGSSYVVEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSINIYTDSRYAFATAHVHGAIYKQRGWLTSAGR EIKNKEEILSLLEALHLPKRLAIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLPAGKRTADGSEFEKRTADGSEFESPKKKAKVE
43	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGGSSPAPGGLDDEYRLY SPLVKPDQNIQFWLEQFPQAWAETAGMGLAKQVPPQVIQLKASATPVSVRQYPLSKEAQEGIRPHVQRLIQQGILVPVQSPWNTPLLPVRKPGTNDYRPV QDLREVNKRVQDIHPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGTGRTGQLTWTRLPQGFKNSPTIFNEALHRDLANFRI QHPQVTLLQYVDDLLLAGATKQDCLEGTKALLLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWLTEARKKTVVQIPAPTTAKQVREFLGKAGFCRL FIPGFATLAAPLYPLTKPKGEFSWAPEHQKAFDAIKKALLSAPALALPDVTKPFTLYVDERKGVARGVLTQTLGPWRRPVAYLSKKLDPVASGWPVCLKA IAAVAILVKDADKLTLGQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNPATLLPEETDEPVTHDCHQLLIEETGVRKDLTDI PLTGEVLTWFTDGSSYVVEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSINIYTDSRYAFATAHVHGAIYKQRGWLTSAGREIK NKEEILSLLEALHLPKRLAIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLPAGKRTADGSEFEKRTADGSEFESPKKKAKVE
47	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL

	LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSSPAPGGLDDEYRLYSPL VKPDQNIQFWLEQFPQAWAETAGMGLAKQVPPQVIQLKASATPVSVRQYPLSKEAQEGIRPHVQRLIQQGILVPVQSPWNTPLLPVRKPGTNDYRPVQDL REVNKRVQDIHPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGTGRTGQLTWTRLPQGFKNSPTIFNEALHRDLANFRIQHP QVTLLQYVDDLLLAGATKQDCLEGTKALLLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWLTEARKKTVVQIPAPTTAKQVREFLGKAGFCRLFIP GFATLAAPLYPLTKPKGEFSWAPEHQKAFDAIKKALLSAPALALPDVTKPFTLYVDERKGVARGVLTQTLGPWRRPVAYLSKKLDPVASGWPVCLKAIAA VAILVKDADKLTLGQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNPATLLPEETDEPVTHDCHQLLIEETGVRKDLTDIPLT GEVLTWFTDGSSYVVEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSINIYTDSRYAFATAHVHGAIYKQRGWLTSAGREIKNKE EILSLLEALHLPKRLAIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLPAGKRTADGSEFEKRTADGSEFESPKKKAKVE
48	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKGGGGGLDDEYRLYS PLVKPDQNIQFWLEQFPQAWAETAGMGLAKQVPPQVIQLKASATPVSVRQYPLSKEAQEGIRPHVQRLIQQGILVPVQSPWNTPLLPVRKPGTNDYRPVQ DLREVNKRVQDIHPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGTGRTGQLTWTRLPQGFKNSPTIFNEALHRDLANFRIQ HPQVTLLQYVDDLLLAGATKQDCLEGTKALLLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWLTEARKKTVVQIPAPTTAKQVREFLGKAGFCRLF IPGFATLAAPLYPLTKPKGEFSWAPEHQKAFDAIKKALLSAPALALPDVTKPFTLYVDERKGVARGVLTQTLGPWRRPVAYLSKKLDPVASGWPVCLKAI AAVAILVKDADKLTLGQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNPATLLPEETDEPVTHDCHQLLIEETGVRKDLTDIP LTGEVLTWFTDGSSYVVEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSINIYTDSRYAFATAHVHGAIYKQRGWLTSAGREIKN KEEILSLLEALHLPKRLAIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLPAGKRTADGSEFEKRTADGSEFESPKKKAKVE
49	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL

	FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGSEAAAKPAPGGLDDEYR LYSPLVKPDQNIQFWLEQFPQAWAETAGMGLAKQVPPQVIQLKASATPVSVRQYPLSKEAQEGIRPHVQRLIQQGILVPVQSPWNTPLLPVRKPGTNDYR PVQDLREVNKRVQDIHPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGTGRTGQLTWTRLPQGFKNSPTIFNEALHRDLANF RIQHPQVTLLQYVDDLLLAGATKQDCLEGTKALLLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWLTEARKKTVVQIPAPTTAKQVREFLGKAGFC RLFIPGFATLAAPLYPLTKPKGEFSWAPEHQKAFDAIKKALLSAPALALPDVTKPFTLYVDERKGVARGVLTQTLGPWRRPVAYLSKKLDPVASGWPVCL KAIAAVAILVKDADKLTLGQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNPATLLPEETDEPVTHDCHQLLIEETGVRKDLT DIPLTGEVLTWFTDGSSYVVEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSINIYTDSRYAFATAHVHGAIYKQRGWLTSAGRE IKNKEEILSLLEALHLPKRLAIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLPAGKRTADGSEFEKRTADGSEFESPKKKAKVE
51	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGGSGGGGSGGGGSGGLD DEYRLYSPLVKPDQNIQFWLEQFPQAWAETAGMGLAKQVPPQVIQLKASATPVSVRQYPLSKEAQEGIRPHVQRLIQQGILVPVQSPWNTPLLPVRKPGT NDYRPVQDLREVNKRVQDIHPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGTGRTGQLTWTRLPQGFKNSPTIFNEALHRD LANFRIQHPQVTLLQYVDDLLLAGATKQDCLEGTKALLLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWLTEARKKTVVQIPAPTTAKQVREFLGK AGFCRLFIPGFATLAAPLYPLTKPKGEFSWAPEHQKAFDAIKKALLSAPALALPDVTKPFTLYVDERKGVARGVLTQTLGPWRRPVAYLSKKLDPVASGW PVCLKAIAAVAILVKDADKLTLGQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNPATLLPEETDEPVTHDCHQLLIEETGVR KDLTDIPLTGEVLTWFTDGSSYVVEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSINIYTDSRYAFATAHVHGAIYKQRGWLTS AGREIKNKEEILSLLEALHLPKRLAIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLPAGKRTADGSEFEKRTADGSEFESPKKKAKVE
62	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV

	QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPAPAPAPAPGGLDDEYR LYSPLVKPDQNIQFWLEQFPQAWAETAGMGLAKQVPPQVIQLKASATPVSVRQYPLSKEAQEGIRPHVQRLIQQGILVPVQSPWNTPLLPVRKPGTNDYR PVQDLREVNKRVQDIHPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGTGRTGQLTWTRLPQGFKNSPTIFNEALHRDLANF RIQHPQVTLLQYVDDLLLAGATKQDCLEGTKALLLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWLTEARKKTVVQIPAPTTAKQVREFLGKAGFC RLFIPGFATLAAPLYPLTKPKGEFSWAPEHQKAFDAIKKALLSAPALALPDVTKPFTLYVDERKGVARGVLTQTLGPWRRPVAYLSKKLDPVASGWPVCL KAIAAVAILVKDADKLTLGQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNPATLLPEETDEPVTHDCHQLLIEETGVRKDLT DIPLTGEVLTWFTDGSSYVVEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSINIYTDSRYAFATAHVHGAIYKQRGWLTSAGRE IKNKEEILSLLEALHLPKRLAIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLPAGKRTADGSEFEKRTADGSEFESPKKKAKVE
65	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGGEAAAKGGSGGLDDEYR LYSPLVKPDQNIQFWLEQFPQAWAETAGMGLAKQVPPQVIQLKASATPVSVRQYPLSKEAQEGIRPHVQRLIQQGILVPVQSPWNTPLLPVRKPGTNDYR PVQDLREVNKRVQDIHPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGTGRTGQLTWTRLPQGFKNSPTIFNEALHRDLANF RIQHPQVTLLQYVDDLLLAGATKQDCLEGTKALLLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWLTEARKKTVVQIPAPTTAKQVREFLGKAGFC RLFIPGFATLAAPLYPLTKPKGEFSWAPEHQKAFDAIKKALLSAPALALPDVTKPFTLYVDERKGVARGVLTQTLGPWRRPVAYLSKKLDPVASGWPVCL KAIAAVAILVKDADKLTLGQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNPATLLPEETDEPVTHDCHQLLIEETGVRKDLT DIPLTGEVLTWFTDGSSYVVEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSINIYTDSRYAFATAHVHGAIYKQRGWLTSAGRE IKNKEEILSLLEALHLPKRLAIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLPAGKRTADGSEFEKRTADGSEFESPKKKAKVE

83	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKGSSGGSGGLDDEYR LYSPLVKPDQNIQFWLEQFPQAWAETAGMGLAKQVPPQVIQLKASATPVSVRQYPLSKEAQEGIRPHVQRLIQQGILVPVQSPWNTPLLPVRKPGTNDYR PVQDLREVNKRVQDIHPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGTGRTGQLTWTRLPQGFKNSPTIFNEALHRDLANF RIQHPQVTLLQYVDDLLLAGATKQDCLEGTKALLLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWLTEARKKTVVQIPAPTTAKQVREFLGKAGFC RLFIPGFATLAAPLYPLTKPKGEFSWAPEHQKAFDAIKKALLSAPALALPDVTKPFTLYVDERKGVARGVLTQTLGPWRRPVAYLSKKLDPVASGWPVCL KAIAAVAILVKDADKLTLGQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNPATLLPEETDEPVTHDCHQLLIEETGVRKDLT DIPLTGEVLTWFTDGSSYVVEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSINIYTDSRYAFATAHVHGAIYKQRGWLTSAGRE IKNKEEILSLLEALHLPKRLAIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLPAGKRTADGSEFEKRTADGSEFESPKKKAKVE
90	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGSGSETPGTSESATPESGGL DDEYRLYSPLVKPDQNIQFWLEQFPQAWAETAGMGLAKQVPPQVIQLKASATPVSVRQYPLSKEAQEGIRPHVQRLIQQGILVPVQSPWNTPLLPVRKPG TNDYRPVQDLREVNKRVQDIHPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGTGRTGQLTWTRLPQGFKNSPTIFNEALHR DLANFRIQHPQVTLLQYVDDLLLAGATKQDCLEGTKALLLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWLTEARKKTVVQIPAPTTAKQVREFLG KAGFCRLFIPGFATLAAPLYPLTKPKGEFSWAPEHQKAFDAIKKALLSAPALALPDVTKPFTLYVDERKGVARGVLTQTLGPWRRPVAYLSKKLDPVASG WPVCLKAIAAVAILVKDADKLTLGQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNPATLLPEETDEPVTHDCHQLLIEETGV

	RKDLTDIPLTGEVLTWFTDGSSYVVEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSINIYTDSRYAFATAHVHGAIYKQRGWLT SAGREIKNKEEILSLLEALHLPKRLAIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLPAGKRTADGSEFEKRTADGSEFESPKKKAKVE
97	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKGGGGSEAAAKGGTL QLDDEYRLYSPLVKPDQNIQFWLEQFPQAWAETAGMGLAKQVPPQVIQLKASATPVSVRQYPLSKEAQEGIRPHVQRLIQQGILVPVQSPWNTPLLPVRK PGTNDYRPVQDLREVNKRVQDIHPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGTGRTGQLTWTRLPQGFKNSPTIFDEAL HRDLANFRIQHPQVTLLQYVDDLLLAGATKQDCLEGTKALLLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWLTEARKKTVVQIPAPTTAKQVREF LGTAGFCRLWIPGFATLAAPLYPLTKEKGEFSWAPEHQKAFDAIKKALLSAPALALPDVTKPFTLYVDERKGVARGVLTQTLGPWRRPVAYLSKKLDPVA SGWPVCLKAIAAVAILVKDADKLTLGQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNPATLLPEETDEPVTHDCHQLLIEET GVRKDLTDIPLTGEVLTWFTDGSSYVVEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSINIYTDSRYAFATAHVHGAIYKQRGL LTSAGREIKNKEEILSLLEALHLPKRLAIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
112	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKGGGPAPGGTLQLDD EYRLYSPLVKPDQNIQFWLEQFPQAWAETAGMGLAKQVPPQVIQLKASATPVSVRQYPLSKEAQEGIRPHVQRLIQQGILVPVQSPWNTPLLPVRKPGTN DYRPVQDLREVNKRVQDIHPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGTGRTGQLTWTRLPQGFKNSPTIFDEALHRDL ANFRIQHPQVTLLQYVDDLLLAGATKQDCLEGTKALLLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWLTEARKKTVVQIPAPTTAKQVREFLGTA GFCRLWIPGFATLAAPLYPLTKEKGEFSWAPEHQKAFDAIKKALLSAPALALPDVTKPFTLYVDERKGVARGVLTQTLGPWRRPVAYLSKKLDPVASGWP

	VCLKAIAAVAILVKDADKLTLGQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNPATLLPEETDEPVTHDCHQLLIEETGVRK DLTDIPLTGEVLTWFTDGSSYVVEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSINIYTDSRYAFATAHVHGAIYKQRGLLTSA GREIKNKEEILSLLEALHLPKRLAIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
113	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSSGSSGSSGSSGSSG GTLQLDDEYRLYSPLVKPDQNIQFWLEQFPQAWAETAGMGLAKQVPPQVIQLKASATPVSVRQYPLSKEAQEGIRPHVQRLIQQGILVPVQSPWNTPLLP VRKPGTNDYRPVQDLREVNKRVQDIHPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGTGRTGQLTWTRLPQGFKNSPTIFN EALHRDLANFRIQHPQVTLLQYVDDLLLAGATKQDCLEGTKALLLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWLTEARKKTVVQIPAPTTAKQV REFLGTAGFCRLWIPGFATLAAPLYPLTKPKGEFSWAPEHQKAFDAIKKALLSAPALALPDVTKPFTLYVDERKGVARGVLTQTLGPWRRPVAYLSKKLD PVASGWPVCLKAIAAVAILVKDADKLTLGQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNPATLLPEETDEPVTHDCHQLLI EETGVRKDLTDIPLTGEVLTWFTDGSSYVVEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSINIYTDSRYAFATAHVHGAIYKQ RGWLTSAGREIKNKEEILSLLEALHLPKRLAIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
113	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSSGSSGSSGSSGSSG GTLQLDDEYRLYSPLVKPDQNIQFWLEQFPQAWAETAGMGLAKQVPPQVIQLKASATPVSVRQYPLSKEAQEGIRPHVQRLIQQGILVPVQSPWNTPLLP VRKPGTNDYRPVQDLREVNKRVQDIHPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGTGRTGQLTWTRLPQGFKNSPTIFN EALHRDLANFRIQHPQVTLLQYVDDLLLAGATKQDCLEGTKALLLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWLTEARKKTVVQIPAPTTAKQV

	REFLGTAGFCRLWIPGFATLAAPLYPLTKPKGEFSWAPEHQKAFDAIKKALLSAPALALPDVTKPFTLYVDERKGVARGVLTQTLGPWRRPVAYLSKKLD PVASGWPVCLKAIAAVAILVKDADKLTLGQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNPATLLPEETDEPVTHDCHQLLI EETGVRKDLTDIPLTGEVLTWFTDGSSYVVEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSINIYTDSRYAFATAHVHGAIYKQ RGWLTSAGREIKNKEEILSLLEALHLPKRLAIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
117	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKEAAAKEAAAKEAAA KEAAAKEAAAKGGTLQLDDEYRLYSPLVKPDQNIQFWLEQFPQAWAETAGMGLAKQVPPQVIQLKASATPVSVRQYPLSKEAQEGIRPHVQRLIQQGILV PVQSPWNTPLLPVRKPGTNDYRPVQDLREVNKRVQDIHPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGTGRTGQLTWTRL PQGFKNSPTIFNEALHRDLANFRIQHPQVTLLQYVDDLLLAGATKQDCLEGTKALLLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWLTEARKKTV VQIPAPTTAKQVREFLGTAGFCRLWIPGFATLAAPLYPLTKPKGEFSWAPEHQKAFDAIKKALLSAPALALPDVTKPFTLYVDERKGVARGVLTQTLGPW RRPVAYLSKKLDPVASGWPVCLKAIAAVAILVKDADKLTLGQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNPATLLPEETD EPVTHDCHQLLIEETGVRKDLTDIPLTGEVLTWFTDGSSYVVEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSINIYTDSRYAF ATAHVHGAIYKQRGWLTSAGREIKNKEEILSLLEALHLPKRLAIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLAGKRTADGSEFEKRTADGSEFE SPKKKAKVE
117	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKEAAAKEAAAKEAAA KEAAAKEAAAKGGTLQLDDEYRLYSPLVKPDQNIQFWLEQFPQAWAETAGMGLAKQVPPQVIQLKASATPVSVRQYPLSKEAQEGIRPHVQRLIQQGILV

	PVQSPWNTPLLPVRKPGTNDYRPVQDLREVNKRVQDIHPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGTGRTGQLTWTRL PQGFKNSPTIFNEALHRDLANFRIQHPQVTLLQYVDDLLLAGATKQDCLEGTKALLLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWLTEARKKTV VQIPAPTTAKQVREFLGTAGFCRLWIPGFATLAAPLYPLTKPKGEFSWAPEHQKAFDAIKKALLSAPALALPDVTKPFTLYVDERKGVARGVLTQTLGPW RRPVAYLSKKLDPVASGWPVCLKAIAAVAILVKDADKLTLGQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNPATLLPEETD EPVTHDCHQLLIEETGVRKDLTDIPLTGEVLTWFTDGSSYVVEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSINIYTDSRYAF ATAHVHGAIYKQRGWLTSAGREIKNKEEILSLLEALHLPKRLAIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLAGKRTADGSEFEKRTADGSEFE SPKKKAKVE
121	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGGGSSEAAAKGGTLQLDD EYRLYSPLVKPDQNIQFWLEQFPQAWAETAGMGLAKQVPPQVIQLKASATPVSVRQYPLSKEAQEGIRPHVQRLIQQGILVPVQSPWNTPLLPVRKPGTN DYRPVQDLREVNKRVQDIHPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGTGRTGQLTWTRLPQGFKNSPTIFNEALHRDL ANFRIQHPQVTLLQYVDDLLLAGATKQDCLEGTKALLLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWLTEARKKTVVQIPAPTTAKQVREFLGTA GFCRLWIPGFATLAAPLYPLTKPKGEFSWAPEHQKAFDAIKKALLSAPALALPDVTKPFTLYVDERKGVARGVLTQTLGPWRRPVAYLSKKLDPVASGWP VCLKAIAAVAILVKDADKLTLGQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNPATLLPEETDEPVTHDCHQLLIEETGVRK DLTDIPLTGEVLTWFTDGSSYVVEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSINIYTDSRYAFATAHVHGAIYKQRGWLTSA GREIKNKEEILSLLEALHLPKRLAIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
121	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK

	VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGGGSSEAAAKGGTLQLDD EYRLYSPLVKPDQNIQFWLEQFPQAWAETAGMGLAKQVPPQVIQLKASATPVSVRQYPLSKEAQEGIRPHVQRLIQQGILVPVQSPWNTPLLPVRKPGTN DYRPVQDLREVNKRVQDIHPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGTGRTGQLTWTRLPQGFKNSPTIFNEALHRDL ANFRIQHPQVTLLQYVDDLLLAGATKQDCLEGTKALLLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWLTEARKKTVVQIPAPTTAKQVREFLGTA GFCRLWIPGFATLAAPLYPLTKPKGEFSWAPEHQKAFDAIKKALLSAPALALPDVTKPFTLYVDERKGVARGVLTQTLGPWRRPVAYLSKKLDPVASGWP VCLKAIAAVAILVKDADKLTLGQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNPATLLPEETDEPVTHDCHQLLIEETGVRK DLTDIPLTGEVLTWFTDGSSYVVEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSINIYTDSRYAFATAHVHGAIYKQRGWLTSA GREIKNKEEILSLLEALHLPKRLAIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
122	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGSGSETPGTSESATPESGGT LQLDDEYRLYSPLVKPDQNIQFWLEQFPQAWAETAGMGLAKQVPPQVIQLKASATPVSVRQYPLSKEAQEGIRPHVQRLIQQGILVPVQSPWNTPLLPVR KPGTNDYRPVQDLREVNKRVQDIHPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGTGRTGQLTWTRLPQGFKNSPTIFNEA LHRDLANFRIQHPQVTLLQYVDDLLLAGATKQDCLEGTKALLLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWLTEARKKTVVQIPAPTTAKQVRE FLGTAGFCRLWIPGFATLAAPLYPLTKPKGEFSWAPEHQKAFDAIKKALLSAPALALPDVTKPFTLYVDERKGVARGVLTQTLGPWRRPVAYLSKKLDPV ASGWPVCLKAIAAVAILVKDADKLTLGQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNPATLLPEETDEPVTHDCHQLLIEE TGVRKDLTDIPLTGEVLTWFTDGSSYVVEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSINIYTDSRYAFATAHVHGAIYKQRG WLTSAGREIKNKEEILSLLEALHLPKRLAIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
123	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE

	VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPGSSGGTLQLDDEYRLY SPLVKPDQNIQFWLEQFPQAWAETAGMGLAKQVPPQVIQLKASATPVSVRQYPLSKEAQEGIRPHVQRLIQQGILVPVQSPWNTPLLPVRKPGTNDYRPV QDLREVNKRVQDIHPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGTGRTGQLTWTRLPQGFKNSPTIFNEALHRDLANFRI QHPQVTLLQYVDDLLLAGATKQDCLEGTKALLLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWLTEARKKTVVQIPAPTTAKQVREFLGTAGFCRL WIPGFATLAAPLYPLTKPKGEFSWAPEHQKAFDAIKKALLSAPALALPDVTKPFTLYVDERKGVARGVLTQTLGPWRRPVAYLSKKLDPVASGWPVCLKA IAAVAILVKDADKLTLGQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNPATLLPEETDEPVTHDCHQLLIEETGVRKDLTDI PLTGEVLTWFTDGSSYVVEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSINIYTDSRYAFATAHVHGAIYKQRGWLTSAGREIK NKEEILSLLEALHLPKRLAIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
124	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPEAAAKGGGGGTLQLDD EYRLYSPLVKPDQNIQFWLEQFPQAWAETAGMGLAKQVPPQVIQLKASATPVSVRQYPLSKEAQEGIRPHVQRLIQQGILVPVQSPWNTPLLPVRKPGTN DYRPVQDLREVNKRVQDIHPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGTGRTGQLTWTRLPQGFKNSPTIFNEALHRDL ANFRIQHPQVTLLQYVDDLLLAGATKQDCLEGTKALLLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWLTEARKKTVVQIPAPTTAKQVREFLGTA GFCRLWIPGFATLAAPLYPLTKPKGEFSWAPEHQKAFDAIKKALLSAPALALPDVTKPFTLYVDERKGVARGVLTQTLGPWRRPVAYLSKKLDPVASGWP VCLKAIAAVAILVKDADKLTLGQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNPATLLPEETDEPVTHDCHQLLIEETGVRK DLTDIPLTGEVLTWFTDGSSYVVEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSINIYTDSRYAFATAHVHGAIYKQRGWLTSA GREIKNKEEILSLLEALHLPKRLAIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
126	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM

	PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKGGGGGTLQLDDEYR LYSPLVKPDQNIQFWLEQFPQAWAETAGMGLAKQVPPQVIQLKASATPVSVRQYPLSKEAQEGIRPHVQRLIQQGILVPVQSPWNTPLLPVRKPGTNDYR PVQDLREVNKRVQDIHPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGTGRTGQLTWTRLPQGFKNSPTIFNEALHRDLANF RIQHPQVTLLQYVDDLLLAGATKQDCLEGTKALLLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWLTEARKKTVVQIPAPTTAKQVREFLGTAGFC RLWIPGFATLAAPLYPLTKPKGEFSWAPEHQKAFDAIKKALLSAPALALPDVTKPFTLYVDERKGVARGVLTQTLGPWRRPVAYLSKKLDPVASGWPVCL KAIAAVAILVKDADKLTLGQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNPATLLPEETDEPVTHDCHQLLIEETGVRKDLT DIPLTGEVLTWFTDGSSYVVEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSINIYTDSRYAFATAHVHGAIYKQRGWLTSAGRE IKNKEEILSLLEALHLPKRLAIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
127	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPGGGEAAAKGGTLQLDD EYRLYSPLVKPDQNIQFWLEQFPQAWAETAGMGLAKQVPPQVIQLKASATPVSVRQYPLSKEAQEGIRPHVQRLIQQGILVPVQSPWNTPLLPVRKPGTN DYRPVQDLREVNKRVQDIHPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGTGRTGQLTWTRLPQGFKNSPTIFNEALHRDL ANFRIQHPQVTLLQYVDDLLLAGATKQDCLEGTKALLLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWLTEARKKTVVQIPAPTTAKQVREFLGTA GFCRLWIPGFATLAAPLYPLTKPKGEFSWAPEHQKAFDAIKKALLSAPALALPDVTKPFTLYVDERKGVARGVLTQTLGPWRRPVAYLSKKLDPVASGWP VCLKAIAAVAILVKDADKLTLGQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNPATLLPEETDEPVTHDCHQLLIEETGVRK DLTDIPLTGEVLTWFTDGSSYVVEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSINIYTDSRYAFATAHVHGAIYKQRGWLTSA GREIKNKEEILSLLEALHLPKRLAIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
133	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL

	NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSSEAAAKGGGGGTLQLDD EYRLYSPLVKPDQNIQFWLEQFPQAWAETAGMGLAKQVPPQVIQLKASATPVSVRQYPLSKEAQEGIRPHVQRLIQQGILVPVQSPWNTPLLPVRKPGTN DYRPVQDLREVNKRVQDIHPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGTGRTGQLTWTRLPQGFKNSPTIFNEALHRDL ANFRIQHPQVTLLQYVDDLLLAGATKQDCLEGTKALLLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWLTEARKKTVVQIPAPTTAKQVREFLGTA GFCRLWIPGFATLAAPLYPLTKPKGEFSWAPEHQKAFDAIKKALLSAPALALPDVTKPFTLYVDERKGVARGVLTQTLGPWRRPVAYLSKKLDPVASGWP VCLKAIAAVAILVKDADKLTLGQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNPATLLPEETDEPVTHDCHQLLIEETGVRK DLTDIPLTGEVLTWFTDGSSYVVEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSINIYTDSRYAFATAHVHGAIYKQRGWLTSA GREIKNKEEILSLLEALHLPKRLAIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
138	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPGGSEAAAKGGTLQLDD EYRLYSPLVKPDQNIQFWLEQFPQAWAETAGMGLAKQVPPQVIQLKASATPVSVRQYPLSKEAQEGIRPHVQRLIQQGILVPVQSPWNTPLLPVRKPGTN DYRPVQDLREVNKRVQDIHPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGTGRTGQLTWTRLPQGFKNSPTIFNEALHRDL ANFRIQHPQVTLLQYVDDLLLAGATKQDCLEGTKALLLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWLTEARKKTVVQIPAPTTAKQVREFLGTA GFCRLWIPGFATLAAPLYPLTKPKGEFSWAPEHQKAFDAIKKALLSAPALALPDVTKPFTLYVDERKGVARGVLTQTLGPWRRPVAYLSKKLDPVASGWP VCLKAIAAVAILVKDADKLTLGQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNPATLLPEETDEPVTHDCHQLLIEETGVRK DLTDIPLTGEVLTWFTDGSSYVVEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSINIYTDSRYAFATAHVHGAIYKQRGWLTSA GREIKNKEEILSLLEALHLPKRLAIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
139	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA

	KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGSGSSEAAAKGGTLQLDD EYRLYSPLVKPDQNIQFWLEQFPQAWAETAGMGLAKQVPPQVIQLKASATPVSVRQYPLSKEAQEGIRPHVQRLIQQGILVPVQSPWNTPLLPVRKPGTN DYRPVQDLREVNKRVQDIHPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGTGRTGQLTWTRLPQGFKNSPTIFNEALHRDL ANFRIQHPQVTLLQYVDDLLLAGATKQDCLEGTKALLLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWLTEARKKTVVQIPAPTTAKQVREFLGTA GFCRLWIPGFATLAAPLYPLTKPKGEFSWAPEHQKAFDAIKKALLSAPALALPDVTKPFTLYVDERKGVARGVLTQTLGPWRRPVAYLSKKLDPVASGWP VCLKAIAAVAILVKDADKLTLGQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNPATLLPEETDEPVTHDCHQLLIEETGVRK DLTDIPLTGEVLTWFTDGSSYVVEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSINIYTDSRYAFATAHVHGAIYKQRGWLTSA GREIKNKEEILSLLEALHLPKRLAIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
140	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGSGGSSGGSSGSETPGTSES ATPESSGGSSGGSSGGTLQLDDEYRLYSPLVKPDQNIQFWLEQFPQAWAETAGMGLAKQVPPQVIQLKASATPVSVRQYPLSKEAQEGIRPHVQRLIQQG ILVPVQSPWNTPLLPVRKPGTNDYRPVQDLREVNKRVQDIHPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGTGRTGQLTW TRLPQGFKNSPTIFNEALHRDLANFRIQHPQVTLLQYVDDLLLAGATKQDCLEGTKALLLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWLTEARK KTVVQIPAPTTAKQVREFLGTAGFCRLWIPGFATLAAPLYPLTKPKGEFSWAPEHQKAFDAIKKALLSAPALALPDVTKPFTLYVDERKGVARGVLTQTL GPWRRPVAYLSKKLDPVASGWPVCLKAIAAVAILVKDADKLTLGQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNPATLLPE ETDEPVTHDCHQLLIEETGVRKDLTDIPLTGEVLTWFTDGSSYVVEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSINIYTDSR YAFATAHVHGAIYKQRGWLTSAGREIKNKEEILSLLEALHLPKRLAIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLAGKRTADGSEFEKRTADGS EFESPKKKAKVE
141	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA

	NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKGGSPAPGGTLQLDD EYRLYSPLVKPDQNIQFWLEQFPQAWAETAGMGLAKQVPPQVIQLKASATPVSVRQYPLSKEAQEGIRPHVQRLIQQGILVPVQSPWNTPLLPVRKPGTN DYRPVQDLREVNKRVQDIHPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGTGRTGQLTWTRLPQGFKNSPTIFNEALHRDL ANFRIQHPQVTLLQYVDDLLLAGATKQDCLEGTKALLLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWLTEARKKTVVQIPAPTTAKQVREFLGTA GFCRLWIPGFATLAAPLYPLTKPKGEFSWAPEHQKAFDAIKKALLSAPALALPDVTKPFTLYVDERKGVARGVLTQTLGPWRRPVAYLSKKLDPVASGWP VCLKAIAAVAILVKDADKLTLGQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNPATLLPEETDEPVTHDCHQLLIEETGVRK DLTDIPLTGEVLTWFTDGSSYVVEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSINIYTDSRYAFATAHVHGAIYKQRGWLTSA GREIKNKEEILSLLEALHLPKRLAIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
142	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSGGSGGSGGSGGSG GTLQLDDEYRLYSPLVKPDQNIQFWLEQFPQAWAETAGMGLAKQVPPQVIQLKASATPVSVRQYPLSKEAQEGIRPHVQRLIQQGILVPVQSPWNTPLLP VRKPGTNDYRPVQDLREVNKRVQDIHPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGTGRTGQLTWTRLPQGFKNSPTIFN EALHRDLANFRIQHPQVTLLQYVDDLLLAGATKQDCLEGTKALLLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWLTEARKKTVVQIPAPTTAKQV REFLGTAGFCRLWIPGFATLAAPLYPLTKPKGEFSWAPEHQKAFDAIKKALLSAPALALPDVTKPFTLYVDERKGVARGVLTQTLGPWRRPVAYLSKKLD PVASGWPVCLKAIAAVAILVKDADKLTLGQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNPATLLPEETDEPVTHDCHQLLI EETGVRKDLTDIPLTGEVLTWFTDGSSYVVEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSINIYTDSRYAFATAHVHGAIYKQ RGWLTSAGREIKNKEEILSLLEALHLPKRLAIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
142	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA

	SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGSGGSGGSGGSGGSG GTLQLDDEYRLYSPLVKPDQNIQFWLEQFPQAWAETAGMGLAKQVPPQVIQLKASATPVSVRQYPLSKEAQEGIRPHVQRLIQQGILVPVQSPWNTPLLP VRKPGTNDYRPVQDLREVNKRVQDIHPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGTGRTGQLTWTRLPQGFKNSPTIFN EALHRDLANFRIQHPQVTLLQYVDDLLLAGATKQDCLEGTKALLLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWLTEARKKTVVQIPAPTTAKQV REFLGTAGFCRLWIPGFATLAAPLYPLTKPKGEFSWAPEHQKAFDAIKKALLSAPALALPDVTKPFTLYVDERKGVARGVLTQTLGPWRRPVAYLSKKLD PVASGWPVCLKAIAAVAILVKDADKLTLGQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNPATLLPEETDEPVTHDCHQLLI EETGVRKDLTDIPLTGEVLTWFTDGSSYVVEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSINIYTDSRYAFATAHVHGAIYKQ RGWLTSAGREIKNKEEILSLLEALHLPKRLAIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
144	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGSGSSGGGGGTLQLDDEY RLYSPLVKPDQNIQFWLEQFPQAWAETAGMGLAKQVPPQVIQLKASATPVSVRQYPLSKEAQEGIRPHVQRLIQQGILVPVQSPWNTPLLPVRKPGTNDY RPVQDLREVNKRVQDIHPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGTGRTGQLTWTRLPQGFKNSPTIFNEALHRDLAN FRIQHPQVTLLQYVDDLLLAGATKQDCLEGTKALLLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWLTEARKKTVVQIPAPTTAKQVREFLGTAGF CRLWIPGFATLAAPLYPLTKPKGEFSWAPEHQKAFDAIKKALLSAPALALPDVTKPFTLYVDERKGVARGVLTQTLGPWRRPVAYLSKKLDPVASGWPVC LKAIAAVAILVKDADKLTLGQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNPATLLPEETDEPVTHDCHQLLIEETGVRKDL TDIPLTGEVLTWFTDGSSYVVEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSINIYTDSRYAFATAHVHGAIYKQRGWLTSAGR EIKNKEEILSLLEALHLPKRLAIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
147	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ

	SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGGGSGGTLQLDDEYRLYS PLVKPDQNIQFWLEQFPQAWAETAGMGLAKQVPPQVIQLKASATPVSVRQYPLSKEAQEGIRPHVQRLIQQGILVPVQSPWNTPLLPVRKPGTNDYRPVQ DLREVNKRVQDIHPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGTGRTGQLTWTRLPQGFKNSPTIFNEALHRDLANFRIQ HPQVTLLQYVDDLLLAGATKQDCLEGTKALLLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWLTEARKKTVVQIPAPTTAKQVREFLGTAGFCRLW IPGFATLAAPLYPLTKPKGEFSWAPEHQKAFDAIKKALLSAPALALPDVTKPFTLYVDERKGVARGVLTQTLGPWRRPVAYLSKKLDPVASGWPVCLKAI AAVAILVKDADKLTLGQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNPATLLPEETDEPVTHDCHQLLIEETGVRKDLTDIP LTGEVLTWFTDGSSYVVEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSINIYTDSRYAFATAHVHGAIYKQRGWLTSAGREIKN KEEILSLLEALHLPKRLAIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
151	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKGGTLQLDDEYRLYS PLVKPDQNIQFWLEQFPQAWAETAGMGLAKQVPPQVIQLKASATPVSVRQYPLSKEAQEGIRPHVQRLIQQGILVPVQSPWNTPLLPVRKPGTNDYRPVQ DLREVNKRVQDIHPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGTGRTGQLTWTRLPQGFKNSPTIFNEALHRDLANFRIQ HPQVTLLQYVDDLLLAGATKQDCLEGTKALLLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWLTEARKKTVVQIPAPTTAKQVREFLGTAGFCRLW IPGFATLAAPLYPLTKPKGEFSWAPEHQKAFDAIKKALLSAPALALPDVTKPFTLYVDERKGVARGVLTQTLGPWRRPVAYLSKKLDPVASGWPVCLKAI AAVAILVKDADKLTLGQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNPATLLPEETDEPVTHDCHQLLIEETGVRKDLTDIP LTGEVLTWFTDGSSYVVEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSINIYTDSRYAFATAHVHGAIYKQRGWLTSAGREIKN KEEILSLLEALHLPKRLAIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
156	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL

	LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGAEAAAKEAAAKEAAAKEAA AKALEAEAAAKEAAAKEAAAKEAAAKAGGTLQLDDEYRLYSPLVKPDQNIQFWLEQFPQAWAETAGMGLAKQVPPQVIQLKASATPVSVRQYPLSKEAQE GIRPHVQRLIQQGILVPVQSPWNTPLLPVRKPGTNDYRPVQDLREVNKRVQDIHPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAFEW RDPGTGRTGQLTWTRLPQGFKNSPTIFNEALHRDLANFRIQHPQVTLLQYVDDLLLAGATKQDCLEGTKALLLELSDLGYRASAKKAQICRREVTYLGYS LRDGQRWLTEARKKTVVQIPAPTTAKQVREFLGTAGFCRLWIPGFATLAAPLYPLTKPKGEFSWAPEHQKAFDAIKKALLSAPALALPDVTKPFTLYVDE RKGVARGVLTQTLGPWRRPVAYLSKKLDPVASGWPVCLKAIAAVAILVKDADKLTLGQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFA PPAALNPATLLPEETDEPVTHDCHQLLIEETGVRKDLTDIPLTGEVLTWFTDGSSYVVEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRL AEGKSINIYTDSRYAFATAHVHGAIYKQRGWLTSAGREIKNKEEILSLLEALHLPKRLAIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLAGKRTA DGSEFEKRTADGSEFESPKKKAKVE
156	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGAEAAAKEAAAKEAAAKEAA AKALEAEAAAKEAAAKEAAAKEAAAKAGGTLQLDDEYRLYSPLVKPDQNIQFWLEQFPQAWAETAGMGLAKQVPPQVIQLKASATPVSVRQYPLSKEAQE GIRPHVQRLIQQGILVPVQSPWNTPLLPVRKPGTNDYRPVQDLREVNKRVQDIHPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAFEW RDPGTGRTGQLTWTRLPQGFKNSPTIFNEALHRDLANFRIQHPQVTLLQYVDDLLLAGATKQDCLEGTKALLLELSDLGYRASAKKAQICRREVTYLGYS LRDGQRWLTEARKKTVVQIPAPTTAKQVREFLGTAGFCRLWIPGFATLAAPLYPLTKPKGEFSWAPEHQKAFDAIKKALLSAPALALPDVTKPFTLYVDE RKGVARGVLTQTLGPWRRPVAYLSKKLDPVASGWPVCLKAIAAVAILVKDADKLTLGQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFA PPAALNPATLLPEETDEPVTHDCHQLLIEETGVRKDLTDIPLTGEVLTWFTDGSSYVVEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRL AEGKSINIYTDSRYAFATAHVHGAIYKQRGWLTSAGREIKNKEEILSLLEALHLPKRLAIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLAGKRTA DGSEFEKRTADGSEFESPKKKAKVE

157	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPAPAPAPAPGGTLQL DDEYRLYSPLVKPDQNIQFWLEQFPQAWAETAGMGLAKQVPPQVIQLKASATPVSVRQYPLSKEAQEGIRPHVQRLIQQGILVPVQSPWNTPLLPVRKPG TNDYRPVQDLREVNKRVQDIHPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGTGRTGQLTWTRLPQGFKNSPTIFNEALHR DLANFRIQHPQVTLLQYVDDLLLAGATKQDCLEGTKALLLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWLTEARKKTVVQIPAPTTAKQVREFLG TAGFCRLWIPGFATLAAPLYPLTKPKGEFSWAPEHQKAFDAIKKALLSAPALALPDVTKPFTLYVDERKGVARGVLTQTLGPWRRPVAYLSKKLDPVASG WPVCLKAIAAVAILVKDADKLTLGQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNPATLLPEETDEPVTHDCHQLLIEETGV RKDLTDIPLTGEVLTWFTDGSSYVVEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSINIYTDSRYAFATAHVHGAIYKQRGWLT SAGREIKNKEEILSLLEALHLPKRLAIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
164	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGSPAPEAAAKGGTLQLDD EYRLYSPLVKPDQNIQFWLEQFPQAWAETAGMGLAKQVPPQVIQLKASATPVSVRQYPLSKEAQEGIRPHVQRLIQQGILVPVQSPWNTPLLPVRKPGTN DYRPVQDLREVNKRVQDIHPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGTGRTGQLTWTRLPQGFKNSPTIFNEALHRDL ANFRIQHPQVTLLQYVDDLLLAGATKQDCLEGTKALLLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWLTEARKKTVVQIPAPTTAKQVREFLGTA GFCRLWIPGFATLAAPLYPLTKPKGEFSWAPEHQKAFDAIKKALLSAPALALPDVTKPFTLYVDERKGVARGVLTQTLGPWRRPVAYLSKKLDPVASGWP VCLKAIAAVAILVKDADKLTLGQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNPATLLPEETDEPVTHDCHQLLIEETGVRK

	DLTDIPLTGEVLTWFTDGSSYVVEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSINIYTDSRYAFATAHVHGAIYKQRGWLTSA GREIKNKEEILSLLEALHLPKRLAIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
168	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKPAPGGSGGTLQLDD EYRLYSPLVKPDQNIQFWLEQFPQAWAETAGMGLAKQVPPQVIQLKASATPVSVRQYPLSKEAQEGIRPHVQRLIQQGILVPVQSPWNTPLLPVRKPGTN DYRPVQDLREVNKRVQDIHPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGTGRTGQLTWTRLPQGFKNSPTIFNEALHRDL ANFRIQHPQVTLLQYVDDLLLAGATKQDCLEGTKALLLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWLTEARKKTVVQIPAPTTAKQVREFLGTA GFCRLWIPGFATLAAPLYPLTKPKGEFSWAPEHQKAFDAIKKALLSAPALALPDVTKPFTLYVDERKGVARGVLTQTLGPWRRPVAYLSKKLDPVASGWP VCLKAIAAVAILVKDADKLTLGQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNPATLLPEETDEPVTHDCHQLLIEETGVRK DLTDIPLTGEVLTWFTDGSSYVVEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSINIYTDSRYAFATAHVHGAIYKQRGWLTSA GREIKNKEEILSLLEALHLPKRLAIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
173	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPGGGGGSGGTLQLDDEY RLYSPLVKPDQNIQFWLEQFPQAWAETAGMGLAKQVPPQVIQLKASATPVSVRQYPLSKEAQEGIRPHVQRLIQQGILVPVQSPWNTPLLPVRKPGTNDY RPVQDLREVNKRVQDIHPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGTGRTGQLTWTRLPQGFKNSPTIFNEALHRDLAN FRIQHPQVTLLQYVDDLLLAGATKQDCLEGTKALLLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWLTEARKKTVVQIPAPTTAKQVREFLGTAGF CRLWIPGFATLAAPLYPLTKPKGEFSWAPEHQKAFDAIKKALLSAPALALPDVTKPFTLYVDERKGVARGVLTQTLGPWRRPVAYLSKKLDPVASGWPVC

	LKAIAAVAILVKDADKLTLGQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNPATLLPEETDEPVTHDCHQLLIEETGVRKDL TDIPLTGEVLTWFTDGSSYVVEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSINIYTDSRYAFATAHVHGAIYKQRGWLTSAGR EIKNKEEILSLLEALHLPKRLAIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
190	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGAEAAAKEAAAKEAAAKEAA AKALEAEAAAKEAAAKEAAAKEAAAKAGGLDDEYRLYSPLVKPDQNIQFWLEQFPQAWAETAGMGLAKQVPPQVIQLKASATPVSVRQYPLSKEAQEGIR PHVQRLIQQGILVPVQSPWNTPLLPVRKPGTNDYRPVQDLREVNKRVQDIHPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDP GTGRTGQLTWTRLPQGFKNSPTIFNEALHRDLANFRIQHPQVTLLQYVDDLLLAGATKQDCLEGTKALLLELSDLGYRASAKKAQICRREVTYLGYSLRD GQRWLTEARKKTVVQIPAPTTAKQVREFLGKAGFCRLFIPGFATLAAPLYPLTKPKGEFSWAPEHQKAFDAIKKALLSAPALALPDVTKPFTLYVDERKG VARGVLTQTLGPWRRPVAYLSKKLDPVASGWPVCLKAIAAVAILVKDADKLTLGQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPA ALNPATLLPEETDEPVTHDCHQLLIEETGVRKDLTDIPLTGEVLTWFTDGSSYVVEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEG KSINIYTDSRYAFATAHVHGAIYKQRGWLTSAGREIKNKEEILSLLEALHLPKRLAIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLPAGKRTADG SEFEKRTADGSEFESPKKKAKVE
190	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGAEAAAKEAAAKEAAAKEAA AKALEAEAAAKEAAAKEAAAKEAAAKAGGLDDEYRLYSPLVKPDQNIQFWLEQFPQAWAETAGMGLAKQVPPQVIQLKASATPVSVRQYPLSKEAQEGIR PHVQRLIQQGILVPVQSPWNTPLLPVRKPGTNDYRPVQDLREVNKRVQDIHPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDP

	GTGRTGQLTWTRLPQGFKNSPTIFNEALHRDLANFRIQHPQVTLLQYVDDLLLAGATKQDCLEGTKALLLELSDLGYRASAKKAQICRREVTYLGYSLRD GQRWLTEARKKTVVQIPAPTTAKQVREFLGKAGFCRLFIPGFATLAAPLYPLTKPKGEFSWAPEHQKAFDAIKKALLSAPALALPDVTKPFTLYVDERKG VARGVLTQTLGPWRRPVAYLSKKLDPVASGWPVCLKAIAAVAILVKDADKLTLGQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPA ALNPATLLPEETDEPVTHDCHQLLIEETGVRKDLTDIPLTGEVLTWFTDGSSYVVEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEG KSINIYTDSRYAFATAHVHGAIYKQRGWLTSAGREIKNKEEILSLLEALHLPKRLAIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLPAGKRTADG SEFEKRTADGSEFESPKKKAKVE
191	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSGGSGGSGGSGGSGG GLDDEYRLYSPLVKPDQNIQFWLEQFPQAWAETAGMGLAKQVPPQVIQLKASATPVSVRQYPLSKEAQEGIRPHVQRLIQQGILVPVQSPWNTPLLPVRK PGTNDYRPVQDLREVNKRVQDIHPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGTGRTGQLTWTRLPQGFKNSPTIFNEAL HRDLANFRIQHPQVTLLQYVDDLLLAGATKQDCLEGTKALLLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWLTEARKKTVVQIPAPTTAKQVREF LGKAGFCRLFIPGFATLAAPLYPLTKPKGEFSWAPEHQKAFDAIKKALLSAPALALPDVTKPFTLYVDERKGVARGVLTQTLGPWRRPVAYLSKKLDPVA SGWPVCLKAIAAVAILVKDADKLTLGQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNPATLLPEETDEPVTHDCHQLLIEET GVRKDLTDIPLTGEVLTWFTDGSSYVVEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSINIYTDSRYAFATAHVHGAIYKQRGW LTSAGREIKNKEEILSLLEALHLPKRLAIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLPAGKRTADGSEFEKRTADGSEFESPKKKAKVE
192	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPEAAAKGGGGGLDDEYR

	LYSPLVKPDQNIQFWLEQFPQAWAETAGMGLAKQVPPQVIQLKASATPVSVRQYPLSKEAQEGIRPHVQRLIQQGILVPVQSPWNTPLLPVRKPGTNDYR PVQDLREVNKRVQDIHPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGTGRTGQLTWTRLPQGFKNSPTIFNEALHRDLANF RIQHPQVTLLQYVDDLLLAGATKQDCLEGTKALLLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWLTEARKKTVVQIPAPTTAKQVREFLGKAGFC RLFIPGFATLAAPLYPLTKPKGEFSWAPEHQKAFDAIKKALLSAPALALPDVTKPFTLYVDERKGVARGVLTQTLGPWRRPVAYLSKKLDPVASGWPVCL KAIAAVAILVKDADKLTLGQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNPATLLPEETDEPVTHDCHQLLIEETGVRKDLT DIPLTGEVLTWFTDGSSYVVEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSINIYTDSRYAFATAHVHGAIYKQRGWLTSAGRE IKNKEEILSLLEALHLPKRLAIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLPAGKRTADGSEFEKRTADGSEFESPKKKAKVE
193	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKEAAAKEAAAKEAAA KEAAAKEAAAKGGLDDEYRLYSPLVKPDQNIQFWLEQFPQAWAETAGMGLAKQVPPQVIQLKASATPVSVRQYPLSKEAQEGIRPHVQRLIQQGILVPVQ SPWNTPLLPVRKPGTNDYRPVQDLREVNKRVQDIHPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGTGRTGQLTWTRLPQG FKNSPTIFNEALHRDLANFRIQHPQVTLLQYVDDLLLAGATKQDCLEGTKALLLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWLTEARKKTVVQI PAPTTAKQVREFLGKAGFCRLFIPGFATLAAPLYPLTKPKGEFSWAPEHQKAFDAIKKALLSAPALALPDVTKPFTLYVDERKGVARGVLTQTLGPWRRP VAYLSKKLDPVASGWPVCLKAIAAVAILVKDADKLTLGQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNPATLLPEETDEPV THDCHQLLIEETGVRKDLTDIPLTGEVLTWFTDGSSYVVEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSINIYTDSRYAFATA HVHGAIYKQRGWLTSAGREIKNKEEILSLLEALHLPKRLAIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLPAGKRTADGSEFEKRTADGSEFESP KKKAKVE
195	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE

	VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKGGSPAPGGLDDEYR LYSPLVKPDQNIQFWLEQFPQAWAETAGMGLAKQVPPQVIQLKASATPVSVRQYPLSKEAQEGIRPHVQRLIQQGILVPVQSPWNTPLLPVRKPGTNDYR PVQDLREVNKRVQDIHPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGTGRTGQLTWTRLPQGFKNSPTIFNEALHRDLANF RIQHPQVTLLQYVDDLLLAGATKQDCLEGTKALLLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWLTEARKKTVVQIPAPTTAKQVREFLGKAGFC RLFIPGFATLAAPLYPLTKPKGEFSWAPEHQKAFDAIKKALLSAPALALPDVTKPFTLYVDERKGVARGVLTQTLGPWRRPVAYLSKKLDPVASGWPVCL KAIAAVAILVKDADKLTLGQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNPATLLPEETDEPVTHDCHQLLIEETGVRKDLT DIPLTGEVLTWFTDGSSYVVEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSINIYTDSRYAFATAHVHGAIYKQRGWLTSAGRE IKNKEEILSLLEALHLPKRLAIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLPAGKRTADGSEFEKRTADGSEFESPKKKAKVE
195	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKGGSPAPGGLDDEYR LYSPLVKPDQNIQFWLEQFPQAWAETAGMGLAKQVPPQVIQLKASATPVSVRQYPLSKEAQEGIRPHVQRLIQQGILVPVQSPWNTPLLPVRKPGTNDYR PVQDLREVNKRVQDIHPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGTGRTGQLTWTRLPQGFKNSPTIFNEALHRDLANF RIQHPQVTLLQYVDDLLLAGATKQDCLEGTKALLLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWLTEARKKTVVQIPAPTTAKQVREFLGKAGFC RLFIPGFATLAAPLYPLTKPKGEFSWAPEHQKAFDAIKKALLSAPALALPDVTKPFTLYVDERKGVARGVLTQTLGPWRRPVAYLSKKLDPVASGWPVCL KAIAAVAILVKDADKLTLGQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNPATLLPEETDEPVTHDCHQLLIEETGVRKDLT DIPLTGEVLTWFTDGSSYVVEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSINIYTDSRYAFATAHVHGAIYKQRGWLTSAGRE IKNKEEILSLLEALHLPKRLAIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLPAGKRTADGSEFEKRTADGSEFESPKKKAKVE
196	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM

	PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGSGSETPGTSESATPESGGL DDEYRLYSPLVKPDQNIQFWLEQFPQAWAETAGMGLAKQVPPQVIQLKASATPVSVRQYPLSKEAQEGIRPHVQRLIQQGILVPVQSPWNTPLLPVRKPG TNDYRPVQDLREVNKRVQDIHPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGTGRTGQLTWTRLPQGFKNSPTIFNEALHR DLANFRIQHPQVTLLQYVDDLLLAGATKQDCLEGTKALLLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWLTEARKKTVVQIPAPTTAKQVREFLG KAGFCRLFIPGFATLAAPLYPLTKPKGEFSWAPEHQKAFDAIKKALLSAPALALPDVTKPFTLYVDERKGVARGVLTQTLGPWRRPVAYLSKKLDPVASG WPVCLKAIAAVAILVKDADKLTLGQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNPATLLPEETDEPVTHDCHQLLIEETGV RKDLTDIPLTGEVLTWFTDGSSYVVEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSINIYTDSRYAFATAHVHGAIYKQRGWLT SAGREIKNKEEILSLLEALHLPKRLAIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLPAGKRTADGSEFEKRTADGSEFESPKKKAKVE
199	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGSSGGGEAAAKGGLDDEYR LYSPLVKPDQNIQFWLEQFPQAWAETAGMGLAKQVPPQVIQLKASATPVSVRQYPLSKEAQEGIRPHVQRLIQQGILVPVQSPWNTPLLPVRKPGTNDYR PVQDLREVNKRVQDIHPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGTGRTGQLTWTRLPQGFKNSPTIFNEALHRDLANF RIQHPQVTLLQYVDDLLLAGATKQDCLEGTKALLLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWLTEARKKTVVQIPAPTTAKQVREFLGKAGFC RLFIPGFATLAAPLYPLTKPKGEFSWAPEHQKAFDAIKKALLSAPALALPDVTKPFTLYVDERKGVARGVLTQTLGPWRRPVAYLSKKLDPVASGWPVCL KAIAAVAILVKDADKLTLGQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNPATLLPEETDEPVTHDCHQLLIEETGVRKDLT DIPLTGEVLTWFTDGSSYVVEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSINIYTDSRYAFATAHVHGAIYKQRGWLTSAGRE IKNKEEILSLLEALHLPKRLAIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLPAGKRTADGSEFEKRTADGSEFESPKKKAKVE
199	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL

	NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSSGGGEAAAKGGLDDEYR LYSPLVKPDQNIQFWLEQFPQAWAETAGMGLAKQVPPQVIQLKASATPVSVRQYPLSKEAQEGIRPHVQRLIQQGILVPVQSPWNTPLLPVRKPGTNDYR PVQDLREVNKRVQDIHPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGTGRTGQLTWTRLPQGFKNSPTIFNEALHRDLANF RIQHPQVTLLQYVDDLLLAGATKQDCLEGTKALLLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWLTEARKKTVVQIPAPTTAKQVREFLGKAGFC RLFIPGFATLAAPLYPLTKPKGEFSWAPEHQKAFDAIKKALLSAPALALPDVTKPFTLYVDERKGVARGVLTQTLGPWRRPVAYLSKKLDPVASGWPVCL KAIAAVAILVKDADKLTLGQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNPATLLPEETDEPVTHDCHQLLIEETGVRKDLT DIPLTGEVLTWFTDGSSYVVEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSINIYTDSRYAFATAHVHGAIYKQRGWLTSAGRE IKNKEEILSLLEALHLPKRLAIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLPAGKRTADGSEFEKRTADGSEFESPKKKAKVE
202	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSSGSSGSSGSSGSSGGLD DEYRLYSPLVKPDQNIQFWLEQFPQAWAETAGMGLAKQVPPQVIQLKASATPVSVRQYPLSKEAQEGIRPHVQRLIQQGILVPVQSPWNTPLLPVRKPGT NDYRPVQDLREVNKRVQDIHPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGTGRTGQLTWTRLPQGFKNSPTIFNEALHRD LANFRIQHPQVTLLQYVDDLLLAGATKQDCLEGTKALLLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWLTEARKKTVVQIPAPTTAKQVREFLGK AGFCRLFIPGFATLAAPLYPLTKPKGEFSWAPEHQKAFDAIKKALLSAPALALPDVTKPFTLYVDERKGVARGVLTQTLGPWRRPVAYLSKKLDPVASGW PVCLKAIAAVAILVKDADKLTLGQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNPATLLPEETDEPVTHDCHQLLIEETGVR KDLTDIPLTGEVLTWFTDGSSYVVEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSINIYTDSRYAFATAHVHGAIYKQRGWLTS AGREIKNKEEILSLLEALHLPKRLAIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLPAGKRTADGSEFEKRTADGSEFESPKKKAKVE
207	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA

	KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGGGSSPAPGGLDDEYRLY SPLVKPDQNIQFWLEQFPQAWAETAGMGLAKQVPPQVIQLKASATPVSVRQYPLSKEAQEGIRPHVQRLIQQGILVPVQSPWNTPLLPVRKPGTNDYRPV QDLREVNKRVQDIHPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGTGRTGQLTWTRLPQGFKNSPTIFNEALHRDLANFRI QHPQVTLLQYVDDLLLAGATKQDCLEGTKALLLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWLTEARKKTVVQIPAPTTAKQVREFLGKAGFCRL FIPGFATLAAPLYPLTKPKGEFSWAPEHQKAFDAIKKALLSAPALALPDVTKPFTLYVDERKGVARGVLTQTLGPWRRPVAYLSKKLDPVASGWPVCLKA IAAVAILVKDADKLTLGQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNPATLLPEETDEPVTHDCHQLLIEETGVRKDLTDI PLTGEVLTWFTDGSSYVVEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSINIYTDSRYAFATAHVHGAIYKQRGWLTSAGREIK NKEEILSLLEALHLPKRLAIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLPAGKRTADGSEFEKRTADGSEFESPKKKAKVE
208	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSSGSSGSSGGLDDEYRLY SPLVKPDQNIQFWLEQFPQAWAETAGMGLAKQVPPQVIQLKASATPVSVRQYPLSKEAQEGIRPHVQRLIQQGILVPVQSPWNTPLLPVRKPGTNDYRPV QDLREVNKRVQDIHPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGTGRTGQLTWTRLPQGFKNSPTIFNEALHRDLANFRI QHPQVTLLQYVDDLLLAGATKQDCLEGTKALLLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWLTEARKKTVVQIPAPTTAKQVREFLGKAGFCRL FIPGFATLAAPLYPLTKPKGEFSWAPEHQKAFDAIKKALLSAPALALPDVTKPFTLYVDERKGVARGVLTQTLGPWRRPVAYLSKKLDPVASGWPVCLKA IAAVAILVKDADKLTLGQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNPATLLPEETDEPVTHDCHQLLIEETGVRKDLTDI PLTGEVLTWFTDGSSYVVEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSINIYTDSRYAFATAHVHGAIYKQRGWLTSAGREIK NKEEILSLLEALHLPKRLAIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLPAGKRTADGSEFEKRTADGSEFESPKKKAKVE
212	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK

	ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGSGSSGGLDDEYRLYSPL VKPDQNIQFWLEQFPQAWAETAGMGLAKQVPPQVIQLKASATPVSVRQYPLSKEAQEGIRPHVQRLIQQGILVPVQSPWNTPLLPVRKPGTNDYRPVQDL REVNKRVQDIHPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGTGRTGQLTWTRLPQGFKNSPTIFNEALHRDLANFRIQHP QVTLLQYVDDLLLAGATKQDCLEGTKALLLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWLTEARKKTVVQIPAPTTAKQVREFLGKAGFCRLFIP GFATLAAPLYPLTKPKGEFSWAPEHQKAFDAIKKALLSAPALALPDVTKPFTLYVDERKGVARGVLTQTLGPWRRPVAYLSKKLDPVASGWPVCLKAIAA VAILVKDADKLTLGQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNPATLLPEETDEPVTHDCHQLLIEETGVRKDLTDIPLT GEVLTWFTDGSSYVVEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSINIYTDSRYAFATAHVHGAIYKQRGWLTSAGREIKNKE EILSLLEALHLPKRLAIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLPAGKRTADGSEFEKRTADGSEFESPKKKAKVE
213	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGSGGGPAPGGLDDEYRLY SPLVKPDQNIQFWLEQFPQAWAETAGMGLAKQVPPQVIQLKASATPVSVRQYPLSKEAQEGIRPHVQRLIQQGILVPVQSPWNTPLLPVRKPGTNDYRPV QDLREVNKRVQDIHPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGTGRTGQLTWTRLPQGFKNSPTIFNEALHRDLANFRI QHPQVTLLQYVDDLLLAGATKQDCLEGTKALLLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWLTEARKKTVVQIPAPTTAKQVREFLGKAGFCRL FIPGFATLAAPLYPLTKPKGEFSWAPEHQKAFDAIKKALLSAPALALPDVTKPFTLYVDERKGVARGVLTQTLGPWRRPVAYLSKKLDPVASGWPVCLKA IAAVAILVKDADKLTLGQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNPATLLPEETDEPVTHDCHQLLIEETGVRKDLTDI PLTGEVLTWFTDGSSYVVEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSINIYTDSRYAFATAHVHGAIYKQRGWLTSAGREIK NKEEILSLLEALHLPKRLAIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLPAGKRTADGSEFEKRTADGSEFESPKKKAKVE
216	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA

	NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGGGSGGGGSGGGGSGGLD DEYRLYSPLVKPDQNIQFWLEQFPQAWAETAGMGLAKQVPPQVIQLKASATPVSVRQYPLSKEAQEGIRPHVQRLIQQGILVPVQSPWNTPLLPVRKPGT NDYRPVQDLREVNKRVQDIHPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGTGRTGQLTWTRLPQGFKNSPTIFNEALHRD LANFRIQHPQVTLLQYVDDLLLAGATKQDCLEGTKALLLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWLTEARKKTVVQIPAPTTAKQVREFLGK AGFCRLFIPGFATLAAPLYPLTKPKGEFSWAPEHQKAFDAIKKALLSAPALALPDVTKPFTLYVDERKGVARGVLTQTLGPWRRPVAYLSKKLDPVASGW PVCLKAIAAVAILVKDADKLTLGQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNPATLLPEETDEPVTHDCHQLLIEETGVR KDLTDIPLTGEVLTWFTDGSSYVVEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSINIYTDSRYAFATAHVHGAIYKQRGWLTS AGREIKNKEEILSLLEALHLPKRLAIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLPAGKRTADGSEFEKRTADGSEFESPKKKAKVE
217	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPGGSEAAAKGGLDDEYR LYSPLVKPDQNIQFWLEQFPQAWAETAGMGLAKQVPPQVIQLKASATPVSVRQYPLSKEAQEGIRPHVQRLIQQGILVPVQSPWNTPLLPVRKPGTNDYR PVQDLREVNKRVQDIHPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGTGRTGQLTWTRLPQGFKNSPTIFNEALHRDLANF RIQHPQVTLLQYVDDLLLAGATKQDCLEGTKALLLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWLTEARKKTVVQIPAPTTAKQVREFLGKAGFC RLFIPGFATLAAPLYPLTKPKGEFSWAPEHQKAFDAIKKALLSAPALALPDVTKPFTLYVDERKGVARGVLTQTLGPWRRPVAYLSKKLDPVASGWPVCL KAIAAVAILVKDADKLTLGQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNPATLLPEETDEPVTHDCHQLLIEETGVRKDLT DIPLTGEVLTWFTDGSSYVVEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSINIYTDSRYAFATAHVHGAIYKQRGWLTSAGRE IKNKEEILSLLEALHLPKRLAIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLPAGKRTADGSEFEKRTADGSEFESPKKKAKVE
219	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA

	SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKGGGGGLDDEYRLYS PLVKPDQNIQFWLEQFPQAWAETAGMGLAKQVPPQVIQLKASATPVSVRQYPLSKEAQEGIRPHVQRLIQQGILVPVQSPWNTPLLPVRKPGTNDYRPVQ DLREVNKRVQDIHPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGTGRTGQLTWTRLPQGFKNSPTIFNEALHRDLANFRIQ HPQVTLLQYVDDLLLAGATKQDCLEGTKALLLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWLTEARKKTVVQIPAPTTAKQVREFLGKAGFCRLF IPGFATLAAPLYPLTKPKGEFSWAPEHQKAFDAIKKALLSAPALALPDVTKPFTLYVDERKGVARGVLTQTLGPWRRPVAYLSKKLDPVASGWPVCLKAI AAVAILVKDADKLTLGQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNPATLLPEETDEPVTHDCHQLLIEETGVRKDLTDIP LTGEVLTWFTDGSSYVVEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSINIYTDSRYAFATAHVHGAIYKQRGWLTSAGREIKN KEEILSLLEALHLPKRLAIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLPAGKRTADGSEFEKRTADGSEFESPKKKAKVE
223	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSSPAPGGLDDEYRLYSPL VKPDQNIQFWLEQFPQAWAETAGMGLAKQVPPQVIQLKASATPVSVRQYPLSKEAQEGIRPHVQRLIQQGILVPVQSPWNTPLLPVRKPGTNDYRPVQDL REVNKRVQDIHPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGTGRTGQLTWTRLPQGFKNSPTIFNEALHRDLANFRIQHP QVTLLQYVDDLLLAGATKQDCLEGTKALLLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWLTEARKKTVVQIPAPTTAKQVREFLGKAGFCRLFIP GFATLAAPLYPLTKPKGEFSWAPEHQKAFDAIKKALLSAPALALPDVTKPFTLYVDERKGVARGVLTQTLGPWRRPVAYLSKKLDPVASGWPVCLKAIAA VAILVKDADKLTLGQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNPATLLPEETDEPVTHDCHQLLIEETGVRKDLTDIPLT GEVLTWFTDGSSYVVEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSINIYTDSRYAFATAHVHGAIYKQRGWLTSAGREIKNKE EILSLLEALHLPKRLAIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLPAGKRTADGSEFEKRTADGSEFESPKKKAKVE
224	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ

	SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKPAPGSSGGLDDEYR LYSPLVKPDQNIQFWLEQFPQAWAETAGMGLAKQVPPQVIQLKASATPVSVRQYPLSKEAQEGIRPHVQRLIQQGILVPVQSPWNTPLLPVRKPGTNDYR PVQDLREVNKRVQDIHPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGTGRTGQLTWTRLPQGFKNSPTIFNEALHRDLANF RIQHPQVTLLQYVDDLLLAGATKQDCLEGTKALLLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWLTEARKKTVVQIPAPTTAKQVREFLGKAGFC RLFIPGFATLAAPLYPLTKPKGEFSWAPEHQKAFDAIKKALLSAPALALPDVTKPFTLYVDERKGVARGVLTQTLGPWRRPVAYLSKKLDPVASGWPVCL KAIAAVAILVKDADKLTLGQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNPATLLPEETDEPVTHDCHQLLIEETGVRKDLT DIPLTGEVLTWFTDGSSYVVEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSINIYTDSRYAFATAHVHGAIYKQRGWLTSAGRE IKNKEEILSLLEALHLPKRLAIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLPAGKRTADGSEFEKRTADGSEFESPKKKAKVE
225	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPGSSEAAAKGGLDDEYR LYSPLVKPDQNIQFWLEQFPQAWAETAGMGLAKQVPPQVIQLKASATPVSVRQYPLSKEAQEGIRPHVQRLIQQGILVPVQSPWNTPLLPVRKPGTNDYR PVQDLREVNKRVQDIHPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGTGRTGQLTWTRLPQGFKNSPTIFNEALHRDLANF RIQHPQVTLLQYVDDLLLAGATKQDCLEGTKALLLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWLTEARKKTVVQIPAPTTAKQVREFLGKAGFC RLFIPGFATLAAPLYPLTKPKGEFSWAPEHQKAFDAIKKALLSAPALALPDVTKPFTLYVDERKGVARGVLTQTLGPWRRPVAYLSKKLDPVASGWPVCL KAIAAVAILVKDADKLTLGQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNPATLLPEETDEPVTHDCHQLLIEETGVRKDLT DIPLTGEVLTWFTDGSSYVVEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSINIYTDSRYAFATAHVHGAIYKQRGWLTSAGRE IKNKEEILSLLEALHLPKRLAIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLPAGKRTADGSEFEKRTADGSEFESPKKKAKVE
228	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL

	LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSSGSSGSSGSSGGLDDEY RLYSPLVKPDQNIQFWLEQFPQAWAETAGMGLAKQVPPQVIQLKASATPVSVRQYPLSKEAQEGIRPHVQRLIQQGILVPVQSPWNTPLLPVRKPGTNDY RPVQDLREVNKRVQDIHPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGTGRTGQLTWTRLPQGFKNSPTIFNEALHRDLAN FRIQHPQVTLLQYVDDLLLAGATKQDCLEGTKALLLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWLTEARKKTVVQIPAPTTAKQVREFLGKAGF CRLFIPGFATLAAPLYPLTKPKGEFSWAPEHQKAFDAIKKALLSAPALALPDVTKPFTLYVDERKGVARGVLTQTLGPWRRPVAYLSKKLDPVASGWPVC LKAIAAVAILVKDADKLTLGQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNPATLLPEETDEPVTHDCHQLLIEETGVRKDL TDIPLTGEVLTWFTDGSSYVVEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSINIYTDSRYAFATAHVHGAIYKQRGWLTSAGR EIKNKEEILSLLEALHLPKRLAIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLPAGKRTADGSEFEKRTADGSEFESPKKKAKVE
228	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSSGSSGSSGSSGGLDDEY RLYSPLVKPDQNIQFWLEQFPQAWAETAGMGLAKQVPPQVIQLKASATPVSVRQYPLSKEAQEGIRPHVQRLIQQGILVPVQSPWNTPLLPVRKPGTNDY RPVQDLREVNKRVQDIHPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGTGRTGQLTWTRLPQGFKNSPTIFNEALHRDLAN FRIQHPQVTLLQYVDDLLLAGATKQDCLEGTKALLLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWLTEARKKTVVQIPAPTTAKQVREFLGKAGF CRLFIPGFATLAAPLYPLTKPKGEFSWAPEHQKAFDAIKKALLSAPALALPDVTKPFTLYVDERKGVARGVLTQTLGPWRRPVAYLSKKLDPVASGWPVC LKAIAAVAILVKDADKLTLGQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNPATLLPEETDEPVTHDCHQLLIEETGVRKDL TDIPLTGEVLTWFTDGSSYVVEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSINIYTDSRYAFATAHVHGAIYKQRGWLTSAGR EIKNKEEILSLLEALHLPKRLAIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLPAGKRTADGSEFEKRTADGSEFESPKKKAKVE
229	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL

	FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGGEAAAKGGSGGLDDEYR LYSPLVKPDQNIQFWLEQFPQAWAETAGMGLAKQVPPQVIQLKASATPVSVRQYPLSKEAQEGIRPHVQRLIQQGILVPVQSPWNTPLLPVRKPGTNDYR PVQDLREVNKRVQDIHPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGTGRTGQLTWTRLPQGFKNSPTIFNEALHRDLANF RIQHPQVTLLQYVDDLLLAGATKQDCLEGTKALLLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWLTEARKKTVVQIPAPTTAKQVREFLGKAGFC RLFIPGFATLAAPLYPLTKPKGEFSWAPEHQKAFDAIKKALLSAPALALPDVTKPFTLYVDERKGVARGVLTQTLGPWRRPVAYLSKKLDPVASGWPVCL KAIAAVAILVKDADKLTLGQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNPATLLPEETDEPVTHDCHQLLIEETGVRKDLT DIPLTGEVLTWFTDGSSYVVEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSINIYTDSRYAFATAHVHGAIYKQRGWLTSAGRE IKNKEEILSLLEALHLPKRLAIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLPAGKRTADGSEFEKRTADGSEFESPKKKAKVE
232	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKEAAAKEAAAKEAAA KEAAAKGGLDDEYRLYSPLVKPDQNIQFWLEQFPQAWAETAGMGLAKQVPPQVIQLKASATPVSVRQYPLSKEAQEGIRPHVQRLIQQGILVPVQSPWNT PLLPVRKPGTNDYRPVQDLREVNKRVQDIHPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGTGRTGQLTWTRLPQGFKNSP TIFNEALHRDLANFRIQHPQVTLLQYVDDLLLAGATKQDCLEGTKALLLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWLTEARKKTVVQIPAPTT AKQVREFLGKAGFCRLFIPGFATLAAPLYPLTKPKGEFSWAPEHQKAFDAIKKALLSAPALALPDVTKPFTLYVDERKGVARGVLTQTLGPWRRPVAYLS KKLDPVASGWPVCLKAIAAVAILVKDADKLTLGQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNPATLLPEETDEPVTHDCH QLLIEETGVRKDLTDIPLTGEVLTWFTDGSSYVVEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSINIYTDSRYAFATAHVHGA IYKQRGWLTSAGREIKNKEEILSLLEALHLPKRLAIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLPAGKRTADGSEFEKRTADGSEFESPKKKAK VE

235	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSSGSSGGLDDEYRLYSPL VKPDQNIQFWLEQFPQAWAETAGMGLAKQVPPQVIQLKASATPVSVRQYPLSKEAQEGIRPHVQRLIQQGILVPVQSPWNTPLLPVRKPGTNDYRPVQDL REVNKRVQDIHPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGTGRTGQLTWTRLPQGFKNSPTIFNEALHRDLANFRIQHP QVTLLQYVDDLLLAGATKQDCLEGTKALLLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWLTEARKKTVVQIPAPTTAKQVREFLGKAGFCRLFIP GFATLAAPLYPLTKPKGEFSWAPEHQKAFDAIKKALLSAPALALPDVTKPFTLYVDERKGVARGVLTQTLGPWRRPVAYLSKKLDPVASGWPVCLKAIAA VAILVKDADKLTLGQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNPATLLPEETDEPVTHDCHQLLIEETGVRKDLTDIPLT GEVLTWFTDGSSYVVEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSINIYTDSRYAFATAHVHGAIYKQRGWLTSAGREIKNKE EILSLLEALHLPKRLAIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLPAGKRTADGSEFEKRTADGSEFESPKKKAKVE
239	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSEAAAKPAPGGLDDEYR LYSPLVKPDQNIQFWLEQFPQAWAETAGMGLAKQVPPQVIQLKASATPVSVRQYPLSKEAQEGIRPHVQRLIQQGILVPVQSPWNTPLLPVRKPGTNDYR PVQDLREVNKRVQDIHPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGTGRTGQLTWTRLPQGFKNSPTIFNEALHRDLANF RIQHPQVTLLQYVDDLLLAGATKQDCLEGTKALLLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWLTEARKKTVVQIPAPTTAKQVREFLGKAGFC RLFIPGFATLAAPLYPLTKPKGEFSWAPEHQKAFDAIKKALLSAPALALPDVTKPFTLYVDERKGVARGVLTQTLGPWRRPVAYLSKKLDPVASGWPVCL KAIAAVAILVKDADKLTLGQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNPATLLPEETDEPVTHDCHQLLIEETGVRKDLT

	DIPLTGEVLTWFTDGSSYVVEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSINIYTDSRYAFATAHVHGAIYKQRGWLTSAGRE IKNKEEILSLLEALHLPKRLAIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLPAGKRTADGSEFEKRTADGSEFESPKKKAKVE
252	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPGGSGGLDDEYRLYSPL VKPDQNIQFWLEQFPQAWAETAGMGLAKQVPPQVIQLKASATPVSVRQYPLSKEAQEGIRPHVQRLIQQGILVPVQSPWNTPLLPVRKPGTNDYRPVQDL REVNKRVQDIHPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGTGRTGQLTWTRLPQGFKNSPTIFNEALHRDLANFRIQHP QVTLLQYVDDLLLAGATKQDCLEGTKALLLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWLTEARKKTVVQIPAPTTAKQVREFLGKAGFCRLFIP GFATLAAPLYPLTKPKGEFSWAPEHQKAFDAIKKALLSAPALALPDVTKPFTLYVDERKGVARGVLTQTLGPWRRPVAYLSKKLDPVASGWPVCLKAIAA VAILVKDADKLTLGQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNPATLLPEETDEPVTHDCHQLLIEETGVRKDLTDIPLT GEVLTWFTDGSSYVVEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSINIYTDSRYAFATAHVHGAIYKQRGWLTSAGREIKNKE EILSLLEALHLPKRLAIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLPAGKRTADGSEFEKRTADGSEFESPKKKAKVE
258	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSSEAAAKGGSGGLDDEYR LYSPLVKPDQNIQFWLEQFPQAWAETAGMGLAKQVPPQVIQLKASATPVSVRQYPLSKEAQEGIRPHVQRLIQQGILVPVQSPWNTPLLPVRKPGTNDYR PVQDLREVNKRVQDIHPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGTGRTGQLTWTRLPQGFKNSPTIFNEALHRDLANF RIQHPQVTLLQYVDDLLLAGATKQDCLEGTKALLLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWLTEARKKTVVQIPAPTTAKQVREFLGKAGFC RLFIPGFATLAAPLYPLTKPKGEFSWAPEHQKAFDAIKKALLSAPALALPDVTKPFTLYVDERKGVARGVLTQTLGPWRRPVAYLSKKLDPVASGWPVCL

	KAIAAVAILVKDADKLTLGQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNPATLLPEETDEPVTHDCHQLLIEETGVRKDLT DIPLTGEVLTWFTDGSSYVVEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSINIYTDSRYAFATAHVHGAIYKQRGWLTSAGRE IKNKEEILSLLEALHLPKRLAIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLPAGKRTADGSEFEKRTADGSEFESPKKKAKVE
268	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSGSSPAPGGLDDEYRLY SPLVKPDQNIQFWLEQFPQAWAETAGMGLAKQVPPQVIQLKASATPVSVRQYPLSKEAQEGIRPHVQRLIQQGILVPVQSPWNTPLLPVRKPGTNDYRPV QDLREVNKRVQDIHPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGTGRTGQLTWTRLPQGFKNSPTIFNEALHRDLANFRI QHPQVTLLQYVDDLLLAGATKQDCLEGTKALLLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWLTEARKKTVVQIPAPTTAKQVREFLGKAGFCRL FIPGFATLAAPLYPLTKPKGEFSWAPEHQKAFDAIKKALLSAPALALPDVTKPFTLYVDERKGVARGVLTQTLGPWRRPVAYLSKKLDPVASGWPVCLKA IAAVAILVKDADKLTLGQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNPATLLPEETDEPVTHDCHQLLIEETGVRKDLTDI PLTGEVLTWFTDGSSYVVEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSINIYTDSRYAFATAHVHGAIYKQRGWLTSAGREIK NKEEILSLLEALHLPKRLAIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLPAGKRTADGSEFEKRTADGSEFESPKKKAKVE
278	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKGGGPAPGGTLQLDD EYRLYSPLVKPDQNIQFWLEQFPQAWAETAGMGLAKQVPPQVIQLKASATPVSVRQYPLSKEAQEGIRPHVQRLIQQGILVPVQSPWNTPLLPVRKPGTN DYRPVQDLREVNKRVQDIHPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGTGRTGQLTWTRLPQGFKNSPTIFDEALHRDL ANFRIQHPQVTLLQYVDDLLLAGATKQDCLEGTKALLLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWLTEARKKTVVQIPAPTTAKQVREFLGTA

	GFCRLWIPGFATLAAPLYPLTKEKGEFSWAPEHQKAFDAIKKALLSAPALALPDVTKPFTLYVDERKGVARGVLTQTLGPWRRPVAYLSKKLDPVASGWP VCLKAIAAVAILVKDADKLTLGQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNPATLLPEETDEPVTHDCHQLLIEETGVRK DLTDIPLTGEVLTWFTDGSSYVVEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSINIYTDSRYAFATAHVHGAIYKQRGLLTSA GREIKNKEEILSLLEALHLPKRLAIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
279	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKEAAAKEAAAKGGTL QLDDEYRLYSPLVKPDQNIQFWLEQFPQAWAETAGMGLAKQVPPQVIQLKASATPVSVRQYPLSKEAQEGIRPHVQRLIQQGILVPVQSPWNTPLLPVRK PGTNDYRPVQDLREVNKRVQDIHPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGTGRTGQLTWTRLPQGFKNSPTIFDEAL HRDLANFRIQHPQVTLLQYVDDLLLAGATKQDCLEGTKALLLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWLTEARKKTVVQIPAPTTAKQVREF LGTAGFCRLWIPGFATLAAPLYPLTKEKGEFSWAPEHQKAFDAIKKALLSAPALALPDVTKPFTLYVDERKGVARGVLTQTLGPWRRPVAYLSKKLDPVA SGWPVCLKAIAAVAILVKDADKLTLGQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNPATLLPEETDEPVTHDCHQLLIEET GVRKDLTDIPLTGEVLTWFTDGSSYVVEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSINIYTDSRYAFATAHVHGAIYKQRGL LTSAGREIKNKEEILSLLEALHLPKRLAIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
280	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKEAAAKEAAAKEAAA KEAAAKEAAAKGGTLQLDDEYRLYSPLVKPDQNIQFWLEQFPQAWAETAGMGLAKQVPPQVIQLKASATPVSVRQYPLSKEAQEGIRPHVQRLIQQGILV PVQSPWNTPLLPVRKPGTNDYRPVQDLREVNKRVQDIHPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGTGRTGQLTWTRL

	PQGFKNSPTIFDEALHRDLANFRIQHPQVTLLQYVDDLLLAGATKQDCLEGTKALLLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWLTEARKKTV VQIPAPTTAKQVREFLGTAGFCRLWIPGFATLAAPLYPLTKEKGEFSWAPEHQKAFDAIKKALLSAPALALPDVTKPFTLYVDERKGVARGVLTQTLGPW RRPVAYLSKKLDPVASGWPVCLKAIAAVAILVKDADKLTLGQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNPATLLPEETD EPVTHDCHQLLIEETGVRKDLTDIPLTGEVLTWFTDGSSYVVEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSINIYTDSRYAF ATAHVHGAIYKQRGLLTSAGREIKNKEEILSLLEALHLPKRLAIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLAGKRTADGSEFEKRTADGSEFE SPKKKAKVE
298	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKEAAAKEAAAKGGTL QLDDEYRLYSPLVKPDQNIQFWLEQFPQAWAETAGMGLAKQVPPQVIQLKASATPVSVRQYPLSKEAQEGIRPHVQRLIQQGILVPVQSPWNTPLLPVRK PGTNDYRPVQDLREVNKRVQDIHPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGTGRTGQLTWTRLPQGFKNSPTIFNEAL HRDLANFRIQHPQVTLLQYVDDLLLAGATKQDCLEGTKALLLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWLTEARKKTVVQIPAPTTAKQVREF LGTAGFCRLWIPGFATLAAPLYPLTKPKGEFSWAPEHQKAFDAIKKALLSAPALALPDVTKPFTLYVDERKGVARGVLTQTLGPWRRPVAYLSKKLDPVA SGWPVCLKAIAAVAILVKDADKLTLGQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNPATLLPEETDEPVTHDCHQLLIEET GVRKDLTDIPLTGEVLTWFTDGSSYVVEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSINIYTDSRYAFATAHVHGAIYKQRGW LTSAGREIKNKEEILSLLEALHLPKRLAIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
299	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKGGSGGGGGTLQLDD

	EYRLYSPLVKPDQNIQFWLEQFPQAWAETAGMGLAKQVPPQVIQLKASATPVSVRQYPLSKEAQEGIRPHVQRLIQQGILVPVQSPWNTPLLPVRKPGTN DYRPVQDLREVNKRVQDIHPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGTGRTGQLTWTRLPQGFKNSPTIFNEALHRDL ANFRIQHPQVTLLQYVDDLLLAGATKQDCLEGTKALLLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWLTEARKKTVVQIPAPTTAKQVREFLGTA GFCRLWIPGFATLAAPLYPLTKPKGEFSWAPEHQKAFDAIKKALLSAPALALPDVTKPFTLYVDERKGVARGVLTQTLGPWRRPVAYLSKKLDPVASGWP VCLKAIAAVAILVKDADKLTLGQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNPATLLPEETDEPVTHDCHQLLIEETGVRK DLTDIPLTGEVLTWFTDGSSYVVEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSINIYTDSRYAFATAHVHGAIYKQRGWLTSA GREIKNKEEILSLLEALHLPKRLAIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
300	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGAEAAAKEAAAKEAAAKEAA AKALEAEAAAKEAAAKEAAAKEAAAKAGGTLQLDDEYRLYSPLVKPDQNIQFWLEQFPQAWAETAGMGLAKQVPPQVIQLKASATPVSVRQYPLSKEAQE GIRPHVQRLIQQGILVPVQSPWNTPLLPVRKPGTNDYRPVQDLREVNKRVQDIHPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAFEW RDPGTGRTGQLTWTRLPQGFKNSPTIFNEALHRDLANFRIQHPQVTLLQYVDDLLLAGATKQDCLEGTKALLLELSDLGYRASAKKAQICRREVTYLGYS LRDGQRWLTEARKKTVVQIPAPTTAKQVREFLGTAGFCRLWIPGFATLAAPLYPLTKPKGEFSWAPEHQKAFDAIKKALLSAPALALPDVTKPFTLYVDE RKGVARGVLTQTLGPWRRPVAYLSKKLDPVASGWPVCLKAIAAVAILVKDADKLTLGQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFA PPAALNPATLLPEETDEPVTHDCHQLLIEETGVRKDLTDIPLTGEVLTWFTDGSSYVVEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRL AEGKSINIYTDSRYAFATAHVHGAIYKQRGWLTSAGREIKNKEEILSLLEALHLPKRLAIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLAGKRTA DGSEFEKRTADGSEFESPKKKAKVE
300	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE

	VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGAEAAAKEAAAKEAAAKEAA AKALEAEAAAKEAAAKEAAAKEAAAKAGGTLQLDDEYRLYSPLVKPDQNIQFWLEQFPQAWAETAGMGLAKQVPPQVIQLKASATPVSVRQYPLSKEAQE GIRPHVQRLIQQGILVPVQSPWNTPLLPVRKPGTNDYRPVQDLREVNKRVQDIHPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAFEW RDPGTGRTGQLTWTRLPQGFKNSPTIFNEALHRDLANFRIQHPQVTLLQYVDDLLLAGATKQDCLEGTKALLLELSDLGYRASAKKAQICRREVTYLGYS LRDGQRWLTEARKKTVVQIPAPTTAKQVREFLGTAGFCRLWIPGFATLAAPLYPLTKPKGEFSWAPEHQKAFDAIKKALLSAPALALPDVTKPFTLYVDE RKGVARGVLTQTLGPWRRPVAYLSKKLDPVASGWPVCLKAIAAVAILVKDADKLTLGQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFA PPAALNPATLLPEETDEPVTHDCHQLLIEETGVRKDLTDIPLTGEVLTWFTDGSSYVVEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRL AEGKSINIYTDSRYAFATAHVHGAIYKQRGWLTSAGREIKNKEEILSLLEALHLPKRLAIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLAGKRTA DGSEFEKRTADGSEFESPKKKAKVE
302	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGSPAPEAAAKGGTLQLDD EYRLYSPLVKPDQNIQFWLEQFPQAWAETAGMGLAKQVPPQVIQLKASATPVSVRQYPLSKEAQEGIRPHVQRLIQQGILVPVQSPWNTPLLPVRKPGTN DYRPVQDLREVNKRVQDIHPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGTGRTGQLTWTRLPQGFKNSPTIFNEALHRDL ANFRIQHPQVTLLQYVDDLLLAGATKQDCLEGTKALLLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWLTEARKKTVVQIPAPTTAKQVREFLGTA GFCRLWIPGFATLAAPLYPLTKPKGEFSWAPEHQKAFDAIKKALLSAPALALPDVTKPFTLYVDERKGVARGVLTQTLGPWRRPVAYLSKKLDPVASGWP VCLKAIAAVAILVKDADKLTLGQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNPATLLPEETDEPVTHDCHQLLIEETGVRK DLTDIPLTGEVLTWFTDGSSYVVEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSINIYTDSRYAFATAHVHGAIYKQRGWLTSA GREIKNKEEILSLLEALHLPKRLAIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
303	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL

	NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGSGGSSGGSSGSETPGTSES ATPESSGGSSGGSSGGTLQLDDEYRLYSPLVKPDQNIQFWLEQFPQAWAETAGMGLAKQVPPQVIQLKASATPVSVRQYPLSKEAQEGIRPHVQRLIQQG ILVPVQSPWNTPLLPVRKPGTNDYRPVQDLREVNKRVQDIHPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGTGRTGQLTW TRLPQGFKNSPTIFNEALHRDLANFRIQHPQVTLLQYVDDLLLAGATKQDCLEGTKALLLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWLTEARK KTVVQIPAPTTAKQVREFLGTAGFCRLWIPGFATLAAPLYPLTKPKGEFSWAPEHQKAFDAIKKALLSAPALALPDVTKPFTLYVDERKGVARGVLTQTL GPWRRPVAYLSKKLDPVASGWPVCLKAIAAVAILVKDADKLTLGQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNPATLLPE ETDEPVTHDCHQLLIEETGVRKDLTDIPLTGEVLTWFTDGSSYVVEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSINIYTDSR YAFATAHVHGAIYKQRGWLTSAGREIKNKEEILSLLEALHLPKRLAIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLAGKRTADGSEFEKRTADGS EFESPKKKAKVE
304	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKPAPGSSGGTLQLDD EYRLYSPLVKPDQNIQFWLEQFPQAWAETAGMGLAKQVPPQVIQLKASATPVSVRQYPLSKEAQEGIRPHVQRLIQQGILVPVQSPWNTPLLPVRKPGTN DYRPVQDLREVNKRVQDIHPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGTGRTGQLTWTRLPQGFKNSPTIFNEALHRDL ANFRIQHPQVTLLQYVDDLLLAGATKQDCLEGTKALLLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWLTEARKKTVVQIPAPTTAKQVREFLGTA GFCRLWIPGFATLAAPLYPLTKPKGEFSWAPEHQKAFDAIKKALLSAPALALPDVTKPFTLYVDERKGVARGVLTQTLGPWRRPVAYLSKKLDPVASGWP VCLKAIAAVAILVKDADKLTLGQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNPATLLPEETDEPVTHDCHQLLIEETGVRK DLTDIPLTGEVLTWFTDGSSYVVEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSINIYTDSRYAFATAHVHGAIYKQRGWLTSA GREIKNKEEILSLLEALHLPKRLAIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
305	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK

	ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPGGGEAAAKGGTLQLDD EYRLYSPLVKPDQNIQFWLEQFPQAWAETAGMGLAKQVPPQVIQLKASATPVSVRQYPLSKEAQEGIRPHVQRLIQQGILVPVQSPWNTPLLPVRKPGTN DYRPVQDLREVNKRVQDIHPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGTGRTGQLTWTRLPQGFKNSPTIFNEALHRDL ANFRIQHPQVTLLQYVDDLLLAGATKQDCLEGTKALLLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWLTEARKKTVVQIPAPTTAKQVREFLGTA GFCRLWIPGFATLAAPLYPLTKPKGEFSWAPEHQKAFDAIKKALLSAPALALPDVTKPFTLYVDERKGVARGVLTQTLGPWRRPVAYLSKKLDPVASGWP VCLKAIAAVAILVKDADKLTLGQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNPATLLPEETDEPVTHDCHQLLIEETGVRK DLTDIPLTGEVLTWFTDGSSYVVEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSINIYTDSRYAFATAHVHGAIYKQRGWLTSA GREIKNKEEILSLLEALHLPKRLAIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
306	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKGGGGGTLQLDDEYR LYSPLVKPDQNIQFWLEQFPQAWAETAGMGLAKQVPPQVIQLKASATPVSVRQYPLSKEAQEGIRPHVQRLIQQGILVPVQSPWNTPLLPVRKPGTNDYR PVQDLREVNKRVQDIHPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGTGRTGQLTWTRLPQGFKNSPTIFNEALHRDLANF RIQHPQVTLLQYVDDLLLAGATKQDCLEGTKALLLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWLTEARKKTVVQIPAPTTAKQVREFLGTAGFC RLWIPGFATLAAPLYPLTKPKGEFSWAPEHQKAFDAIKKALLSAPALALPDVTKPFTLYVDERKGVARGVLTQTLGPWRRPVAYLSKKLDPVASGWPVCL KAIAAVAILVKDADKLTLGQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNPATLLPEETDEPVTHDCHQLLIEETGVRKDLT DIPLTGEVLTWFTDGSSYVVEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSINIYTDSRYAFATAHVHGAIYKQRGWLTSAGRE IKNKEEILSLLEALHLPKRLAIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
307	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA

	NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGGGSSPAPGGTLQLDDEY RLYSPLVKPDQNIQFWLEQFPQAWAETAGMGLAKQVPPQVIQLKASATPVSVRQYPLSKEAQEGIRPHVQRLIQQGILVPVQSPWNTPLLPVRKPGTNDY RPVQDLREVNKRVQDIHPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGTGRTGQLTWTRLPQGFKNSPTIFNEALHRDLAN FRIQHPQVTLLQYVDDLLLAGATKQDCLEGTKALLLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWLTEARKKTVVQIPAPTTAKQVREFLGTAGF CRLWIPGFATLAAPLYPLTKPKGEFSWAPEHQKAFDAIKKALLSAPALALPDVTKPFTLYVDERKGVARGVLTQTLGPWRRPVAYLSKKLDPVASGWPVC LKAIAAVAILVKDADKLTLGQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNPATLLPEETDEPVTHDCHQLLIEETGVRKDL TDIPLTGEVLTWFTDGSSYVVEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSINIYTDSRYAFATAHVHGAIYKQRGWLTSAGR EIKNKEEILSLLEALHLPKRLAIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
308	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKGGTLQLDDEYRLYS PLVKPDQNIQFWLEQFPQAWAETAGMGLAKQVPPQVIQLKASATPVSVRQYPLSKEAQEGIRPHVQRLIQQGILVPVQSPWNTPLLPVRKPGTNDYRPVQ DLREVNKRVQDIHPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGTGRTGQLTWTRLPQGFKNSPTIFNEALHRDLANFRIQ HPQVTLLQYVDDLLLAGATKQDCLEGTKALLLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWLTEARKKTVVQIPAPTTAKQVREFLGTAGFCRLW IPGFATLAAPLYPLTKPKGEFSWAPEHQKAFDAIKKALLSAPALALPDVTKPFTLYVDERKGVARGVLTQTLGPWRRPVAYLSKKLDPVASGWPVCLKAI AAVAILVKDADKLTLGQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNPATLLPEETDEPVTHDCHQLLIEETGVRKDLTDIP LTGEVLTWFTDGSSYVVEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSINIYTDSRYAFATAHVHGAIYKQRGWLTSAGREIKN KEEILSLLEALHLPKRLAIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
309	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA

	SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPAPAPAPAPGGTLQL DDEYRLYSPLVKPDQNIQFWLEQFPQAWAETAGMGLAKQVPPQVIQLKASATPVSVRQYPLSKEAQEGIRPHVQRLIQQGILVPVQSPWNTPLLPVRKPG TNDYRPVQDLREVNKRVQDIHPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGTGRTGQLTWTRLPQGFKNSPTIFNEALHR DLANFRIQHPQVTLLQYVDDLLLAGATKQDCLEGTKALLLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWLTEARKKTVVQIPAPTTAKQVREFLG TAGFCRLWIPGFATLAAPLYPLTKPKGEFSWAPEHQKAFDAIKKALLSAPALALPDVTKPFTLYVDERKGVARGVLTQTLGPWRRPVAYLSKKLDPVASG WPVCLKAIAAVAILVKDADKLTLGQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNPATLLPEETDEPVTHDCHQLLIEETGV RKDLTDIPLTGEVLTWFTDGSSYVVEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSINIYTDSRYAFATAHVHGAIYKQRGWLT SAGREIKNKEEILSLLEALHLPKRLAIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
311	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGGGGSEAAAKGGTLQLDD EYRLYSPLVKPDQNIQFWLEQFPQAWAETAGMGLAKQVPPQVIQLKASATPVSVRQYPLSKEAQEGIRPHVQRLIQQGILVPVQSPWNTPLLPVRKPGTN DYRPVQDLREVNKRVQDIHPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGTGRTGQLTWTRLPQGFKNSPTIFNEALHRDL ANFRIQHPQVTLLQYVDDLLLAGATKQDCLEGTKALLLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWLTEARKKTVVQIPAPTTAKQVREFLGTA GFCRLWIPGFATLAAPLYPLTKPKGEFSWAPEHQKAFDAIKKALLSAPALALPDVTKPFTLYVDERKGVARGVLTQTLGPWRRPVAYLSKKLDPVASGWP VCLKAIAAVAILVKDADKLTLGQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNPATLLPEETDEPVTHDCHQLLIEETGVRK DLTDIPLTGEVLTWFTDGSSYVVEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSINIYTDSRYAFATAHVHGAIYKQRGWLTSA GREIKNKEEILSLLEALHLPKRLAIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
313	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ

	SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKEAAAKEAAAKEAAA KEAAAKEAAAKGGTLQLDDEYRLYSPLVKPDQNIQFWLEQFPQAWAETAGMGLAKQVPPQVIQLKASATPVSVRQYPLSKEAQEGIRPHVQRLIQQGILV PVQSPWNTPLLPVRKPGTNDYRPVQDLREVNKRVQDIHPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGTGRTGQLTWTRL PQGFKNSPTIFNEALHRDLANFRIQHPQVTLLQYVDDLLLAGATKQDCLEGTKALLLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWLTEARKKTV VQIPAPTTAKQVREFLGTAGFCRLWIPGFATLAAPLYPLTKPKGEFSWAPEHQKAFDAIKKALLSAPALALPDVTKPFTLYVDERKGVARGVLTQTLGPW RRPVAYLSKKLDPVASGWPVCLKAIAAVAILVKDADKLTLGQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNPATLLPEETD EPVTHDCHQLLIEETGVRKDLTDIPLTGEVLTWFTDGSSYVVEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSINIYTDSRYAF ATAHVHGAIYKQRGWLTSAGREIKNKEEILSLLEALHLPKRLAIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLAGKRTADGSEFEKRTADGSEFE SPKKKAKVE
313	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKEAAAKEAAAKEAAA KEAAAKEAAAKGGTLQLDDEYRLYSPLVKPDQNIQFWLEQFPQAWAETAGMGLAKQVPPQVIQLKASATPVSVRQYPLSKEAQEGIRPHVQRLIQQGILV PVQSPWNTPLLPVRKPGTNDYRPVQDLREVNKRVQDIHPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGTGRTGQLTWTRL PQGFKNSPTIFNEALHRDLANFRIQHPQVTLLQYVDDLLLAGATKQDCLEGTKALLLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWLTEARKKTV VQIPAPTTAKQVREFLGTAGFCRLWIPGFATLAAPLYPLTKPKGEFSWAPEHQKAFDAIKKALLSAPALALPDVTKPFTLYVDERKGVARGVLTQTLGPW RRPVAYLSKKLDPVASGWPVCLKAIAAVAILVKDADKLTLGQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNPATLLPEETD EPVTHDCHQLLIEETGVRKDLTDIPLTGEVLTWFTDGSSYVVEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSINIYTDSRYAF ATAHVHGAIYKQRGWLTSAGREIKNKEEILSLLEALHLPKRLAIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLAGKRTADGSEFEKRTADGSEFE SPKKKAKVE
314	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV

	QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGGPAPGSSGGTLQLDDEY RLYSPLVKPDQNIQFWLEQFPQAWAETAGMGLAKQVPPQVIQLKASATPVSVRQYPLSKEAQEGIRPHVQRLIQQGILVPVQSPWNTPLLPVRKPGTNDY RPVQDLREVNKRVQDIHPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGTGRTGQLTWTRLPQGFKNSPTIFNEALHRDLAN FRIQHPQVTLLQYVDDLLLAGATKQDCLEGTKALLLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWLTEARKKTVVQIPAPTTAKQVREFLGTAGF CRLWIPGFATLAAPLYPLTKPKGEFSWAPEHQKAFDAIKKALLSAPALALPDVTKPFTLYVDERKGVARGVLTQTLGPWRRPVAYLSKKLDPVASGWPVC LKAIAAVAILVKDADKLTLGQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNPATLLPEETDEPVTHDCHQLLIEETGVRKDL TDIPLTGEVLTWFTDGSSYVVEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSINIYTDSRYAFATAHVHGAIYKQRGWLTSAGR EIKNKEEILSLLEALHLPKRLAIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
316	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGSGGSGGSGGSGGSGG GTLQLDDEYRLYSPLVKPDQNIQFWLEQFPQAWAETAGMGLAKQVPPQVIQLKASATPVSVRQYPLSKEAQEGIRPHVQRLIQQGILVPVQSPWNTPLLP VRKPGTNDYRPVQDLREVNKRVQDIHPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGTGRTGQLTWTRLPQGFKNSPTIFN EALHRDLANFRIQHPQVTLLQYVDDLLLAGATKQDCLEGTKALLLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWLTEARKKTVVQIPAPTTAKQV REFLGTAGFCRLWIPGFATLAAPLYPLTKPKGEFSWAPEHQKAFDAIKKALLSAPALALPDVTKPFTLYVDERKGVARGVLTQTLGPWRRPVAYLSKKLD PVASGWPVCLKAIAAVAILVKDADKLTLGQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNPATLLPEETDEPVTHDCHQLLI EETGVRKDLTDIPLTGEVLTWFTDGSSYVVEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSINIYTDSRYAFATAHVHGAIYKQ RGWLTSAGREIKNKEEILSLLEALHLPKRLAIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE

316	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSGGSGGSGGSGGSGG GTLQLDDEYRLYSPLVKPDQNIQFWLEQFPQAWAETAGMGLAKQVPPQVIQLKASATPVSVRQYPLSKEAQEGIRPHVQRLIQQGILVPVQSPWNTPLLP VRKPGTNDYRPVQDLREVNKRVQDIHPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGTGRTGQLTWTRLPQGFKNSPTIFN EALHRDLANFRIQHPQVTLLQYVDDLLLAGATKQDCLEGTKALLLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWLTEARKKTVVQIPAPTTAKQV REFLGTAGFCRLWIPGFATLAAPLYPLTKPKGEFSWAPEHQKAFDAIKKALLSAPALALPDVTKPFTLYVDERKGVARGVLTQTLGPWRRPVAYLSKKLD PVASGWPVCLKAIAAVAILVKDADKLTLGQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNPATLLPEETDEPVTHDCHQLLI EETGVRKDLTDIPLTGEVLTWFTDGSSYVVEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSINIYTDSRYAFATAHVHGAIYKQ RGWLTSAGREIKNKEEILSLLEALHLPKRLAIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
317	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSSGGGEAAAKGGTLQLDD EYRLYSPLVKPDQNIQFWLEQFPQAWAETAGMGLAKQVPPQVIQLKASATPVSVRQYPLSKEAQEGIRPHVQRLIQQGILVPVQSPWNTPLLPVRKPGTN DYRPVQDLREVNKRVQDIHPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGTGRTGQLTWTRLPQGFKNSPTIFNEALHRDL ANFRIQHPQVTLLQYVDDLLLAGATKQDCLEGTKALLLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWLTEARKKTVVQIPAPTTAKQVREFLGTA GFCRLWIPGFATLAAPLYPLTKPKGEFSWAPEHQKAFDAIKKALLSAPALALPDVTKPFTLYVDERKGVARGVLTQTLGPWRRPVAYLSKKLDPVASGWP VCLKAIAAVAILVKDADKLTLGQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNPATLLPEETDEPVTHDCHQLLIEETGVRK

	DLTDIPLTGEVLTWFTDGSSYVVEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSINIYTDSRYAFATAHVHGAIYKQRGWLTSA GREIKNKEEILSLLEALHLPKRLAIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
317	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSSGGGEAAAKGGTLQLDD EYRLYSPLVKPDQNIQFWLEQFPQAWAETAGMGLAKQVPPQVIQLKASATPVSVRQYPLSKEAQEGIRPHVQRLIQQGILVPVQSPWNTPLLPVRKPGTN DYRPVQDLREVNKRVQDIHPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGTGRTGQLTWTRLPQGFKNSPTIFNEALHRDL ANFRIQHPQVTLLQYVDDLLLAGATKQDCLEGTKALLLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWLTEARKKTVVQIPAPTTAKQVREFLGTA GFCRLWIPGFATLAAPLYPLTKPKGEFSWAPEHQKAFDAIKKALLSAPALALPDVTKPFTLYVDERKGVARGVLTQTLGPWRRPVAYLSKKLDPVASGWP VCLKAIAAVAILVKDADKLTLGQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNPATLLPEETDEPVTHDCHQLLIEETGVRK DLTDIPLTGEVLTWFTDGSSYVVEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSINIYTDSRYAFATAHVHGAIYKQRGWLTSA GREIKNKEEILSLLEALHLPKRLAIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
318	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGGSSEAAAKGGTLQLDD EYRLYSPLVKPDQNIQFWLEQFPQAWAETAGMGLAKQVPPQVIQLKASATPVSVRQYPLSKEAQEGIRPHVQRLIQQGILVPVQSPWNTPLLPVRKPGTN DYRPVQDLREVNKRVQDIHPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGTGRTGQLTWTRLPQGFKNSPTIFNEALHRDL ANFRIQHPQVTLLQYVDDLLLAGATKQDCLEGTKALLLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWLTEARKKTVVQIPAPTTAKQVREFLGTA GFCRLWIPGFATLAAPLYPLTKPKGEFSWAPEHQKAFDAIKKALLSAPALALPDVTKPFTLYVDERKGVARGVLTQTLGPWRRPVAYLSKKLDPVASGWP

	VCLKAIAAVAILVKDADKLTLGQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNPATLLPEETDEPVTHDCHQLLIEETGVRK DLTDIPLTGEVLTWFTDGSSYVVEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSINIYTDSRYAFATAHVHGAIYKQRGWLTSA GREIKNKEEILSLLEALHLPKRLAIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
318	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGGGSSEAAAKGGTLQLDD EYRLYSPLVKPDQNIQFWLEQFPQAWAETAGMGLAKQVPPQVIQLKASATPVSVRQYPLSKEAQEGIRPHVQRLIQQGILVPVQSPWNTPLLPVRKPGTN DYRPVQDLREVNKRVQDIHPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGTGRTGQLTWTRLPQGFKNSPTIFNEALHRDL ANFRIQHPQVTLLQYVDDLLLAGATKQDCLEGTKALLLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWLTEARKKTVVQIPAPTTAKQVREFLGTA GFCRLWIPGFATLAAPLYPLTKPKGEFSWAPEHQKAFDAIKKALLSAPALALPDVTKPFTLYVDERKGVARGVLTQTLGPWRRPVAYLSKKLDPVASGWP VCLKAIAAVAILVKDADKLTLGQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNPATLLPEETDEPVTHDCHQLLIEETGVRK DLTDIPLTGEVLTWFTDGSSYVVEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSINIYTDSRYAFATAHVHGAIYKQRGWLTSA GREIKNKEEILSLLEALHLPKRLAIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
319	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPEAAAKGGGGGTLQLDD EYRLYSPLVKPDQNIQFWLEQFPQAWAETAGMGLAKQVPPQVIQLKASATPVSVRQYPLSKEAQEGIRPHVQRLIQQGILVPVQSPWNTPLLPVRKPGTN DYRPVQDLREVNKRVQDIHPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGTGRTGQLTWTRLPQGFKNSPTIFNEALHRDL ANFRIQHPQVTLLQYVDDLLLAGATKQDCLEGTKALLLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWLTEARKKTVVQIPAPTTAKQVREFLGTA

	GFCRLWIPGFATLAAPLYPLTKPKGEFSWAPEHQKAFDAIKKALLSAPALALPDVTKPFTLYVDERKGVARGVLTQTLGPWRRPVAYLSKKLDPVASGWP VCLKAIAAVAILVKDADKLTLGQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNPATLLPEETDEPVTHDCHQLLIEETGVRK DLTDIPLTGEVLTWFTDGSSYVVEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSINIYTDSRYAFATAHVHGAIYKQRGWLTSA GREIKNKEEILSLLEALHLPKRLAIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
320	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGGGGSGSSGGTLQLDDEY RLYSPLVKPDQNIQFWLEQFPQAWAETAGMGLAKQVPPQVIQLKASATPVSVRQYPLSKEAQEGIRPHVQRLIQQGILVPVQSPWNTPLLPVRKPGTNDY RPVQDLREVNKRVQDIHPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGTGRTGQLTWTRLPQGFKNSPTIFNEALHRDLAN FRIQHPQVTLLQYVDDLLLAGATKQDCLEGTKALLLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWLTEARKKTVVQIPAPTTAKQVREFLGTAGF CRLWIPGFATLAAPLYPLTKPKGEFSWAPEHQKAFDAIKKALLSAPALALPDVTKPFTLYVDERKGVARGVLTQTLGPWRRPVAYLSKKLDPVASGWPVC LKAIAAVAILVKDADKLTLGQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNPATLLPEETDEPVTHDCHQLLIEETGVRKDL TDIPLTGEVLTWFTDGSSYVVEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSINIYTDSRYAFATAHVHGAIYKQRGWLTSAGR EIKNKEEILSLLEALHLPKRLAIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
320	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGGGGSGSSGGTLQLDDEY RLYSPLVKPDQNIQFWLEQFPQAWAETAGMGLAKQVPPQVIQLKASATPVSVRQYPLSKEAQEGIRPHVQRLIQQGILVPVQSPWNTPLLPVRKPGTNDY RPVQDLREVNKRVQDIHPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGTGRTGQLTWTRLPQGFKNSPTIFNEALHRDLAN

	FRIQHPQVTLLQYVDDLLLAGATKQDCLEGTKALLLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWLTEARKKTVVQIPAPTTAKQVREFLGTAGF CRLWIPGFATLAAPLYPLTKPKGEFSWAPEHQKAFDAIKKALLSAPALALPDVTKPFTLYVDERKGVARGVLTQTLGPWRRPVAYLSKKLDPVASGWPVC LKAIAAVAILVKDADKLTLGQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNPATLLPEETDEPVTHDCHQLLIEETGVRKDL TDIPLTGEVLTWFTDGSSYVVEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSINIYTDSRYAFATAHVHGAIYKQRGWLTSAGR EIKNKEEILSLLEALHLPKRLAIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
321	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPGGSEAAAKGGTLQLDD EYRLYSPLVKPDQNIQFWLEQFPQAWAETAGMGLAKQVPPQVIQLKASATPVSVRQYPLSKEAQEGIRPHVQRLIQQGILVPVQSPWNTPLLPVRKPGTN DYRPVQDLREVNKRVQDIHPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGTGRTGQLTWTRLPQGFKNSPTIFNEALHRDL ANFRIQHPQVTLLQYVDDLLLAGATKQDCLEGTKALLLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWLTEARKKTVVQIPAPTTAKQVREFLGTA GFCRLWIPGFATLAAPLYPLTKPKGEFSWAPEHQKAFDAIKKALLSAPALALPDVTKPFTLYVDERKGVARGVLTQTLGPWRRPVAYLSKKLDPVASGWP VCLKAIAAVAILVKDADKLTLGQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNPATLLPEETDEPVTHDCHQLLIEETGVRK DLTDIPLTGEVLTWFTDGSSYVVEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSINIYTDSRYAFATAHVHGAIYKQRGWLTSA GREIKNKEEILSLLEALHLPKRLAIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
322	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGGEAAAKGGSGGTLQLDD EYRLYSPLVKPDQNIQFWLEQFPQAWAETAGMGLAKQVPPQVIQLKASATPVSVRQYPLSKEAQEGIRPHVQRLIQQGILVPVQSPWNTPLLPVRKPGTN

	DYRPVQDLREVNKRVQDIHPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGTGRTGQLTWTRLPQGFKNSPTIFNEALHRDL ANFRIQHPQVTLLQYVDDLLLAGATKQDCLEGTKALLLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWLTEARKKTVVQIPAPTTAKQVREFLGTA GFCRLWIPGFATLAAPLYPLTKPKGEFSWAPEHQKAFDAIKKALLSAPALALPDVTKPFTLYVDERKGVARGVLTQTLGPWRRPVAYLSKKLDPVASGWP VCLKAIAAVAILVKDADKLTLGQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNPATLLPEETDEPVTHDCHQLLIEETGVRK DLTDIPLTGEVLTWFTDGSSYVVEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSINIYTDSRYAFATAHVHGAIYKQRGWLTSA GREIKNKEEILSLLEALHLPKRLAIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
324	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGGEAAAKPAPGGTLQLDD EYRLYSPLVKPDQNIQFWLEQFPQAWAETAGMGLAKQVPPQVIQLKASATPVSVRQYPLSKEAQEGIRPHVQRLIQQGILVPVQSPWNTPLLPVRKPGTN DYRPVQDLREVNKRVQDIHPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGTGRTGQLTWTRLPQGFKNSPTIFNEALHRDL ANFRIQHPQVTLLQYVDDLLLAGATKQDCLEGTKALLLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWLTEARKKTVVQIPAPTTAKQVREFLGTA GFCRLWIPGFATLAAPLYPLTKPKGEFSWAPEHQKAFDAIKKALLSAPALALPDVTKPFTLYVDERKGVARGVLTQTLGPWRRPVAYLSKKLDPVASGWP VCLKAIAAVAILVKDADKLTLGQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNPATLLPEETDEPVTHDCHQLLIEETGVRK DLTDIPLTGEVLTWFTDGSSYVVEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSINIYTDSRYAFATAHVHGAIYKQRGWLTSA GREIKNKEEILSLLEALHLPKRLAIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
328	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGSGSETPGTSESATPESGGT

	LQLDDEYRLYSPLVKPDQNIQFWLEQFPQAWAETAGMGLAKQVPPQVIQLKASATPVSVRQYPLSKEAQEGIRPHVQRLIQQGILVPVQSPWNTPLLPVR KPGTNDYRPVQDLREVNKRVQDIHPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGTGRTGQLTWTRLPQGFKNSPTIFNEA LHRDLANFRIQHPQVTLLQYVDDLLLAGATKQDCLEGTKALLLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWLTEARKKTVVQIPAPTTAKQVRE FLGTAGFCRLWIPGFATLAAPLYPLTKPKGEFSWAPEHQKAFDAIKKALLSAPALALPDVTKPFTLYVDERKGVARGVLTQTLGPWRRPVAYLSKKLDPV ASGWPVCLKAIAAVAILVKDADKLTLGQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNPATLLPEETDEPVTHDCHQLLIEE TGVRKDLTDIPLTGEVLTWFTDGSSYVVEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSINIYTDSRYAFATAHVHGAIYKQRG WLTSAGREIKNKEEILSLLEALHLPKRLAIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
332	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPGGGGGTLQLDDEYRLY SPLVKPDQNIQFWLEQFPQAWAETAGMGLAKQVPPQVIQLKASATPVSVRQYPLSKEAQEGIRPHVQRLIQQGILVPVQSPWNTPLLPVRKPGTNDYRPV QDLREVNKRVQDIHPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGTGRTGQLTWTRLPQGFKNSPTIFNEALHRDLANFRI QHPQVTLLQYVDDLLLAGATKQDCLEGTKALLLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWLTEARKKTVVQIPAPTTAKQVREFLGTAGFCRL WIPGFATLAAPLYPLTKPKGEFSWAPEHQKAFDAIKKALLSAPALALPDVTKPFTLYVDERKGVARGVLTQTLGPWRRPVAYLSKKLDPVASGWPVCLKA IAAVAILVKDADKLTLGQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNPATLLPEETDEPVTHDCHQLLIEETGVRKDLTDI PLTGEVLTWFTDGSSYVVEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSINIYTDSRYAFATAHVHGAIYKQRGWLTSAGREIK NKEEILSLLEALHLPKRLAIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
340	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK

	VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPGGGGGSGGTLQLDDEY RLYSPLVKPDQNIQFWLEQFPQAWAETAGMGLAKQVPPQVIQLKASATPVSVRQYPLSKEAQEGIRPHVQRLIQQGILVPVQSPWNTPLLPVRKPGTNDY RPVQDLREVNKRVQDIHPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGTGRTGQLTWTRLPQGFKNSPTIFNEALHRDLAN FRIQHPQVTLLQYVDDLLLAGATKQDCLEGTKALLLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWLTEARKKTVVQIPAPTTAKQVREFLGTAGF CRLWIPGFATLAAPLYPLTKPKGEFSWAPEHQKAFDAIKKALLSAPALALPDVTKPFTLYVDERKGVARGVLTQTLGPWRRPVAYLSKKLDPVASGWPVC LKAIAAVAILVKDADKLTLGQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNPATLLPEETDEPVTHDCHQLLIEETGVRKDL TDIPLTGEVLTWFTDGSSYVVEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSINIYTDSRYAFATAHVHGAIYKQRGWLTSAGR EIKNKEEILSLLEALHLPKRLAIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
341	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKGGSPAPGGTLQLDD EYRLYSPLVKPDQNIQFWLEQFPQAWAETAGMGLAKQVPPQVIQLKASATPVSVRQYPLSKEAQEGIRPHVQRLIQQGILVPVQSPWNTPLLPVRKPGTN DYRPVQDLREVNKRVQDIHPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGTGRTGQLTWTRLPQGFKNSPTIFNEALHRDL ANFRIQHPQVTLLQYVDDLLLAGATKQDCLEGTKALLLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWLTEARKKTVVQIPAPTTAKQVREFLGTA GFCRLWIPGFATLAAPLYPLTKPKGEFSWAPEHQKAFDAIKKALLSAPALALPDVTKPFTLYVDERKGVARGVLTQTLGPWRRPVAYLSKKLDPVASGWP VCLKAIAAVAILVKDADKLTLGQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNPATLLPEETDEPVTHDCHQLLIEETGVRK DLTDIPLTGEVLTWFTDGSSYVVEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSINIYTDSRYAFATAHVHGAIYKQRGWLTSA GREIKNKEEILSLLEALHLPKRLAIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
346	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE

	VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGGPAPEAAAKGGTLQLDD EYRLYSPLVKPDQNIQFWLEQFPQAWAETAGMGLAKQVPPQVIQLKASATPVSVRQYPLSKEAQEGIRPHVQRLIQQGILVPVQSPWNTPLLPVRKPGTN DYRPVQDLREVNKRVQDIHPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGTGRTGQLTWTRLPQGFKNSPTIFNEALHRDL ANFRIQHPQVTLLQYVDDLLLAGATKQDCLEGTKALLLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWLTEARKKTVVQIPAPTTAKQVREFLGTA GFCRLWIPGFATLAAPLYPLTKPKGEFSWAPEHQKAFDAIKKALLSAPALALPDVTKPFTLYVDERKGVARGVLTQTLGPWRRPVAYLSKKLDPVASGWP VCLKAIAAVAILVKDADKLTLGQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNPATLLPEETDEPVTHDCHQLLIEETGVRK DLTDIPLTGEVLTWFTDGSSYVVEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSINIYTDSRYAFATAHVHGAIYKQRGWLTSA GREIKNKEEILSLLEALHLPKRLAIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
352	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGSEAAAKGGGGGTLQLDD EYRLYSPLVKPDQNIQFWLEQFPQAWAETAGMGLAKQVPPQVIQLKASATPVSVRQYPLSKEAQEGIRPHVQRLIQQGILVPVQSPWNTPLLPVRKPGTN DYRPVQDLREVNKRVQDIHPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGTGRTGQLTWTRLPQGFKNSPTIFNEALHRDL ANFRIQHPQVTLLQYVDDLLLAGATKQDCLEGTKALLLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWLTEARKKTVVQIPAPTTAKQVREFLGTA GFCRLWIPGFATLAAPLYPLTKPKGEFSWAPEHQKAFDAIKKALLSAPALALPDVTKPFTLYVDERKGVARGVLTQTLGPWRRPVAYLSKKLDPVASGWP VCLKAIAAVAILVKDADKLTLGQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNPATLLPEETDEPVTHDCHQLLIEETGVRK DLTDIPLTGEVLTWFTDGSSYVVEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSINIYTDSRYAFATAHVHGAIYKQRGWLTSA GREIKNKEEILSLLEALHLPKRLAIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
352	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM

	PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGSEAAAKGGGGGTLQLDD EYRLYSPLVKPDQNIQFWLEQFPQAWAETAGMGLAKQVPPQVIQLKASATPVSVRQYPLSKEAQEGIRPHVQRLIQQGILVPVQSPWNTPLLPVRKPGTN DYRPVQDLREVNKRVQDIHPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGTGRTGQLTWTRLPQGFKNSPTIFNEALHRDL ANFRIQHPQVTLLQYVDDLLLAGATKQDCLEGTKALLLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWLTEARKKTVVQIPAPTTAKQVREFLGTA GFCRLWIPGFATLAAPLYPLTKPKGEFSWAPEHQKAFDAIKKALLSAPALALPDVTKPFTLYVDERKGVARGVLTQTLGPWRRPVAYLSKKLDPVASGWP VCLKAIAAVAILVKDADKLTLGQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNPATLLPEETDEPVTHDCHQLLIEETGVRK DLTDIPLTGEVLTWFTDGSSYVVEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSINIYTDSRYAFATAHVHGAIYKQRGWLTSA GREIKNKEEILSLLEALHLPKRLAIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
358	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKPAPGGGGGTLQLDD EYRLYSPLVKPDQNIQFWLEQFPQAWAETAGMGLAKQVPPQVIQLKASATPVSVRQYPLSKEAQEGIRPHVQRLIQQGILVPVQSPWNTPLLPVRKPGTN DYRPVQDLREVNKRVQDIHPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGTGRTGQLTWTRLPQGFKNSPTIFNEALHRDL ANFRIQHPQVTLLQYVDDLLLAGATKQDCLEGTKALLLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWLTEARKKTVVQIPAPTTAKQVREFLGTA GFCRLWIPGFATLAAPLYPLTKPKGEFSWAPEHQKAFDAIKKALLSAPALALPDVTKPFTLYVDERKGVARGVLTQTLGPWRRPVAYLSKKLDPVASGWP VCLKAIAAVAILVKDADKLTLGQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNPATLLPEETDEPVTHDCHQLLIEETGVRK DLTDIPLTGEVLTWFTDGSSYVVEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSINIYTDSRYAFATAHVHGAIYKQRGWLTSA GREIKNKEEILSLLEALHLPKRLAIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
363	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL

	NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGSGSSEAAAKGGTLQLDD EYRLYSPLVKPDQNIQFWLEQFPQAWAETAGMGLAKQVPPQVIQLKASATPVSVRQYPLSKEAQEGIRPHVQRLIQQGILVPVQSPWNTPLLPVRKPGTN DYRPVQDLREVNKRVQDIHPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGTGRTGQLTWTRLPQGFKNSPTIFNEALHRDL ANFRIQHPQVTLLQYVDDLLLAGATKQDCLEGTKALLLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWLTEARKKTVVQIPAPTTAKQVREFLGTA GFCRLWIPGFATLAAPLYPLTKPKGEFSWAPEHQKAFDAIKKALLSAPALALPDVTKPFTLYVDERKGVARGVLTQTLGPWRRPVAYLSKKLDPVASGWP VCLKAIAAVAILVKDADKLTLGQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNPATLLPEETDEPVTHDCHQLLIEETGVRK DLTDIPLTGEVLTWFTDGSSYVVEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSINIYTDSRYAFATAHVHGAIYKQRGWLTSA GREIKNKEEILSLLEALHLPKRLAIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
365	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSSEAAAKGGGGGTLQLDD EYRLYSPLVKPDQNIQFWLEQFPQAWAETAGMGLAKQVPPQVIQLKASATPVSVRQYPLSKEAQEGIRPHVQRLIQQGILVPVQSPWNTPLLPVRKPGTN DYRPVQDLREVNKRVQDIHPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGTGRTGQLTWTRLPQGFKNSPTIFNEALHRDL ANFRIQHPQVTLLQYVDDLLLAGATKQDCLEGTKALLLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWLTEARKKTVVQIPAPTTAKQVREFLGTA GFCRLWIPGFATLAAPLYPLTKPKGEFSWAPEHQKAFDAIKKALLSAPALALPDVTKPFTLYVDERKGVARGVLTQTLGPWRRPVAYLSKKLDPVASGWP VCLKAIAAVAILVKDADKLTLGQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNPATLLPEETDEPVTHDCHQLLIEETGVRK DLTDIPLTGEVLTWFTDGSSYVVEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSINIYTDSRYAFATAHVHGAIYKQRGWLTSA GREIKNKEEILSLLEALHLPKRLAIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
384	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA

	KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGSGSSGGGGGTLQLDDEY RLYSPLVKPDQNIQFWLEQFPQAWAETAGMGLAKQVPPQVIQLKASATPVSVRQYPLSKEAQEGIRPHVQRLIQQGILVPVQSPWNTPLLPVRKPGTNDY RPVQDLREVNKRVQDIHPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGTGRTGQLTWTRLPQGFKNSPTIFNEALHRDLAN FRIQHPQVTLLQYVDDLLLAGATKQDCLEGTKALLLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWLTEARKKTVVQIPAPTTAKQVREFLGTAGF CRLWIPGFATLAAPLYPLTKPKGEFSWAPEHQKAFDAIKKALLSAPALALPDVTKPFTLYVDERKGVARGVLTQTLGPWRRPVAYLSKKLDPVASGWPVC LKAIAAVAILVKDADKLTLGQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNPATLLPEETDEPVTHDCHQLLIEETGVRKDL TDIPLTGEVLTWFTDGSSYVVEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSINIYTDSRYAFATAHVHGAIYKQRGWLTSAGR EIKNKEEILSLLEALHLPKRLAIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
386	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPGSSGGTLQLDDEYRLY SPLVKPDQNIQFWLEQFPQAWAETAGMGLAKQVPPQVIQLKASATPVSVRQYPLSKEAQEGIRPHVQRLIQQGILVPVQSPWNTPLLPVRKPGTNDYRPV QDLREVNKRVQDIHPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGTGRTGQLTWTRLPQGFKNSPTIFNEALHRDLANFRI QHPQVTLLQYVDDLLLAGATKQDCLEGTKALLLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWLTEARKKTVVQIPAPTTAKQVREFLGTAGFCRL WIPGFATLAAPLYPLTKPKGEFSWAPEHQKAFDAIKKALLSAPALALPDVTKPFTLYVDERKGVARGVLTQTLGPWRRPVAYLSKKLDPVASGWPVCLKA IAAVAILVKDADKLTLGQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNPATLLPEETDEPVTHDCHQLLIEETGVRKDLTDI PLTGEVLTWFTDGSSYVVEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSINIYTDSRYAFATAHVHGAIYKQRGWLTSAGREIK NKEEILSLLEALHLPKRLAIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
392	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK

	ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGGGSGGTLQLDDEYRLYS PLVKPDQNIQFWLEQFPQAWAETAGMGLAKQVPPQVIQLKASATPVSVRQYPLSKEAQEGIRPHVQRLIQQGILVPVQSPWNTPLLPVRKPGTNDYRPVQ DLREVNKRVQDIHPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGTGRTGQLTWTRLPQGFKNSPTIFNEALHRDLANFRIQ HPQVTLLQYVDDLLLAGATKQDCLEGTKALLLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWLTEARKKTVVQIPAPTTAKQVREFLGTAGFCRLW IPGFATLAAPLYPLTKPKGEFSWAPEHQKAFDAIKKALLSAPALALPDVTKPFTLYVDERKGVARGVLTQTLGPWRRPVAYLSKKLDPVASGWPVCLKAI AAVAILVKDADKLTLGQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNPATLLPEETDEPVTHDCHQLLIEETGVRKDLTDIP LTGEVLTWFTDGSSYVVEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSINIYTDSRYAFATAHVHGAIYKQRGWLTSAGREIKN KEEILSLLEALHLPKRLAIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
396	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSSGSSGSSGSSGSSG GTLQLDDEYRLYSPLVKPDQNIQFWLEQFPQAWAETAGMGLAKQVPPQVIQLKASATPVSVRQYPLSKEAQEGIRPHVQRLIQQGILVPVQSPWNTPLLP VRKPGTNDYRPVQDLREVNKRVQDIHPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGTGRTGQLTWTRLPQGFKNSPTIFN EALHRDLANFRIQHPQVTLLQYVDDLLLAGATKQDCLEGTKALLLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWLTEARKKTVVQIPAPTTAKQV REFLGTAGFCRLWIPGFATLAAPLYPLTKPKGEFSWAPEHQKAFDAIKKALLSAPALALPDVTKPFTLYVDERKGVARGVLTQTLGPWRRPVAYLSKKLD PVASGWPVCLKAIAAVAILVKDADKLTLGQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNPATLLPEETDEPVTHDCHQLLI EETGVRKDLTDIPLTGEVLTWFTDGSSYVVEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSINIYTDSRYAFATAHVHGAIYKQ RGWLTSAGREIKNKEEILSLLEALHLPKRLAIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
396	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA

	NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGSSGSSGSSGSSGSSGSSG GTLQLDDEYRLYSPLVKPDQNIQFWLEQFPQAWAETAGMGLAKQVPPQVIQLKASATPVSVRQYPLSKEAQEGIRPHVQRLIQQGILVPVQSPWNTPLLP VRKPGTNDYRPVQDLREVNKRVQDIHPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGTGRTGQLTWTRLPQGFKNSPTIFN EALHRDLANFRIQHPQVTLLQYVDDLLLAGATKQDCLEGTKALLLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWLTEARKKTVVQIPAPTTAKQV REFLGTAGFCRLWIPGFATLAAPLYPLTKPKGEFSWAPEHQKAFDAIKKALLSAPALALPDVTKPFTLYVDERKGVARGVLTQTLGPWRRPVAYLSKKLD PVASGWPVCLKAIAAVAILVKDADKLTLGQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNPATLLPEETDEPVTHDCHQLLI EETGVRKDLTDIPLTGEVLTWFTDGSSYVVEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSINIYTDSRYAFATAHVHGAIYKQ RGWLTSAGREIKNKEEILSLLEALHLPKRLAIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
480	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGAEAAAKEAAAKEAAAKEAA AKALEAEAAAKEAAAKEAAAKEAAAKAGGMDPLQLLQPLEAEIKGTKLKAHWNSGATITCVPEAFLEDERPIQTMLIKTIHGEKQQDVYYLTFKVQGRKV EAEVLASPYDYILLNPSDVPWLMKKPLQLTVLVPLHEYQERLLQQTALPKEQKELLQKLFLKYDALWQHWENQVGHRRIKPHNIATGTLAPRPQKQYPIN PKAKPSIQIVIDDLLKQGVLIQQNSTMNTPVYPVPKPDGKWRMVLDYREVNKTIPLIAAQNQHSAGILSSIYRGKYKTTLDLTNGFWAHPITPESYWLTA FTWQGKQYCWTRLPQGFLNSPALFNADVVDLLKEIPNVQAYVDDIYISHDDPQEHLEQLEKIFSILLNAGYVVSLKKSEIAQREVEFLGFNITKEGRGLT DTFKQKLLNITPPKDLKQLQSILGKLNFARNFIPNYSELVKPLYTIVAPANGKFISWTEDNSNQLQHIISVLNQADNLEERNPETRLIIKVNSSPSAGYI RYYNEGSKRPIMYVNYIFSKAEAKFTQTEKLLTTMHKGLIKAMDLAMGQEILVYSPIVSMTKIQRTPLPERKALPVRWITWMTYLEDPRIQFHYDKSLPE LQQIPNVTEDVIAKTKHPSEFAMVFYTDGSAIKHPDVNKSHSAGMGIAQVQFIPEYKIVHQWSIPLGDHTAQLAEIAAVEFACKKALKISGPVLIVTDSF YVAESANKELPYWKSNGFLNNKKKPLRHVSKWKSIAECLQLKPDIIIMHEKGHQQPMTTLHTEGNNLADKLATQGSYVVHAGKRTADGSEFEKRTADGSE FESPKKKAKVE
550	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL

	LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKEAAAKEAAAKEAAA KEAAAKEAAAKGGIPWLMKKPLQLTTLVPLQEYEERLLKQTMLTGSYKEKLQSLFLKYDALWQHWENQVGHRRIKPHHIATGTVNPRPQKQYPINPKAKA SIQTVINDLLKQGVLIQQNSIMNTPVYPVPKPDGKWRMVLDYREVNKTIPLIAAQNQHSAGILSSIFRGKYKTTLDLSNGFWAHSITPESYWLTAFTWLG QQYCWTRLPQGFLNSPALFNADVVDLLKEVPNVQVYVDDIYISHDDPREHLEQLEKVFSLLLNAGYVVSLKKSEIAQHEVEFLGFNITKEGRGLTETFKQ KLLNITPPRDLKQLQSILGKLNFARNFIPNFSELVKPLYNIIATAPGKYITWTTDNSQQLQNIISMLNSAENLEERNPEVRLIMKVNTSPSAGYIRFYNE FAKRPIMYLNYVYTKAEVKFTNTEKLLTTIHKGLIKALDLGMGQEILVYSPIVSMTKIQKTPLPERKALPIRWITWMSYLEDPRIQFHYDKTLPELQQVP TVTDDIIAKIKHPSEFSMVFYTDGSAIKHPNVNKSHNAGMGIAQVQFKPEFTVINTWSIPLGDHTAQLAEVAAVEFACKKALKIDGPVLIVTDSFYVAES VNKELPYWQSNGFFNNKKKPLKHVSKWKSIADCIQLKPDIIIIHEKGHQPTASTFHTEGNNLADKLATQGSYVVNAGKRTADGSEFEKRTADGSEFESPK KKAKVE
590	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKEAAAKEAAAKEAAA KEAAAKEAAAKGGMDPLQLLQPLEAEIKGTKLKAHWNSGATITCVPQAFLEEEVPIKNIWIKTIHGEKEQPVYYLTFKIQGRKVEAEVISSPYDYILVSP SDIPWLMKKPLQLTTLVPLQEYEERLLKQTMLTGSYKEKLQSLFLKYDALWQHWENQVGHRRIKPHHIATGTVNPRPQKQYPINPKAKASIQTVINDLLK QGVLIQQNSIMNTPVYPVPKPDGKWRMVLDYREVNKTIPLIAAQNQHSAGILSSIFRGKYKTTLDLSNGFWAHSITPESYWLTAFTWLGQQYCWTRLPQG FLNSPALFNADVVDLLKEVPNVQVYVDDIYISHDDPREHLEQLEKVFSLLLNAGYVVSLKKSEIAQHEVEFLGFNITKEGRGLTETFKQKLLNITPPRDL KQLQSILGLLNFARNFIPNFSELVKPLYNIIATAPGKYITWTTDNSQQLQNIISMLNSAENLEERNPEVRLIMKVNTSPSAGYIRFYNEFAKRPIMYLNY VYTKAEVKFTNTEKLLTTIHKGLIKALDLGMGQEILVYSPIVSMTKIQKTPLPERKALPIRWITWMSYLEDPRIQFHYDKTLPELQQVPTVTDDIIAKIK HPSEFSMVFYTDGSAIKHPNVNKSHNAGMGIAQVQFKPEFTVINTWSIPLGDHTAQLAEVAAVEFACKKALKIDGPVLIVTDSFYVAESVNKELPYWQSN GFFNNKKKPLKHVSKWKSIADCIQLKPDIIIIHEKGHQPTASTFHTEGNNLADKLATQGSYVVNAGKRTADGSEFEKRTADGSEFESPKKKAKVE

591	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGAEAAAKEAAAKEAAAKEAA AKALEAEAAAKEAAAKEAAAKEAAAKAGGMDPLQLLQPLEAEIKGTKLKAHWNSGATITCVPQAFLEEEVPIKNIWIKTIHGEKEQPVYYLTFKIQGRKV EAEVISSPYDYILVSPSDIPWLMKKPLQLTTLVPLQEYEERLLKQTMLTGSYKEKLQSLFLKYDALWQHWENQVGHRRIKPHHIATGTVNPRPQKQYPIN PKAKASIQTVINDLLKQGVLIQQNSIMNTPVYPVPKPDGKWRMVLDYREVNKTIPLIAAQNQHSAGILSSIFRGKYKTTLDLSNGFWAHSITPESYWLTA FTWLGQQYCWTRLPQGFLNSPALFNADVVDLLKEVPNVQVYVDDIYISHDDPREHLEQLEKVFSLLLNAGYVVSLKKSEIAQHEVEFLGFNITKEGRGLT ETFKQKLLNITPPRDLKQLQSILGLLNFARNFIPNFSELVKPLYNIIATAPGKYITWTTDNSQQLQNIISMLNSAENLEERNPEVRLIMKVNTSPSAGYI RFYNEFAKRPIMYLNYVYTKAEVKFTNTEKLLTTIHKGLIKALDLGMGQEILVYSPIVSMTKIQKTPLPERKALPIRWITWMSYLEDPRIQFHYDKTLPE LQQVPTVTDDIIAKIKHPSEFSMVFYTDGSAIKHPNVNKSHNAGMGIAQVQFKPEFTVINTWSIPLGDHTAQLAEVAAVEFACKKALKIDGPVLIVTDSF YVAESVNKELPYWQSNGFFNNKKKPLKHVSKWKSIADCIQLKPDIIIIHEKGHQPTASTFHTEGNNLADKLATQGSYVVNAGKRTADGSEFEKRTADGSE FESPKKKAKVE
647	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGAEAAAKEAAAKEAAAKEAA AKALEAEAAAKEAAAKEAAAKEAAAKAGGMDPLQLLQPLEAEIKGTKLKAHWNSGATITCVPQAFLEEEVPIKNIWIKTIHGEKEQPVYYLTFKIQGRKV EAEVISSPYDYILVSPSDIPWLMKKPLQLTTLVPLQEYEERLLKQTMLTGSYKEKLQSLFLKYDALWQHWENQVGHRRIKPHHIATGTVNPRPQKQYPIN PKAKASIQTVINDLLKQGVLIQQNSIMNTPVYPVPKPDGKWRMVLDYREVNKTIPLIAAQNQHSAGILSSIFRGKYKTTLDLSNGFWAHSITPESYWLTA FTWLGQQYCWTRLPQGFLNSPALFNADVVDLLKEVPNVQVYVDDIYISHDDPREHLEQLEKVFSLLLNAGYVVSLKKSEIAQHEVEFLGFNITKEGRGLT

	ETFKQKLLNITPPRDLKQLQSILGKLNFARNFIPNFSELVKPLYNIIATAPGKYITWTTDNSQQLQNIISMLNSAENLEERNPEVRLIMKVNTSPSAGYI RFYNEFAKRPIMYLNYVYTKAEVKFTNTEKLLTTIHKGLIKALDLGMGQEILVYSPIVSMTKIQKTPLPERKALPIRWITWMSYLEDPRIQFHYDKTLPE LQQVPTVTDDIIAKIKHPSEFSMVFYTDGSAIKHPNVNKSHNAGMGIAQVQFKPEFTVINTWSIPLGDHTAQLAEVAAVEFACKKALKIDGPVLIVTDSF YVAESVNKELPYWQSNGFFNNKKKPLKHVSKWKSIADCIQLKPDIIIIHEKGHQPTASTFHTEGNNLADKLATQGSYVVNAGKRTADGSEFEKRTADGSE FESPKKKAKVE
715	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGAEAAAKEAAAKEAAAKEAA AKALEAEAAAKEAAAKEAAAKEAAAKAGGMDLLKPLTVERKGVKIKGYWNSQADITCVPKDLLQGEEPVRQQNVTTIHGTQEGDVYYVNLKIDGRRINTE VIGTTLDYAIITPGDVPWILKKPLELTIKLDLEEQQGTLLNNSILSKKGKEELKQLFEKYSALWQSWENQVGHRRIRPHKIATGTVKPTPQKQYHINPKA KPDIQIVINDLLKQGVLIQKESTMNTPVYPVPKPNGRWRMVLDYRAVNKVTPLIAVQNQHSYGILGSLFKGRYKTTIDLSNGFWAHPIVPEDYWITAFTW QGKQYCWTVLPQGFLNSPGLFTGDVVDLLQGIPNVEVYVDDVYISHDSEKEHLEYLDILFNRLKEAGYIISLKKSNIANSIVDFLGFQITNEGRGLTDTF KEKLENITAPTTLKQLQSILGLLNFARNFIPDFTELIAPLYALIPKSTKNYVPWQIEHSTTLETLITKLNGAEYLQGRKGDKTLIMKVNASYTTGYIRYY NEGEKKPISYVSIVFSKTELKFTELEKLLTTVHKGLLKALDLSMGQNIHVYSPIVSMQNIQKTPQTAKKALASRWLSWLSYLEDPRIRFFYDPQMPALKD LPAVDTGKDNKKHPSNFQHIFYTDGSAITSPTKEGHLNAGMGIVYFINKDGNLQKQQEWSISLGNHTAQFAEIAAFEFALKKCLPLGGNILVVTDSNYVA KAYNEELDVWASNGFVNNRKKPLKHISKWKSVADLKRLRPDVVVTHEPGHQKLDSSPHAYGNNLADQLATQASFKVHAGKRTADGSEFEKRTADGSEFES PKKKAKVE
800	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK

	VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGGGGSEAAAKGGVLNLEE EYRLHEKPVPSSIDPSWLQLFPTVWAERAGMGLANQVPPVVVELRSGASPVAVRQYPMSKEAREGIRPHIQRFLDLGVLVPCQSPWNTPLLPVKKPGTND YRPVQDLREINKRVQDIHPTVPNPYNLLSSLPPSHTWYSVLDLKDAFFCLKLHPNSQPLFAFEWRDPEKGNTGQLTWTRLPQGFKNSPTLFNEALHRDLA PFRALNPQVVLLQYVDDLLVAAPTYRDCKEGTQKLLQELSKLGYRVSAKKAQLCQKEVTYLGYLLKEGKRWLTPARKATVMKIPPPTTPRQVREFLGTAG FCRLWIPGFASLAAPLYPLTKPSIPFIWTEEHQKAFDRIKEALLSAPALALPDLTKPFTLYVDERAGVARGVLTQTLGPWRRPVAYLSKKLDPVASGWPT CLKAVAAVALLLKDADKLTLGQNVTVIASHSLESIVRQPPDRWMTNARMTHYQSLLLNERVSFAPPAVLNPATLLPVESEATPVHRCSEILAEETGTRRD LKDQPLPGVPAWYTDGSSFIAEGKRRAGAAIVDGKRTVWASSLPEGTSAQKAELVALTQALRLAEGKDINIYTDSRYAFATAHIHGAIYKQRGWLTSAGK DIKNKEEILALLEAIHLPKRVAIIHCPGHQKGNDPVATGNRRADEAAKQAALSTRVLAETTKPAGKRTADGSEFEKRTADGSEFESPKKKAKVE
801	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGAEAAAKEAAAKEAAAKEAA AKALEAEAAAKEAAAKEAAAKEAAAKAGGVLNLEEEYRLHEKPVPSSIDPSWLQLFPTVWAERAGMGLANQVPPVVVELRSGASPVAVRQYPMSKEAREG IRPHIQRFLDLGVLVPCQSPWNTPLLPVKKPGTNDYRPVQDLREINKRVQDIHPTVPNPYNLLSSLPPSHTWYSVLDLKDAFFCLKLHPNSQPLFAFEWR DPEKGNTGQLTWTRLPQGFKNSPTLFNEALHRDLAPFRALNPQVVLLQYVDDLLVAAPTYRDCKEGTQKLLQELSKLGYRVSAKKAQLCQKEVTYLGYLL KEGKRWLTPARKATVMKIPPPTTPRQVREFLGTAGFCRLWIPGFASLAAPLYPLTKPSIPFIWTEEHQKAFDRIKEALLSAPALALPDLTKPFTLYVDER AGVARGVLTQTLGPWRRPVAYLSKKLDPVASGWPTCLKAVAAVALLLKDADKLTLGQNVTVIASHSLESIVRQPPDRWMTNARMTHYQSLLLNERVSFAP PAVLNPATLLPVESEATPVHRCSEILAEETGTRRDLKDQPLPGVPAWYTDGSSFIAEGKRRAGAAIVDGKRTVWASSLPEGTSAQKAELVALTQALRLAE GKDINIYTDSRYAFATAHIHGAIYKQRGWLTSAGKDIKNKEEILALLEAIHLPKRVAIIHCPGHQKGNDPVATGNRRADEAAKQAALSTRVLAETTKPAG KRTADGSEFEKRTADGSEFESPKKKAKVE
804	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM

	PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGGGSSGGSGGVLNLEEEY RLHEKPVPSSIDPSWLQLFPTVWAERAGMGLANQVPPVVVELRSGASPVAVRQYPMSKEAREGIRPHIQRFLDLGVLVPCQSPWNTPLLPVKKPGTNDYR PVQDLREINKRVQDIHPTVPNPYNLLSSLPPSHTWYSVLDLKDAFFCLKLHPNSQPLFAFEWRDPEKGNTGQLTWTRLPQGFKNSPTLFNEALHRDLAPF RALNPQVVLLQYVDDLLVAAPTYRDCKEGTQKLLQELSKLGYRVSAKKAQLCQKEVTYLGYLLKEGKRWLTPARKATVMKIPPPTTPRQVREFLGTAGFC RLWIPGFASLAAPLYPLTKPSIPFIWTEEHQKAFDRIKEALLSAPALALPDLTKPFTLYVDERAGVARGVLTQTLGPWRRPVAYLSKKLDPVASGWPTCL KAVAAVALLLKDADKLTLGQNVTVIASHSLESIVRQPPDRWMTNARMTHYQSLLLNERVSFAPPAVLNPATLLPVESEATPVHRCSEILAEETGTRRDLK DQPLPGVPAWYTDGSSFIAEGKRRAGAAIVDGKRTVWASSLPEGTSAQKAELVALTQALRLAEGKDINIYTDSRYAFATAHIHGAIYKQRGWLTSAGKDI KNKEEILALLEAIHLPKRVAIIHCPGHQKGNDPVATGNRRADEAAKQAALSTRVLAETTKPAGKRTADGSEFEKRTADGSEFESPKKKAKVE
805	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGGGGGGVLNLEEEYRLH EKPVPSSIDPSWLQLFPTVWAERAGMGLANQVPPVVVELRSGASPVAVRQYPMSKEAREGIRPHIQRFLDLGVLVPCQSPWNTPLLPVKKPGTNDYRPVQ DLREINKRVQDIHPTVPNPYNLLSSLPPSHTWYSVLDLKDAFFCLKLHPNSQPLFAFEWRDPEKGNTGQLTWTRLPQGFKNSPTLFNEALHRDLAPFRAL NPQVVLLQYVDDLLVAAPTYRDCKEGTQKLLQELSKLGYRVSAKKAQLCQKEVTYLGYLLKEGKRWLTPARKATVMKIPPPTTPRQVREFLGTAGFCRLW IPGFASLAAPLYPLTKPSIPFIWTEEHQKAFDRIKEALLSAPALALPDLTKPFTLYVDERAGVARGVLTQTLGPWRRPVAYLSKKLDPVASGWPTCLKAV AAVALLLKDADKLTLGQNVTVIASHSLESIVRQPPDRWMTNARMTHYQSLLLNERVSFAPPAVLNPATLLPVESEATPVHRCSEILAEETGTRRDLKDQP LPGVPAWYTDGSSFIAEGKRRAGAAIVDGKRTVWASSLPEGTSAQKAELVALTQALRLAEGKDINIYTDSRYAFATAHIHGAIYKQRGWLTSAGKDIKNK EEILALLEAIHLPKRVAIIHCPGHQKGNDPVATGNRRADEAAKQAALSTRVLAETTKPAGKRTADGSEFEKRTADGSEFESPKKKAKVE
806	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL

	NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGSGSETPGTSESATPESGGV LNLEEEYRLHEKPVPSSIDPSWLQLFPTVWAERAGMGLANQVPPVVVELRSGASPVAVRQYPMSKEAREGIRPHIQRFLDLGVLVPCQSPWNTPLLPVKK PGTNDYRPVQDLREINKRVQDIHPTVPNPYNLLSSLPPSHTWYSVLDLKDAFFCLKLHPNSQPLFAFEWRDPEKGNTGQLTWTRLPQGFKNSPTLFNEAL HRDLAPFRALNPQVVLLQYVDDLLVAAPTYRDCKEGTQKLLQELSKLGYRVSAKKAQLCQKEVTYLGYLLKEGKRWLTPARKATVMKIPPPTTPRQVREF LGTAGFCRLWIPGFASLAAPLYPLTKPSIPFIWTEEHQKAFDRIKEALLSAPALALPDLTKPFTLYVDERAGVARGVLTQTLGPWRRPVAYLSKKLDPVA SGWPTCLKAVAAVALLLKDADKLTLGQNVTVIASHSLESIVRQPPDRWMTNARMTHYQSLLLNERVSFAPPAVLNPATLLPVESEATPVHRCSEILAEET GTRRDLKDQPLPGVPAWYTDGSSFIAEGKRRAGAAIVDGKRTVWASSLPEGTSAQKAELVALTQALRLAEGKDINIYTDSRYAFATAHIHGAIYKQRGWL TSAGKDIKNKEEILALLEAIHLPKRVAIIHCPGHQKGNDPVATGNRRADEAAKQAALSTRVLAETTKPAGKRTADGSEFEKRTADGSEFESPKKKAKVE
818	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGSSGSSGSSGSSGSSGSSG GVLNLEEEYRLHEKPVPSSIDPSWLQLFPTVWAERAGMGLANQVPPVVVELRSGASPVAVRQYPMSKEAREGIRPHIQRFLDLGVLVPCQSPWNTPLLPV KKPGTNDYRPVQDLREINKRVQDIHPTVPNPYNLLSSLPPSHTWYSVLDLKDAFFCLKLHPNSQPLFAFEWRDPEKGNTGQLTWTRLPQGFKNSPTLFNE ALHRDLAPFRALNPQVVLLQYVDDLLVAAPTYRDCKEGTQKLLQELSKLGYRVSAKKAQLCQKEVTYLGYLLKEGKRWLTPARKATVMKIPPPTTPRQVR EFLGTAGFCRLWIPGFASLAAPLYPLTKPSIPFIWTEEHQKAFDRIKEALLSAPALALPDLTKPFTLYVDERAGVARGVLTQTLGPWRRPVAYLSKKLDP VASGWPTCLKAVAAVALLLKDADKLTLGQNVTVIASHSLESIVRQPPDRWMTNARMTHYQSLLLNERVSFAPPAVLNPATLLPVESEATPVHRCSEILAE ETGTRRDLKDQPLPGVPAWYTDGSSFIAEGKRRAGAAIVDGKRTVWASSLPEGTSAQKAELVALTQALRLAEGKDINIYTDSRYAFATAHIHGAIYKQRG WLTSAGKDIKNKEEILALLEAIHLPKRVAIIHCPGHQKGNDPVATGNRRADEAAKQAALSTRVLAETTKPAGKRTADGSEFEKRTADGSEFESPKKKAKV E
819	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK

	ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPEAAAKGGVLNLEEEYR LHEKPVPSSIDPSWLQLFPTVWAERAGMGLANQVPPVVVELRSGASPVAVRQYPMSKEAREGIRPHIQRFLDLGVLVPCQSPWNTPLLPVKKPGTNDYRP VQDLREINKRVQDIHPTVPNPYNLLSSLPPSHTWYSVLDLKDAFFCLKLHPNSQPLFAFEWRDPEKGNTGQLTWTRLPQGFKNSPTLFNEALHRDLAPFR ALNPQVVLLQYVDDLLVAAPTYRDCKEGTQKLLQELSKLGYRVSAKKAQLCQKEVTYLGYLLKEGKRWLTPARKATVMKIPPPTTPRQVREFLGTAGFCR LWIPGFASLAAPLYPLTKPSIPFIWTEEHQKAFDRIKEALLSAPALALPDLTKPFTLYVDERAGVARGVLTQTLGPWRRPVAYLSKKLDPVASGWPTCLK AVAAVALLLKDADKLTLGQNVTVIASHSLESIVRQPPDRWMTNARMTHYQSLLLNERVSFAPPAVLNPATLLPVESEATPVHRCSEILAEETGTRRDLKD QPLPGVPAWYTDGSSFIAEGKRRAGAAIVDGKRTVWASSLPEGTSAQKAELVALTQALRLAEGKDINIYTDSRYAFATAHIHGAIYKQRGWLTSAGKDIK NKEEILALLEAIHLPKRVAIIHCPGHQKGNDPVATGNRRADEAAKQAALSTRVLAETTKPAGKRTADGSEFEKRTADGSEFESPKKKAKVE
871	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGAEAAAKEAAAKEAAAKEAA AKALEAEAAAKEAAAKEAAAKEAAAKAGGVLNLEEEYRLHEKPVPSSIDPSWLQLFPTVWAERAGMGLANQVPPVVVELRSGASPVAVRQYPMSKEAREG IRPHIQRFLDLGVLVPCQSPWNTPLLPVKKPGTNDYRPVQDLREINKRVQDIHPTVPNPYNLLSSLPPSHTWYSVLDLKDAFFCLKLHPNSQPLFAFEWR DPEKGNTGQLTWTRLPQGFKNSPTLFNEALHRDLAPFRALNPQVVLLQYVDDLLVAAPTYRDCKEGTQKLLQELSKLGYRVSAKKAQLCQKEVTYLGYLL KEGKRWLTPARKATVMKIPPPTTPRQVREFLGKAGFCRLFIPGFASLAAPLYPLTKPSIPFIWTEEHQKAFDRIKEALLSAPALALPDLTKPFTLYVDER AGVARGVLTQTLGPWRRPVAYLSKKLDPVASGWPTCLKAVAAVALLLKDADKLTLGQNVTVIASHSLESIVRQPPDRWMTNARMTHYQSLLLNERVSFAP PAVLNPATLLPVESEATPVHRCSEILAEETGTRRDLKDQPLPGVPAWYTDGSSFIAEGKRRAGAAIVDGKRTVWASSLPEGTSAQKAELVALTQALRLAE GKDINIYTDSRYAFATAHIHGAIYKQRGWLTSAGKDIKNKEEILALLEAIHLPKRVAIIHCPGHQKGNDPVATGNRRADEAAKQAALSTRVLAETTKPAG KRTADGSEFEKRTADGSEFESPKKKAKVE
872	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA

	SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPGGGGSSGGVLNLEEEY RLHEKPVPSSIDPSWLQLFPTVWAERAGMGLANQVPPVVVELRSGASPVAVRQYPMSKEAREGIRPHIQRFLDLGVLVPCQSPWNTPLLPVKKPGTNDYR PVQDLREINKRVQDIHPTVPNPYNLLSSLPPSHTWYSVLDLKDAFFCLKLHPNSQPLFAFEWRDPEKGNTGQLTWTRLPQGFKNSPTLFNEALHRDLAPF RALNPQVVLLQYVDDLLVAAPTYRDCKEGTQKLLQELSKLGYRVSAKKAQLCQKEVTYLGYLLKEGKRWLTPARKATVMKIPPPTTPRQVREFLGKAGFC RLFIPGFASLAAPLYPLTKPSIPFIWTEEHQKAFDRIKEALLSAPALALPDLTKPFTLYVDERAGVARGVLTQTLGPWRRPVAYLSKKLDPVASGWPTCL KAVAAVALLLKDADKLTLGQNVTVIASHSLESIVRQPPDRWMTNARMTHYQSLLLNERVSFAPPAVLNPATLLPVESEATPVHRCSEILAEETGTRRDLK DQPLPGVPAWYTDGSSFIAEGKRRAGAAIVDGKRTVWASSLPEGTSAQKAELVALTQALRLAEGKDINIYTDSRYAFATAHIHGAIYKQRGWLTSAGKDI KNKEEILALLEAIHLPKRVAIIHCPGHQKGNDPVATGNRRADEAAKQAALSTRVLAETTKPAGKRTADGSEFEKRTADGSEFESPKKKAKVE
873	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGGSGGGGSGGGGSGGGG SGGGGSGGVLNLEEEYRLHEKPVPSSIDPSWLQLFPTVWAERAGMGLANQVPPVVVELRSGASPVAVRQYPMSKEAREGIRPHIQRFLDLGVLVPCQSPW NTPLLPVKKPGTNDYRPVQDLREINKRVQDIHPTVPNPYNLLSSLPPSHTWYSVLDLKDAFFCLKLHPNSQPLFAFEWRDPEKGNTGQLTWTRLPQGFKN SPTLFNEALHRDLAPFRALNPQVVLLQYVDDLLVAAPTYRDCKEGTQKLLQELSKLGYRVSAKKAQLCQKEVTYLGYLLKEGKRWLTPARKATVMKIPPP TTPRQVREFLGKAGFCRLFIPGFASLAAPLYPLTKPSIPFIWTEEHQKAFDRIKEALLSAPALALPDLTKPFTLYVDERAGVARGVLTQTLGPWRRPVAY LSKKLDPVASGWPTCLKAVAAVALLLKDADKLTLGQNVTVIASHSLESIVRQPPDRWMTNARMTHYQSLLLNERVSFAPPAVLNPATLLPVESEATPVHR CSEILAEETGTRRDLKDQPLPGVPAWYTDGSSFIAEGKRRAGAAIVDGKRTVWASSLPEGTSAQKAELVALTQALRLAEGKDINIYTDSRYAFATAHIHG AIYKQRGWLTSAGKDIKNKEEILALLEAIHLPKRVAIIHCPGHQKGNDPVATGNRRADEAAKQAALSTRVLAETTKPAGKRTADGSEFEKRTADGSEFES PKKKAKVE
874	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL

	LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKPAPGSSGGVLNLEE EYRLHEKPVPSSIDPSWLQLFPTVWAERAGMGLANQVPPVVVELRSGASPVAVRQYPMSKEAREGIRPHIQRFLDLGVLVPCQSPWNTPLLPVKKPGTND YRPVQDLREINKRVQDIHPTVPNPYNLLSSLPPSHTWYSVLDLKDAFFCLKLHPNSQPLFAFEWRDPEKGNTGQLTWTRLPQGFKNSPTLFNEALHRDLA PFRALNPQVVLLQYVDDLLVAAPTYRDCKEGTQKLLQELSKLGYRVSAKKAQLCQKEVTYLGYLLKEGKRWLTPARKATVMKIPPPTTPRQVREFLGKAG FCRLFIPGFASLAAPLYPLTKPSIPFIWTEEHQKAFDRIKEALLSAPALALPDLTKPFTLYVDERAGVARGVLTQTLGPWRRPVAYLSKKLDPVASGWPT CLKAVAAVALLLKDADKLTLGQNVTVIASHSLESIVRQPPDRWMTNARMTHYQSLLLNERVSFAPPAVLNPATLLPVESEATPVHRCSEILAEETGTRRD LKDQPLPGVPAWYTDGSSFIAEGKRRAGAAIVDGKRTVWASSLPEGTSAQKAELVALTQALRLAEGKDINIYTDSRYAFATAHIHGAIYKQRGWLTSAGK DIKNKEEILALLEAIHLPKRVAIIHCPGHQKGNDPVATGNRRADEAAKQAALSTRVLAETTKPAGKRTADGSEFEKRTADGSEFESPKKKAKVE
876	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSSGGVLNLEEEYRLHEKP VPSSIDPSWLQLFPTVWAERAGMGLANQVPPVVVELRSGASPVAVRQYPMSKEAREGIRPHIQRFLDLGVLVPCQSPWNTPLLPVKKPGTNDYRPVQDLR EINKRVQDIHPTVPNPYNLLSSLPPSHTWYSVLDLKDAFFCLKLHPNSQPLFAFEWRDPEKGNTGQLTWTRLPQGFKNSPTLFNEALHRDLAPFRALNPQ VVLLQYVDDLLVAAPTYRDCKEGTQKLLQELSKLGYRVSAKKAQLCQKEVTYLGYLLKEGKRWLTPARKATVMKIPPPTTPRQVREFLGKAGFCRLFIPG FASLAAPLYPLTKPSIPFIWTEEHQKAFDRIKEALLSAPALALPDLTKPFTLYVDERAGVARGVLTQTLGPWRRPVAYLSKKLDPVASGWPTCLKAVAAV ALLLKDADKLTLGQNVTVIASHSLESIVRQPPDRWMTNARMTHYQSLLLNERVSFAPPAVLNPATLLPVESEATPVHRCSEILAEETGTRRDLKDQPLPG VPAWYTDGSSFIAEGKRRAGAAIVDGKRTVWASSLPEGTSAQKAELVALTQALRLAEGKDINIYTDSRYAFATAHIHGAIYKQRGWLTSAGKDIKNKEEI LALLEAIHLPKRVAIIHCPGHQKGNDPVATGNRRADEAAKQAALSTRVLAETTKPAGKRTADGSEFEKRTADGSEFESPKKKAKVE
878	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL

	FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGGPAPGGSGGVLNLEEEY RLHEKPVPSSIDPSWLQLFPTVWAERAGMGLANQVPPVVVELRSGASPVAVRQYPMSKEAREGIRPHIQRFLDLGVLVPCQSPWNTPLLPVKKPGTNDYR PVQDLREINKRVQDIHPTVPNPYNLLSSLPPSHTWYSVLDLKDAFFCLKLHPNSQPLFAFEWRDPEKGNTGQLTWTRLPQGFKNSPTLFNEALHRDLAPF RALNPQVVLLQYVDDLLVAAPTYRDCKEGTQKLLQELSKLGYRVSAKKAQLCQKEVTYLGYLLKEGKRWLTPARKATVMKIPPPTTPRQVREFLGKAGFC RLFIPGFASLAAPLYPLTKPSIPFIWTEEHQKAFDRIKEALLSAPALALPDLTKPFTLYVDERAGVARGVLTQTLGPWRRPVAYLSKKLDPVASGWPTCL KAVAAVALLLKDADKLTLGQNVTVIASHSLESIVRQPPDRWMTNARMTHYQSLLLNERVSFAPPAVLNPATLLPVESEATPVHRCSEILAEETGTRRDLK DQPLPGVPAWYTDGSSFIAEGKRRAGAAIVDGKRTVWASSLPEGTSAQKAELVALTQALRLAEGKDINIYTDSRYAFATAHIHGAIYKQRGWLTSAGKDI KNKEEILALLEAIHLPKRVAIIHCPGHQKGNDPVATGNRRADEAAKQAALSTRVLAETTKPAGKRTADGSEFEKRTADGSEFESPKKKAKVE
880	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPGGSGSSGGVLNLEEEY RLHEKPVPSSIDPSWLQLFPTVWAERAGMGLANQVPPVVVELRSGASPVAVRQYPMSKEAREGIRPHIQRFLDLGVLVPCQSPWNTPLLPVKKPGTNDYR PVQDLREINKRVQDIHPTVPNPYNLLSSLPPSHTWYSVLDLKDAFFCLKLHPNSQPLFAFEWRDPEKGNTGQLTWTRLPQGFKNSPTLFNEALHRDLAPF RALNPQVVLLQYVDDLLVAAPTYRDCKEGTQKLLQELSKLGYRVSAKKAQLCQKEVTYLGYLLKEGKRWLTPARKATVMKIPPPTTPRQVREFLGKAGFC RLFIPGFASLAAPLYPLTKPSIPFIWTEEHQKAFDRIKEALLSAPALALPDLTKPFTLYVDERAGVARGVLTQTLGPWRRPVAYLSKKLDPVASGWPTCL KAVAAVALLLKDADKLTLGQNVTVIASHSLESIVRQPPDRWMTNARMTHYQSLLLNERVSFAPPAVLNPATLLPVESEATPVHRCSEILAEETGTRRDLK DQPLPGVPAWYTDGSSFIAEGKRRAGAAIVDGKRTVWASSLPEGTSAQKAELVALTQALRLAEGKDINIYTDSRYAFATAHIHGAIYKQRGWLTSAGKDI KNKEEILALLEAIHLPKRVAIIHCPGHQKGNDPVATGNRRADEAAKQAALSTRVLAETTKPAGKRTADGSEFEKRTADGSEFESPKKKAKVE
882	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV

	QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGGGGGGVLNLEEEYRLH EKPVPSSIDPSWLQLFPTVWAERAGMGLANQVPPVVVELRSGASPVAVRQYPMSKEAREGIRPHIQRFLDLGVLVPCQSPWNTPLLPVKKPGTNDYRPVQ DLREINKRVQDIHPTVPNPYNLLSSLPPSHTWYSVLDLKDAFFCLKLHPNSQPLFAFEWRDPEKGNTGQLTWTRLPQGFKNSPTLFNEALHRDLAPFRAL NPQVVLLQYVDDLLVAAPTYRDCKEGTQKLLQELSKLGYRVSAKKAQLCQKEVTYLGYLLKEGKRWLTPARKATVMKIPPPTTPRQVREFLGKAGFCRLF IPGFASLAAPLYPLTKPSIPFIWTEEHQKAFDRIKEALLSAPALALPDLTKPFTLYVDERAGVARGVLTQTLGPWRRPVAYLSKKLDPVASGWPTCLKAV AAVALLLKDADKLTLGQNVTVIASHSLESIVRQPPDRWMTNARMTHYQSLLLNERVSFAPPAVLNPATLLPVESEATPVHRCSEILAEETGTRRDLKDQP LPGVPAWYTDGSSFIAEGKRRAGAAIVDGKRTVWASSLPEGTSAQKAELVALTQALRLAEGKDINIYTDSRYAFATAHIHGAIYKQRGWLTSAGKDIKNK EEILALLEAIHLPKRVAIIHCPGHQKGNDPVATGNRRADEAAKQAALSTRVLAETTKPAGKRTADGSEFEKRTADGSEFESPKKKAKVE
883	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSSEAAAKGGVLNLEEEYR LHEKPVPSSIDPSWLQLFPTVWAERAGMGLANQVPPVVVELRSGASPVAVRQYPMSKEAREGIRPHIQRFLDLGVLVPCQSPWNTPLLPVKKPGTNDYRP VQDLREINKRVQDIHPTVPNPYNLLSSLPPSHTWYSVLDLKDAFFCLKLHPNSQPLFAFEWRDPEKGNTGQLTWTRLPQGFKNSPTLFNEALHRDLAPFR ALNPQVVLLQYVDDLLVAAPTYRDCKEGTQKLLQELSKLGYRVSAKKAQLCQKEVTYLGYLLKEGKRWLTPARKATVMKIPPPTTPRQVREFLGKAGFCR LFIPGFASLAAPLYPLTKPSIPFIWTEEHQKAFDRIKEALLSAPALALPDLTKPFTLYVDERAGVARGVLTQTLGPWRRPVAYLSKKLDPVASGWPTCLK AVAAVALLLKDADKLTLGQNVTVIASHSLESIVRQPPDRWMTNARMTHYQSLLLNERVSFAPPAVLNPATLLPVESEATPVHRCSEILAEETGTRRDLKD QPLPGVPAWYTDGSSFIAEGKRRAGAAIVDGKRTVWASSLPEGTSAQKAELVALTQALRLAEGKDINIYTDSRYAFATAHIHGAIYKQRGWLTSAGKDIK NKEEILALLEAIHLPKRVAIIHCPGHQKGNDPVATGNRRADEAAKQAALSTRVLAETTKPAGKRTADGSEFEKRTADGSEFESPKKKAKVE

884	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSSPAPGGVLNLEEEYRLH EKPVPSSIDPSWLQLFPTVWAERAGMGLANQVPPVVVELRSGASPVAVRQYPMSKEAREGIRPHIQRFLDLGVLVPCQSPWNTPLLPVKKPGTNDYRPVQ DLREINKRVQDIHPTVPNPYNLLSSLPPSHTWYSVLDLKDAFFCLKLHPNSQPLFAFEWRDPEKGNTGQLTWTRLPQGFKNSPTLFNEALHRDLAPFRAL NPQVVLLQYVDDLLVAAPTYRDCKEGTQKLLQELSKLGYRVSAKKAQLCQKEVTYLGYLLKEGKRWLTPARKATVMKIPPPTTPRQVREFLGKAGFCRLF IPGFASLAAPLYPLTKPSIPFIWTEEHQKAFDRIKEALLSAPALALPDLTKPFTLYVDERAGVARGVLTQTLGPWRRPVAYLSKKLDPVASGWPTCLKAV AAVALLLKDADKLTLGQNVTVIASHSLESIVRQPPDRWMTNARMTHYQSLLLNERVSFAPPAVLNPATLLPVESEATPVHRCSEILAEETGTRRDLKDQP LPGVPAWYTDGSSFIAEGKRRAGAAIVDGKRTVWASSLPEGTSAQKAELVALTQALRLAEGKDINIYTDSRYAFATAHIHGAIYKQRGWLTSAGKDIKNK EEILALLEAIHLPKRVAIIHCPGHQKGNDPVATGNRRADEAAKQAALSTRVLAETTKPAGKRTADGSEFEKRTADGSEFESPKKKAKVE
890	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPAPAPAPAPGGVLNL EEEYRLHEKPVPSSIDPSWLQLFPTVWAERAGMGLANQVPPVVVELRSGASPVAVRQYPMSKEAREGIRPHIQRFLDLGVLVPCQSPWNTPLLPVKKPGT NDYRPVQDLREINKRVQDIHPTVPNPYNLLSSLPPSHTWYSVLDLKDAFFCLKLHPNSQPLFAFEWRDPEKGNTGQLTWTRLPQGFKNSPTLFNEALHRD LAPFRALNPQVVLLQYVDDLLVAAPTYRDCKEGTQKLLQELSKLGYRVSAKKAQLCQKEVTYLGYLLKEGKRWLTPARKATVMKIPPPTTPRQVREFLGK AGFCRLFIPGFASLAAPLYPLTKPSIPFIWTEEHQKAFDRIKEALLSAPALALPDLTKPFTLYVDERAGVARGVLTQTLGPWRRPVAYLSKKLDPVASGW PTCLKAVAAVALLLKDADKLTLGQNVTVIASHSLESIVRQPPDRWMTNARMTHYQSLLLNERVSFAPPAVLNPATLLPVESEATPVHRCSEILAEETGTR

	RDLKDQPLPGVPAWYTDGSSFIAEGKRRAGAAIVDGKRTVWASSLPEGTSAQKAELVALTQALRLAEGKDINIYTDSRYAFATAHIHGAIYKQRGWLTSA GKDIKNKEEILALLEAIHLPKRVAIIHCPGHQKGNDPVATGNRRADEAAKQAALSTRVLAETTKPAGKRTADGSEFEKRTADGSEFESPKKKAKVE
898	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGSPAPEAAAKGGVLNLEE EYRLHEKPVPSSIDPSWLQLFPTVWAERAGMGLANQVPPVVVELRSGASPVAVRQYPMSKEAREGIRPHIQRFLDLGVLVPCQSPWNTPLLPVKKPGTND YRPVQDLREINKRVQDIHPTVPNPYNLLSSLPPSHTWYSVLDLKDAFFCLKLHPNSQPLFAFEWRDPEKGNTGQLTWTRLPQGFKNSPTLFNEALHRDLA PFRALNPQVVLLQYVDDLLVAAPTYRDCKEGTQKLLQELSKLGYRVSAKKAQLCQKEVTYLGYLLKEGKRWLTPARKATVMKIPPPTTPRQVREFLGKAG FCRLFIPGFASLAAPLYPLTKPSIPFIWTEEHQKAFDRIKEALLSAPALALPDLTKPFTLYVDERAGVARGVLTQTLGPWRRPVAYLSKKLDPVASGWPT CLKAVAAVALLLKDADKLTLGQNVTVIASHSLESIVRQPPDRWMTNARMTHYQSLLLNERVSFAPPAVLNPATLLPVESEATPVHRCSEILAEETGTRRD LKDQPLPGVPAWYTDGSSFIAEGKRRAGAAIVDGKRTVWASSLPEGTSAQKAELVALTQALRLAEGKDINIYTDSRYAFATAHIHGAIYKQRGWLTSAGK DIKNKEEILALLEAIHLPKRVAIIHCPGHQKGNDPVATGNRRADEAAKQAALSTRVLAETTKPAGKRTADGSEFEKRTADGSEFESPKKKAKVE
900	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKGGGGSEAAAKGGVL NLEEEYRLHEKPVPSSIDPSWLQLFPTVWAERAGMGLANQVPPVVVELRSGASPVAVRQYPMSKEAREGIRPHIQRFLDLGVLVPCQSPWNTPLLPVKKP GTNDYRPVQDLREINKRVQDIHPTVPNPYNLLSSLPPSHTWYSVLDLKDAFFCLKLHPNSQPLFAFEWRDPEKGNTGQLTWTRLPQGFKNSPTLFNEALH RDLAPFRALNPQVVLLQYVDDLLVAAPTYRDCKEGTQKLLQELSKLGYRVSAKKAQLCQKEVTYLGYLLKEGKRWLTPARKATVMKIPPPTTPRQVREFL GKAGFCRLFIPGFASLAAPLYPLTKPSIPFIWTEEHQKAFDRIKEALLSAPALALPDLTKPFTLYVDERAGVARGVLTQTLGPWRRPVAYLSKKLDPVAS

	GWPTCLKAVAAVALLLKDADKLTLGQNVTVIASHSLESIVRQPPDRWMTNARMTHYQSLLLNERVSFAPPAVLNPATLLPVESEATPVHRCSEILAEETG TRRDLKDQPLPGVPAWYTDGSSFIAEGKRRAGAAIVDGKRTVWASSLPEGTSAQKAELVALTQALRLAEGKDINIYTDSRYAFATAHIHGAIYKQRGWLT SAGKDIKNKEEILALLEAIHLPKRVAIIHCPGHQKGNDPVATGNRRADEAAKQAALSTRVLAETTKPAGKRTADGSEFEKRTADGSEFESPKKKAKVE
901	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGGEAAAKGGSGGVLNLEE EYRLHEKPVPSSIDPSWLQLFPTVWAERAGMGLANQVPPVVVELRSGASPVAVRQYPMSKEAREGIRPHIQRFLDLGVLVPCQSPWNTPLLPVKKPGTND YRPVQDLREINKRVQDIHPTVPNPYNLLSSLPPSHTWYSVLDLKDAFFCLKLHPNSQPLFAFEWRDPEKGNTGQLTWTRLPQGFKNSPTLFNEALHRDLA PFRALNPQVVLLQYVDDLLVAAPTYRDCKEGTQKLLQELSKLGYRVSAKKAQLCQKEVTYLGYLLKEGKRWLTPARKATVMKIPPPTTPRQVREFLGKAG FCRLFIPGFASLAAPLYPLTKPSIPFIWTEEHQKAFDRIKEALLSAPALALPDLTKPFTLYVDERAGVARGVLTQTLGPWRRPVAYLSKKLDPVASGWPT CLKAVAAVALLLKDADKLTLGQNVTVIASHSLESIVRQPPDRWMTNARMTHYQSLLLNERVSFAPPAVLNPATLLPVESEATPVHRCSEILAEETGTRRD LKDQPLPGVPAWYTDGSSFIAEGKRRAGAAIVDGKRTVWASSLPEGTSAQKAELVALTQALRLAEGKDINIYTDSRYAFATAHIHGAIYKQRGWLTSAGK DIKNKEEILALLEAIHLPKRVAIIHCPGHQKGNDPVATGNRRADEAAKQAALSTRVLAETTKPAGKRTADGSEFEKRTADGSEFESPKKKAKVE
912	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGSEAAAKPAPGGVLNLEE EYRLHEKPVPSSIDPSWLQLFPTVWAERAGMGLANQVPPVVVELRSGASPVAVRQYPMSKEAREGIRPHIQRFLDLGVLVPCQSPWNTPLLPVKKPGTND YRPVQDLREINKRVQDIHPTVPNPYNLLSSLPPSHTWYSVLDLKDAFFCLKLHPNSQPLFAFEWRDPEKGNTGQLTWTRLPQGFKNSPTLFNEALHRDLA PFRALNPQVVLLQYVDDLLVAAPTYRDCKEGTQKLLQELSKLGYRVSAKKAQLCQKEVTYLGYLLKEGKRWLTPARKATVMKIPPPTTPRQVREFLGKAG

	FCRLFIPGFASLAAPLYPLTKPSIPFIWTEEHQKAFDRIKEALLSAPALALPDLTKPFTLYVDERAGVARGVLTQTLGPWRRPVAYLSKKLDPVASGWPT CLKAVAAVALLLKDADKLTLGQNVTVIASHSLESIVRQPPDRWMTNARMTHYQSLLLNERVSFAPPAVLNPATLLPVESEATPVHRCSEILAEETGTRRD LKDQPLPGVPAWYTDGSSFIAEGKRRAGAAIVDGKRTVWASSLPEGTSAQKAELVALTQALRLAEGKDINIYTDSRYAFATAHIHGAIYKQRGWLTSAGK DIKNKEEILALLEAIHLPKRVAIIHCPGHQKGNDPVATGNRRADEAAKQAALSTRVLAETTKPAGKRTADGSEFEKRTADGSEFESPKKKAKVE
915	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSSGGSEAAAKGGVLNLEE EYRLHEKPVPSSIDPSWLQLFPTVWAERAGMGLANQVPPVVVELRSGASPVAVRQYPMSKEAREGIRPHIQRFLDLGVLVPCQSPWNTPLLPVKKPGTND YRPVQDLREINKRVQDIHPTVPNPYNLLSSLPPSHTWYSVLDLKDAFFCLKLHPNSQPLFAFEWRDPEKGNTGQLTWTRLPQGFKNSPTLFNEALHRDLA PFRALNPQVVLLQYVDDLLVAAPTYRDCKEGTQKLLQELSKLGYRVSAKKAQLCQKEVTYLGYLLKEGKRWLTPARKATVMKIPPPTTPRQVREFLGKAG FCRLFIPGFASLAAPLYPLTKPSIPFIWTEEHQKAFDRIKEALLSAPALALPDLTKPFTLYVDERAGVARGVLTQTLGPWRRPVAYLSKKLDPVASGWPT CLKAVAAVALLLKDADKLTLGQNVTVIASHSLESIVRQPPDRWMTNARMTHYQSLLLNERVSFAPPAVLNPATLLPVESEATPVHRCSEILAEETGTRRD LKDQPLPGVPAWYTDGSSFIAEGKRRAGAAIVDGKRTVWASSLPEGTSAQKAELVALTQALRLAEGKDINIYTDSRYAFATAHIHGAIYKQRGWLTSAGK DIKNKEEILALLEAIHLPKRVAIIHCPGHQKGNDPVATGNRRADEAAKQAALSTRVLAETTKPAGKRTADGSEFEKRTADGSEFESPKKKAKVE
929	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSSGGSSGGSSGGVLNLEEEY RLHEKPVPSSIDPSWLQLFPTVWAERAGMGLANQVPPVVVELRSGASPVAVRQYPMSKEAREGIRPHIQRFLDLGVLVPCQSPWNTPLLPVKKPGTNDYR PVQDLREINKRVQDIHPTVPNPYNLLSSLPPSHTWYSVLDLKDAFFCLKLHPNSQPLFAFEWRDPEKGNTGQLTWTRLPQGFKNSPTLFNEALHRDLAPF

	RALNPQVVLLQYVDDLLVAAPTYRDCKEGTQKLLQELSKLGYRVSAKKAQLCQKEVTYLGYLLKEGKRWLTPARKATVMKIPPPTTPRQVREFLGKAGFC RLFIPGFASLAAPLYPLTKPSIPFIWTEEHQKAFDRIKEALLSAPALALPDLTKPFTLYVDERAGVARGVLTQTLGPWRRPVAYLSKKLDPVASGWPTCL KAVAAVALLLKDADKLTLGQNVTVIASHSLESIVRQPPDRWMTNARMTHYQSLLLNERVSFAPPAVLNPATLLPVESEATPVHRCSEILAEETGTRRDLK DQPLPGVPAWYTDGSSFIAEGKRRAGAAIVDGKRTVWASSLPEGTSAQKAELVALTQALRLAEGKDINIYTDSRYAFATAHIHGAIYKQRGWLTSAGKDI KNKEEILALLEAIHLPKRVAIIHCPGHQKGNDPVATGNRRADEAAKQAALSTRVLAETTKPAGKRTADGSEFEKRTADGSEFESPKKKAKVE
933	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKEAAAKEAAAKGGVL NLEEEYRLHEKPVPSSIDPSWLQLFPTVWAERAGMGLANQVPPVVVELRSGASPVAVRQYPMSKEAREGIRPHIQRFLDLGVLVPCQSPWNTPLLPVKKP GTNDYRPVQDLREINKRVQDIHPTVPNPYNLLSSLPPSHTWYSVLDLKDAFFCLKLHPNSQPLFAFEWRDPEKGNTGQLTWTRLPQGFKNSPTLFNEALH RDLAPFRALNPQVVLLQYVDDLLVAAPTYRDCKEGTQKLLQELSKLGYRVSAKKAQLCQKEVTYLGYLLKEGKRWLTPARKATVMKIPPPTTPRQVREFL GKAGFCRLFIPGFASLAAPLYPLTKPSIPFIWTEEHQKAFDRIKEALLSAPALALPDLTKPFTLYVDERAGVARGVLTQTLGPWRRPVAYLSKKLDPVAS GWPTCLKAVAAVALLLKDADKLTLGQNVTVIASHSLESIVRQPPDRWMTNARMTHYQSLLLNERVSFAPPAVLNPATLLPVESEATPVHRCSEILAEETG TRRDLKDQPLPGVPAWYTDGSSFIAEGKRRAGAAIVDGKRTVWASSLPEGTSAQKAELVALTQALRLAEGKDINIYTDSRYAFATAHIHGAIYKQRGWLT SAGKDIKNKEEILALLEAIHLPKRVAIIHCPGHQKGNDPVATGNRRADEAAKQAALSTRVLAETTKPAGKRTADGSEFEKRTADGSEFESPKKKAKVE
958	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSGGSGGSGGSGGSGG GTLNIEDEYRLHETSKEPDVPLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLL

	PVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLF NEALHRDLADFRIQHPDLILLQYVDDLLLAATSEQDCQRGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQ LREFLGTAGFCRLWIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKL DPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEKEAPHDCLEIL AETHGTRPDLTDQPIPDADYTWYTDGSSFLQEGQRRAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHVHGEIYR RRGWLTSEGREIKNKNEILALLKALFLPKRLSIIHCPGHQKGNSAEARGNRMADQAARE AAMKAVLETSTLLAGKRTADGSEFEKRTADGSEFESPKKKA KVE
960	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKGSSPAPGGTLNIED EYRLHETSKEPDVPLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGT NDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRD LADFRIQHPDLILLQYVDDLLLAATSEQDCQRGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGT AGFCRLWIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGW PPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEKEAPHDCLEILAETHGTR PDLTDQPIPDADYTWYTDGSSFLQEGQRRAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHVHGEIYRRRGWLTS EGREIKNKNEILALLKALFLPKRLSIIHCPGHQKGNSAEARGNRMADQAARE AAMKAVLETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
961	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK

	VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKPAPGGSGGTLNIED EYRLHETSKEPDVPLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGT NDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRD LADFRIQHPDLILLQYVDDLLLAATSEQDCQRGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGT AGFCRLWIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGW PPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEKEAPHDCLEILAETHGTR PDLTDQPIPDADYTWYTDGSSFLQEGQRRAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHVHGEIYRRRGWLTS EGREIKNKNEILALLKALFLPKRLSIIHCPGHQKGNSAEARGNRMADQAARE AAMKAVLETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
963	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKGGGPAPGGTLNIED EYRLHETSKEPDVPLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGT NDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRD LADFRIQHPDLILLQYVDDLLLAATSEQDCQRGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGT AGFCRLWIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGW PPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEKEAPHDCLEILAETHGTR PDLTDQPIPDADYTWYTDGSSFLQEGQRRAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHVHGEIYRRRGWLTS EGREIKNKNEILALLKALFLPKRLSIIHCPGHQKGNSAEARGNRMADQAARE AAMKAVLETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
964	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE

	VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSSGSSGSSGSSGSSGGTL NIEDEYRLHETSKEPDVPLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVK KPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEA LHRDLADFRIQHPDLILLQYVDDLLLAATSEQDCQRGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLRE FLGTAGFCRLWIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPV AAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEKEAPHDCLEILAET HGTRPDLTDQPIPDADYTWYTDGSSFLQEGQRRAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHVHGEIYRRRG WLTSEGREIKNKNEILALLKALFLPKRLSIIHCPGHQKGNSAEARGNRMADQAAREAAMKAVLETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
966	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSSEAAAKGGTLNIEDEYR LHETSKEPDVPLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDY RPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLAD FRIQHPDLILLQYVDDLLLAATSEQDCQRGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGTAGF CRLWIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPC LRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEKEAPHDCLEILAETHGTRPDL TDQPIPDADYTWYTDGSSFLQEGQRRAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHVHGEIYRRRGWLTSEGR EIKNKNEILALLKALFLPKRLSIIHCPGHQKGNSAEARGNRMADQAAREAAMKAVLETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
967	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM

	PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPGSSEAAAKGGTLNIED EYRLHETSKEPDVPLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGT NDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRD LADFRIQHPDLILLQYVDDLLLAATSEQDCQRGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGT AGFCRLWIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGW PPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEKEAPHDCLEILAETHGTR PDLTDQPIPDADYTWYTDGSSFLQEGQRRAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHVHGEIYRRRGWLTS EGREIKNKNEILALLKALFLPKRLSIIHCPGHQKGNSAEARGNRMADQAAREAAMKAVLETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
978	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPAPAPAPGGTLNIEDEY RLHETSKEPDVPLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTND YRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLA DFRIQHPDLILLQYVDDLLLAATSEQDCQRGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGTAG FCRLWIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPP CLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEKEAPHDCLEILAETHGTRPD LTDQPIPDADYTWYTDGSSFLQEGQRRAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHVHGEIYRRRGWLTSEG REIKNKNEILALLKALFLPKRLSIIHCPGHQKGNSAEARGNRMADQAAREAAMKAVLETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
987	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL

	NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSSPAPGGSGGTLNIEDEY RLHETSKEPDVPLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTND YRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLA DFRIQHPDLILLQYVDDLLLAATSEQDCQRGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGTAG FCRLWIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPP CLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEKEAPHDCLEILAETHGTRPD LTDQPIPDADYTWYTDGSSFLQEGQRRAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHVHGEIYRRRGWLTSEG REIKNKNEILALLKALFLPKRLSIIHCPGHQKGNSAEARGNRMADQAAREAAMKAVLETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
1006	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGAEAAAKEAAAKEAAAKEAA AKALEAEAAAKEAAAKEAAAKEAAAKAGGTLNIEDEYRLHETSKEPDVPLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEAR LGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFE WRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSEQDCQRGTRALLQTLGNLGYRASAKKAQICQKQVKYLGY LLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVD EKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQ FGPVVALNPATLLPLPEKEAPHDCLEILAETHGTRPDLTDQPIPDADYTWYTDGSSFLQEGQRRAGAAVTTETEVIWARALPAGTSAQRAELIALTQALK MAEGKKLNVYTDSRYAFATAHVHGEIYRRRGWLTSEGREIKNKNEILALLKALFLPKRLSIIHCPGHQKGNSAEARGNRMADQAAREAAMKAVLETSTLL AGKRTADGSEFEKRTADGSEFESPKKKAKVE
1007	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK

	ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPEAAAKGSSGGTLNIED EYRLHETSKEPDVPLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGT NDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRD LADFRIQHPDLILLQYVDDLLLAATSEQDCQRGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGK AGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGW PPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEKEAPHDCLEILAETHGTR PDLTDQPIPDADYTWYTDGSSFLQEGQRRAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHVHGEIYRRRGWLTS EGREIKNKNEILALLKALFLPKRLSIIHCPGHQKGNSAEARGNRMADQAAREAAMKAVLETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
1008	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKEAAAKEAAAKEAAA KGGTLNIEDEYRLHETSKEPDVPLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTP LLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPT LFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSEQDCQRGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTP RQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSK KLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEKEAPHDCLE ILAETHGTRPDLTDQPIPDADYTWYTDGSSFLQEGQRRAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHVHGEI YRRRGWLTSEGREIKNKNEILALLKALFLPKRLSIIHCPGHQKGNSAEARGNRMADQAAREAAMKAVLETSTLLAGKRTADGSEFEKRTADGSEFESPKK KAKVE
1009	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA

	SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKGGTLNIEDEYRLHE TSKEPDVPLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPV QDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRI QHPDLILLQYVDDLLLAATSEQDCQRGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRL FIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRM VAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEKEAPHDCLEILAETHGTRPDLTDQ PIPDADYTWYTDGSSFLQEGQRRAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHVHGEIYRRRGWLTSEGREIK NKNEILALLKALFLPKRLSIIHCPGHQKGNSAEARGNRMADQAAREAAMKAVLETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
1011	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSSGGTLNIEDEYRLHETS KEPDVPLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQD LREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQH PDLILLQYVDDLLLAATSEQDCQRGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFI PGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVA AIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEKEAPHDCLEILAETHGTRPDLTDQPI PDADYTWYTDGSSFLQEGQRRAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHVHGEIYRRRGWLTSEGREIKNK NEILALLKALFLPKRLSIIHCPGHQKGNSAEARGNRMADQAAREAAMKAVLETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
1012	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ

	SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKGSSGGGGGTLNIED EYRLHETSKEPDVPLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGT NDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRD LADFRIQHPDLILLQYVDDLLLAATSEQDCQRGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGK AGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGW PPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEKEAPHDCLEILAETHGTR PDLTDQPIPDADYTWYTDGSSFLQEGQRRAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHVHGEIYRRRGWLTS EGREIKNKNEILALLKALFLPKRLSIIHCPGHQKGNSAEARGNRMADQAAREAAMKAVLETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
1015	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGGGGSPAPGGTLNIEDEY RLHETSKEPDVPLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTND YRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLA DFRIQHPDLILLQYVDDLLLAATSEQDCQRGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAG FCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPP CLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEKEAPHDCLEILAETHGTRPD LTDQPIPDADYTWYTDGSSFLQEGQRRAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHVHGEIYRRRGWLTSEG REIKNKNEILALLKALFLPKRLSIIHCPGHQKGNSAEARGNRMADQAAREAAMKAVLETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
1016	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL

	LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGSGSSGGTLNIEDEYRLH ETSKEPDVPLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRP VQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFR IQHPDLILLQYVDDLLLAATSEQDCQRGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCR LFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLR MVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEKEAPHDCLEILAETHGTRPDLTD QPIPDADYTWYTDGSSFLQEGQRRAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHVHGEIYRRRGWLTSEGREI KNKNEILALLKALFLPKRLSIIHCPGHQKGNSAEARGNRMADQAAREAAMKAVLETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
1017	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGSPAPGGTLNIEDEYRLH ETSKEPDVPLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRP VQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFR IQHPDLILLQYVDDLLLAATSEQDCQRGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCR LFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLR MVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEKEAPHDCLEILAETHGTRPDLTD QPIPDADYTWYTDGSSFLQEGQRRAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHVHGEIYRRRGWLTSEGREI KNKNEILALLKALFLPKRLSIIHCPGHQKGNSAEARGNRMADQAAREAAMKAVLETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
1018	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL

	FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGGEAAAKGGSGGTLNIED EYRLHETSKEPDVPLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGT NDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRD LADFRIQHPDLILLQYVDDLLLAATSEQDCQRGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGK AGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGW PPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEKEAPHDCLEILAETHGTR PDLTDQPIPDADYTWYTDGSSFLQEGQRRAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHVHGEIYRRRGWLTS EGREIKNKNEILALLKALFLPKRLSIIHCPGHQKGNSAEARGNRMADQAAREAAMKAVLETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
1019	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGSGGSGGSGGSGGTLNIE DEYRLHETSKEPDVPLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPG TNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHR DLADFRIQHPDLILLQYVDDLLLAATSEQDCQRGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLG KAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAG WPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEKEAPHDCLEILAETHGT RPDLTDQPIPDADYTWYTDGSSFLQEGQRRAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHVHGEIYRRRGWLT SEGREIKNKNEILALLKALFLPKRLSIIHCPGHQKGNSAEARGNRMADQAAREAAMKAVLETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
1020	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV

	QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPAPAPAPAPAPGGTLNI EDEYRLHETSKEPDVPLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKP GTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALH RDLADFRIQHPDLILLQYVDDLLLAATSEQDCQRGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFL GKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAA GWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEKEAPHDCLEILAETHG TRPDLTDQPIPDADYTWYTDGSSFLQEGQRRAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHVHGEIYRRRGWL TSEGREIKNKNEILALLKALFLPKRLSIIHCPGHQKGNSAEARGNRMADQAAREAAMKAVLETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
1021	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGGGSGGGGSGGGGSGGGG SGGGGSGGGGSGGTLNIEDEYRLHETSKEPDVPLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGIL VPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTR LPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSEQDCQRGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKET VMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGP WRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLP EKEAPHDCLEILAETHGTRPDLTDQPIPDADYTWYTDGSSFLQEGQRRAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYA FATAHVHGEIYRRRGWLTSEGREIKNKNEILALLKALFLPKRLSIIHCPGHQKGNSAEARGNRMADQAAREAAMKAVLETSTLLAGKRTADGSEFEKRTA DGSEFESPKKKAKVE

1022	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSGSSGGGGTLNIEDEY RLHETSKEPDVPLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTND YRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLA DFRIQHPDLILLQYVDDLLLAATSEQDCQRGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAG FCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPP CLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEKEAPHDCLEILAETHGTRPD LTDQPIPDADYTWYTDGSSFLQEGQRRAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHVHGEIYRRRGWLTSEG REIKNKNEILALLKALFLPKRLSIIHCPGHQKGNSAEARGNRMADQAAREAAMKAVLETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
1023	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKGGSGGTLNIEDEYR LHETSKEPDVPLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDY RPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLAD FRIQHPDLILLQYVDDLLLAATSEQDCQRGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGF CRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPC LRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEKEAPHDCLEILAETHGTRPDL

	TDQPIPDADYTWYTDGSSFLQEGQRRAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHVHGEIYRRRGWLTSEGR EIKNKNEILALLKALFLPKRLSIIHCPGHQKGNSAEARGNRMADQAAREAAMKAVLETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
1025	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGPAPGGSGGTLNIEDEY RLHETSKEPDVPLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTND YRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLA DFRIQHPDLILLQYVDDLLLAATSEQDCQRGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAG FCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPP CLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEKEAPHDCLEILAETHGTRPD LTDQPIPDADYTWYTDGSSFLQEGQRRAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHVHGEIYRRRGWLTSEG REIKNKNEILALLKALFLPKRLSIIHCPGHQKGNSAEARGNRMADQAAREAAMKAVLETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
1029	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKEAAAKEAAAKEAAA KEAAAKGGTLNIEDEYRLHETSKEPDVPLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQS PWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGF KNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSEQDCQRGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQP TPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPV

	AYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEKEAP HDCLEILAETHGTRPDLTDQPIPDADYTWYTDGSSFLQEGQRRAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAH VHGEIYRRRGWLTSEGREIKNKNEILALLKALFLPKRLSIIHCPGHQKGNSAEARGNRMADQAAREAAMKAVLETSTLLAGKRTADGSEFEKRTADGSEF ESPKKKAKVE
1033	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPGSSGGGGGTLNIEDEY RLHETSKEPDVPLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTND YRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLA DFRIQHPDLILLQYVDDLLLAATSEQDCQRGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAG FCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPP CLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEKEAPHDCLEILAETHGTRPD LTDQPIPDADYTWYTDGSSFLQEGQRRAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHVHGEIYRRRGWLTSEG REIKNKNEILALLKALFLPKRLSIIHCPGHQKGNSAEARGNRMADQAAREAAMKAVLETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
1034	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPGGSEAAAKGGTLNIED EYRLHETSKEPDVPLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGT NDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRD

	LADFRIQHPDLILLQYVDDLLLAATSEQDCQRGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGK AGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGW PPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEKEAPHDCLEILAETHGTR PDLTDQPIPDADYTWYTDGSSFLQEGQRRAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHVHGEIYRRRGWLTS EGREIKNKNEILALLKALFLPKRLSIIHCPGHQKGNSAEARGNRMADQAAREAAMKAVLETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
1037	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKGGGGSEAAAKGGTL NIEDEYRLHETSKEPDVPLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVK KPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEA LHRDLADFRIQHPDLILLQYVDDLLLAATSEQDCQRGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLRE FLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPV AAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEKEAPHDCLEILAET HGTRPDLTDQPIPDADYTWYTDGSSFLQEGQRRAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHVHGEIYRRRG WLTSEGREIKNKNEILALLKALFLPKRLSIIHCPGHQKGNSAEARGNRMADQAAREAAMKAVLETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
1038	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSSPAPGGGGGTLNIEDEY RLHETSKEPDVPLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTND

	YRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLA DFRIQHPDLILLQYVDDLLLAATSEQDCQRGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAG FCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPP CLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEKEAPHDCLEILAETHGTRPD LTDQPIPDADYTWYTDGSSFLQEGQRRAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHVHGEIYRRRGWLTSEG REIKNKNEILALLKALFLPKRLSIIHCPGHQKGNSAEARGNRMADQAAREAAMKAVLETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
1039	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKGSSPAPGGTLNIED EYRLHETSKEPDVPLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGT NDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRD LADFRIQHPDLILLQYVDDLLLAATSEQDCQRGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGK AGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGW PPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEKEAPHDCLEILAETHGTR PDLTDQPIPDADYTWYTDGSSFLQEGQRRAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHVHGEIYRRRGWLTS EGREIKNKNEILALLKALFLPKRLSIIHCPGHQKGNSAEARGNRMADQAAREAAMKAVLETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
1043	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPGSSGGSGGTLNIEDEY

	RLHETSKEPDVPLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTND YRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLA DFRIQHPDLILLQYVDDLLLAATSEQDCQRGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAG FCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPP CLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEKEAPHDCLEILAETHGTRPD LTDQPIPDADYTWYTDGSSFLQEGQRRAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHVHGEIYRRRGWLTSEG REIKNKNEILALLKALFLPKRLSIIHCPGHQKGNSAEARGNRMADQAAREAAMKAVLETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
1044	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGGEAAAKGGTLNIEDEYR LHETSKEPDVPLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDY RPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLAD FRIQHPDLILLQYVDDLLLAATSEQDCQRGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGF CRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPC LRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEKEAPHDCLEILAETHGTRPDL TDQPIPDADYTWYTDGSSFLQEGQRRAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHVHGEIYRRRGWLTSEGR EIKNKNEILALLKALFLPKRLSIIHCPGHQKGNSAEARGNRMADQAAREAAMKAVLETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
1046	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK

	VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGSGGGEAAAKGGTLNIED EYRLHETSKEPDVPLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGT NDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRD LADFRIQHPDLILLQYVDDLLLAATSEQDCQRGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGK AGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGW PPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEKEAPHDCLEILAETHGTR PDLTDQPIPDADYTWYTDGSSFLQEGQRRAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHVHGEIYRRRGWLTS EGREIKNKNEILALLKALFLPKRLSIIHCPGHQKGNSAEARGNRMADQAAREAAMKAVLETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
1047	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSSGSSGGTLNIEDEYRLH ETSKEPDVPLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRP VQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFR IQHPDLILLQYVDDLLLAATSEQDCQRGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCR LFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLR MVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEKEAPHDCLEILAETHGTRPDLTD QPIPDADYTWYTDGSSFLQEGQRRAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHVHGEIYRRRGWLTSEGREI KNKNEILALLKALFLPKRLSIIHCPGHQKGNSAEARGNRMADQAAREAAMKAVLETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
1049	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE

	VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGGGSGGGGSGGGGSGGGG SGGTLNIEDEYRLHETSKEPDVPLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTP LLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPT LFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSEQDCQRGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTP RQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSK KLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEKEAPHDCLE ILAETHGTRPDLTDQPIPDADYTWYTDGSSFLQEGQRRAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHVHGEI YRRRGWLTSEGREIKNKNEILALLKALFLPKRLSIIHCPGHQKGNSAEARGNRMADQAAREAAMKAVLETSTLLAGKRTADGSEFEKRTADGSEFESPKK KAKVE
1052	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKEAAAKEAAAKEAAA KEAAAKEAAAKGGTLNIEDEYRLHETSKEPDVPLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGIL VPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTR LPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSEQDCQRGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKET VMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGP WRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLP EKEAPHDCLEILAETHGTRPDLTDQPIPDADYTWYTDGSSFLQEGQRRAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYA FATAHVHGEIYRRRGWLTSEGREIKNKNEILALLKALFLPKRLSIIHCPGHQKGNSAEARGNRMADQAAREAAMKAVLETSTLLAGKRTADGSEFEKRTA DGSEFESPKKKAKVE
1056	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA

	KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKGGGGSSGGTLNIED EYRLHETSKEPDVPLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGT NDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRD LADFRIQHPDLILLQYVDDLLLAATSEQDCQRGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGK AGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGW PPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEKEAPHDCLEILAETHGTR PDLTDQPIPDADYTWYTDGSSFLQEGQRRAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHVHGEIYRRRGWLTS EGREIKNKNEILALLKALFLPKRLSIIHCPGHQKGNSAEARGNRMADQAAREAAMKAVLETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
1059	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSGSSEAAAKGGTLNIED EYRLHETSKEPDVPLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGT NDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRD LADFRIQHPDLILLQYVDDLLLAATSEQDCQRGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGK AGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGW PPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEKEAPHDCLEILAETHGTR PDLTDQPIPDADYTWYTDGSSFLQEGQRRAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHVHGEIYRRRGWLTS EGREIKNKNEILALLKALFLPKRLSIIHCPGHQKGNSAEARGNRMADQAAREAAMKAVLETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
1060	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK

	ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSSGGSEAAAKGGTLNIED EYRLHETSKEPDVPLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGT NDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRD LADFRIQHPDLILLQYVDDLLLAATSEQDCQRGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGK AGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGW PPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEKEAPHDCLEILAETHGTR PDLTDQPIPDADYTWYTDGSSFLQEGQRRAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHVHGEIYRRRGWLTS EGREIKNKNEILALLKALFLPKRLSIIHCPGHQKGNSAEARGNRMADQAAREAAMKAVLETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
1061	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSSGGSPAPGGTLNIEDEY RLHETSKEPDVPLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTND YRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLA DFRIQHPDLILLQYVDDLLLAATSEQDCQRGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAG FCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPP CLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEKEAPHDCLEILAETHGTRPD LTDQPIPDADYTWYTDGSSFLQEGQRRAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHVHGEIYRRRGWLTSEG REIKNKNEILALLKALFLPKRLSIIHCPGHQKGNSAEARGNRMADQAAREAAMKAVLETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
1076	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA

	NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGGPAPEAAAKGGTLNIED EYRLHETSKEPDVPLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGT NDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRD LADFRIQHPDLILLQYVDDLLLAATSEQDCQRGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGK AGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGW PPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEKEAPHDCLEILAETHGTR PDLTDQPIPDADYTWYTDGSSFLQEGQRRAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHVHGEIYRRRGWLTS EGREIKNKNEILALLKALFLPKRLSIIHCPGHQKGNSAEARGNRMADQAAREAAMKAVLETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
1083	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGSEAAAKGGTLNIEDEYR LHETSKEPDVPLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDY RPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLAD FRIQHPDLILLQYVDDLLLAATSEQDCQRGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGF CRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPC LRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEKEAPHDCLEILAETHGTRPDL TDQPIPDADYTWYTDGSSFLQEGQRRAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHVHGEIYRRRGWLTSEGR EIKNKNEILALLKALFLPKRLSIIHCPGHQKGNSAEARGNRMADQAAREAAMKAVLETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
1093	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA

	SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGAEAAAKEAAAKEAAAKEAA AKALEAEAAAKEAAAKEAAAKEAAAKAGGVPWILKKPLELTIKLDLEEQQGTLLNNSILSKKGKEELKQLFEKYSALWQSWENQVGHRRIRPHKIATGTV KPTPQKQYHINPKAKPDIQIVINDLLKQGVLIQKESTMNTPVYPVPKPNGRWRMVLDYRAVNKVTPLIAVQNQHSYGILGSLFKGRYKTTIDLSNGFWAH PIVPEDYWITAFTWQGKQYCWTVLPQGFLNSPGLFNGDVVDLLQGIPNVEVYVDDVYISHDSEKEHLEYLDILFNRLKEAGYIISLKKSNIANSIVDFLG FQITNEGRGLTDTFKEKLENITAPTTLKQLQSILGLLNFARNFIPDFTELIAPLYALIPKSPKNYVPWQIEHSTTLETLITKLNGAEYLQGRKGDKTLIM KVNASYTTGYIRYYNEGEKKPISYVSIVFSKTELKFTELEKLLTTVHKGLLKALDLSMGQNIHVYSPIVSMQNIQKTPQTAKKALASRWLSWLSYLEDPR IRFFYDPQMPALKDLPAVDTGKDNKKHPSNFQHIFYTDGSAITSPTKEGHLNAGMGIVYFINKDGNLQKQQEWSISLGNHTAQFAEIAAFEFALKKCLPL GGNILVVTDSNYVAKAYNEELDVWASNGFVNNRKKPLKHISKWKSVADLKRLRPDVVVTHEPGHQKLDSSPHAYGNNLADQLATQASFKVHAGKRTADGS EFEKRTADGSEFESPKKKAKVE
1115	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGAEAAAKEAAAKEAAAKEAA AKALEAEAAAKEAAAKEAAAKEAAAKAGGMDLLKPLTVERKGVKIKGYWNSQADITCVPKDLLQGEEPVRQQNVTTIHGTQEGDVYYVNLKIDGRRINTE VIGTTLDYAIITPGDVPWILKKPLELTIKLDLEEQQGTLLNNSILSKKGKEELKQLFEKYSALWQSWENQVGHRRIRPHKIATGTVKPTPQKQYHINPKA KPDIQIVINDLLKQGVLIQKESTMNTPVYPVPKPNGRWRMVLDYRAVNKVTPLIAVQNQHSYGILGSLFKGRYKTTIDLSNGFWAHPIVPEDYWITAFTW QGKQYCWTVLPQGFLNSPGLFNGDVVDLLQGIPNVEVYVDDVYISHDSEKEHLEYLDILFNRLKEAGYIISLKKSNIANSIVDFLGFQITNEGRGLTDTF KEKLENITAPTTLKQLQSILGLLNFARNFIPDFTELIAPLYALIPKSPKNYVPWQIEHSTTLETLITKLNGAEYLQGRKGDKTLIMKVNASYTTGYIRYY NEGEKKPISYVSIVFSKTELKFTELEKLLTTVHKGLLKALDLSMGQNIHVYSPIVSMQNIQKTPQTAKKALASRWLSWLSYLEDPRIRFFYDPQMPALKD LPAVDTGKDNKKHPSNFQHIFYTDGSAITSPTKEGHLNAGMGIVYFINKDGNLQKQQEWSISLGNHTAQFAEIAAFEFALKKCLPLGGNILVVTDSNYVA KAYNEELDVWASNGFVNNRKKPLKHISKWKSVADLKRLRPDVVVTHEPGHQKLDSSPHAYGNNLADQLATQASFKVHAGKRTADGSEFEKRTADGSEFES PKKKAKVE
1137	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV

	QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKEAAAKEAAAKEAAA KGGTAPLEEEYRLFLEAPIQNVTLLEQWKREIPKVWAEINPPGLASTQAPIHVQLLSTALPVRVRQYPITLEAKRSLRETIRKFRAAGILRPVHSPWNTP LLPVRKSGTSEYRMVQDLREVNKRVETIHPTVPNPYTLLSLLPPDRIWYSVLDLKDAFFCIPLAPESQLIFAFEWADAEEGESGQLTWTRLPQGFKNSPT LFNEALNRDLQGFRLDHPSVSLLQYVDDLLIAADTQAACLSATRDLLMTLAELGYRVSGKKAQLCQEEVTYLGFKIHKGSRSLSNSRTQAILQIPVPKTK RQVREFLGTIGYCRLWIPGFAELAQPLYAATRPGNDPLVWGEKEEEAFQSLKLALTQPPALALPSLDKPFQLFVEETSGAAKGVLTQALGPWKRPVAYLS KRLDPVAAGWPRCLRAIAAAALLTREASKLTFGQDIEITSSHNLESLLRSPPDKWLTNARITQYQVLLLDPPRVRFKQTAALNPATLLPETDDTLPIHHC LDTLDSLTSTRPDLTDQPLAQAEATLFTDGSSYIRDGKRYAGAAVVTLDSVIWAEPLPIGTSAQKAELIALTKALEWSKDKSVNIYTDSRYAFATLHVHG MIYRERGWLTAGGKAIKNAPEILALLTAVWLPKRVAVMHCKGHQKDDAPTSTGNRRADEVAREVAIRPLSTQATISAGKRTADGSEFEKRTADGSEFESP KKKAKVE
1168	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGGGGSPAPGGTLQLEEEY RLFEPESTQKQEMDIWLKNFPQAWAETGGMGTAHCQAPVLIQLKATATPISIRQYPMPHEAYQGIKPHIRRMLDQGILKPCQSPWNTPLLPVKKPGTEDY RPVQDLREVNKRVEDIHPTVPNPYNLLSTLPPSHPWYTVLDLKDAFFCLRLHSESQLLFAFEWRDPEIGLSGQLTWTRLPQGFKNSPTLFNEALHSDLAD FRVRYPALVLLQYVDDLLLAAATRTECLEGTKALLETLGNKGYRASAKKAQICLQEVTYLGYSLKDGQRWLTKARKEAILSIPVPKNSRQVREFLGTAGY CRLWIPGFAELAAPLYPLTRPGTLFQWGTEQQLAFEDIKKALLSSPALGLPDITKPFELFIDENSGFAKGVLVQKLGPWKRPVAYLSKKLDTVASGWPPC LRMVAAIAILVKDAGKLTLGQPLTILTSHPVEALVRQPPNKWLSNARMTHYQAMLLDAERVHFGPTVSLNPATLLPLPSGGNHHDCLQILAETHGTRPDL TDQPLPDADLTWYTDGSSFIRNGEREAGAAVTTESEVIWAAPLPPGTSAQRAELIALTQALKMAEGKKLTVYTDSRYAFATTHVHGEIYRRRGWLTSEGK EIKNKNEILALLEALFLPKRLSIIHCPGHQKGDSPQAKGNRLADDTAKKAATETHSSLTVLPAGKRTADGSEFEKRTADGSEFESPKKKAKVE

1171	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKEAAAKEAAAKEAAA KEAAAKEAAAKGGTLQLEEEYRLFEPESTQKQEMDIWLKNFPQAWAETGGMGTAHCQAPVLIQLKATATPISIRQYPMPHEAYQGIKPHIRRMLDQGILK PCQSPWNTPLLPVKKPGTEDYRPVQDLREVNKRVEDIHPTVPNPYNLLSTLPPSHPWYTVLDLKDAFFCLRLHSESQLLFAFEWRDPEIGLSGQLTWTRL PQGFKNSPTLFNEALHSDLADFRVRYPALVLLQYVDDLLLAAATRTECLEGTKALLETLGNKGYRASAKKAQICLQEVTYLGYSLKDGQRWLTKARKEAI LSIPVPKNSRQVREFLGTAGYCRLWIPGFAELAAPLYPLTRPGTLFQWGTEQQLAFEDIKKALLSSPALGLPDITKPFELFIDENSGFAKGVLVQKLGPW KRPVAYLSKKLDTVASGWPPCLRMVAAIAILVKDAGKLTLGQPLTILTSHPVEALVRQPPNKWLSNARMTHYQAMLLDAERVHFGPTVSLNPATLLPLPS GGNHHDCLQILAETHGTRPDLTDQPLPDADLTWYTDGSSFIRNGEREAGAAVTTESEVIWAAPLPPGTSAQRAELIALTQALKMAEGKKLTVYTDSRYAF ATTHVHGEIYRRRGWLTSEGKEIKNKNEILALLEALFLPKRLSIIHCPGHQKGDSPQAKGNRLADDTAKKAATETHSSLTVLPAGKRTADGSEFEKRTAD GSEFESPKKKAKVE
1197	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGAEAAAKEAAAKEAAAKEAA AKALEAEAAAKEAAAKEAAAKEAAAKAGGTLQLEEEYRLFEPESTQKQEMDIWLKNFPQAWAETGGMGTAHCQAPVLIQLKATATPISIRQYPMPHEAYQ GIKPHIRRMLDQGILKPCQSPWNTPLLPVKKPGTEDYRPVQDLREVNKRVEDIHPTVPNPYNLLSTLPPSHPWYTVLDLKDAFFCLRLHSESQLLFAFEW RDPEIGLSGQLTWTRLPQGFKNSPTLFNEALHSDLADFRVRYPALVLLQYVDDLLLAAATRTECLEGTKALLETLGNKGYRASAKKAQICLQEVTYLGYS LKDGQRWLTKARKEAILSIPVPKNSRQVREFLGKAGYCRLFIPGFAELAAPLYPLTRPGTLFQWGTEQQLAFEDIKKALLSSPALGLPDITKPFELFIDE NSGFAKGVLVQKLGPWKRPVAYLSKKLDTVASGWPPCLRMVAAIAILVKDAGKLTLGQPLTILTSHPVEALVRQPPNKWLSNARMTHYQAMLLDAERVHF

	GPTVSLNPATLLPLPSGGNHHDCLQILAETHGTRPDLTDQPLPDADLTWYTDGSSFIRNGEREAGAAVTTESEVIWAAPLPPGTSAQRAELIALTQALKM AEGKKLTVYTDSRYAFATTHVHGEIYRRRGWLTSEGKEIKNKNEILALLEALFLPKRLSIIHCPGHQKGDSPQAKGNRLADDTAKKAATETHSSLTVLPA GKRTADGSEFEKRTADGSEFESPKKKAKVE
1198	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKEAAAKEAAAKEAAA KGGTLQLEEEYRLFEPESTQKQEMDIWLKNFPQAWAETGGMGTAHCQAPVLIQLKATATPISIRQYPMPHEAYQGIKPHIRRMLDQGILKPCQSPWNTPL LPVKKPGTEDYRPVQDLREVNKRVEDIHPTVPNPYNLLSTLPPSHPWYTVLDLKDAFFCLRLHSESQLLFAFEWRDPEIGLSGQLTWTRLPQGFKNSPTL FNEALHSDLADFRVRYPALVLLQYVDDLLLAAATRTECLEGTKALLETLGNKGYRASAKKAQICLQEVTYLGYSLKDGQRWLTKARKEAILSIPVPKNSR QVREFLGKAGYCRLFIPGFAELAAPLYPLTRPGTLFQWGTEQQLAFEDIKKALLSSPALGLPDITKPFELFIDENSGFAKGVLVQKLGPWKRPVAYLSKK LDTVASGWPPCLRMVAAIAILVKDAGKLTLGQPLTILTSHPVEALVRQPPNKWLSNARMTHYQAMLLDAERVHFGPTVSLNPATLLPLPSGGNHHDCLQI LAETHGTRPDLTDQPLPDADLTWYTDGSSFIRNGEREAGAAVTTESEVIWAAPLPPGTSAQRAELIALTQALKMAEGKKLTVYTDSRYAFATTHVHGEIY RRRGWLTSEGKEIKNKNEILALLEALFLPKRLSIIHCPGHQKGDSPQAKGNRLADDTAKKAATETHSSLTVLPAGKRTADGSEFEKRTADGSEFESPKKK AKVE
1202	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGGGSGGGGSGGGGSGGGG SGGGGSGGTLQLEEEYRLFEPESTQKQEMDIWLKNFPQAWAETGGMGTAHCQAPVLIQLKATATPISIRQYPMPHEAYQGIKPHIRRMLDQGILKPCQSP WNTPLLPVKKPGTEDYRPVQDLREVNKRVEDIHPTVPNPYNLLSTLPPSHPWYTVLDLKDAFFCLRLHSESQLLFAFEWRDPEIGLSGQLTWTRLPQGFK

	NSPTLFNEALHSDLADFRVRYPALVLLQYVDDLLLAAATRTECLEGTKALLETLGNKGYRASAKKAQICLQEVTYLGYSLKDGQRWLTKARKEAILSIPV PKNSRQVREFLGKAGYCRLFIPGFAELAAPLYPLTRPGTLFQWGTEQQLAFEDIKKALLSSPALGLPDITKPFELFIDENSGFAKGVLVQKLGPWKRPVA YLSKKLDTVASGWPPCLRMVAAIAILVKDAGKLTLGQPLTILTSHPVEALVRQPPNKWLSNARMTHYQAMLLDAERVHFGPTVSLNPATLLPLPSGGNHH DCLQILAETHGTRPDLTDQPLPDADLTWYTDGSSFIRNGEREAGAAVTTESEVIWAAPLPPGTSAQRAELIALTQALKMAEGKKLTVYTDSRYAFATTHV HGEIYRRRGWLTSEGKEIKNKNEILALLEALFLPKRLSIIHCPGHQKGDSPQAKGNRLADDTAKKAATETHSSLTVLPAGKRTADGSEFEKRTADGSEFE SPKKKAKVE
1203	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGGGSEAAAKGGGGSGGTL QLEEEYRLFEPESTQKQEMDIWLKNFPQAWAETGGMGTAHCQAPVLIQLKATATPISIRQYPMPHEAYQGIKPHIRRMLDQGILKPCQSPWNTPLLPVKK PGTEDYRPVQDLREVNKRVEDIHPTVPNPYNLLSTLPPSHPWYTVLDLKDAFFCLRLHSESQLLFAFEWRDPEIGLSGQLTWTRLPQGFKNSPTLFNEAL HSDLADFRVRYPALVLLQYVDDLLLAAATRTECLEGTKALLETLGNKGYRASAKKAQICLQEVTYLGYSLKDGQRWLTKARKEAILSIPVPKNSRQVREF LGKAGYCRLFIPGFAELAAPLYPLTRPGTLFQWGTEQQLAFEDIKKALLSSPALGLPDITKPFELFIDENSGFAKGVLVQKLGPWKRPVAYLSKKLDTVA SGWPPCLRMVAAIAILVKDAGKLTLGQPLTILTSHPVEALVRQPPNKWLSNARMTHYQAMLLDAERVHFGPTVSLNPATLLPLPSGGNHHDCLQILAETH GTRPDLTDQPLPDADLTWYTDGSSFIRNGEREAGAAVTTESEVIWAAPLPPGTSAQRAELIALTQALKMAEGKKLTVYTDSRYAFATTHVHGEIYRRRGW LTSEGKEIKNKNEILALLEALFLPKRLSIIHCPGHQKGDSPQAKGNRLADDTAKKAATETHSSLTVLPAGKRTADGSEFEKRTADGSEFESPKKKAKVE
1210	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKGSSGGGGGTLQLEE

	EYRLFEPESTQKQEMDIWLKNFPQAWAETGGMGTAHCQAPVLIQLKATATPISIRQYPMPHEAYQGIKPHIRRMLDQGILKPCQSPWNTPLLPVKKPGTE DYRPVQDLREVNKRVEDIHPTVPNPYNLLSTLPPSHPWYTVLDLKDAFFCLRLHSESQLLFAFEWRDPEIGLSGQLTWTRLPQGFKNSPTLFNEALHSDL ADFRVRYPALVLLQYVDDLLLAAATRTECLEGTKALLETLGNKGYRASAKKAQICLQEVTYLGYSLKDGQRWLTKARKEAILSIPVPKNSRQVREFLGKA GYCRLFIPGFAELAAPLYPLTRPGTLFQWGTEQQLAFEDIKKALLSSPALGLPDITKPFELFIDENSGFAKGVLVQKLGPWKRPVAYLSKKLDTVASGWP PCLRMVAAIAILVKDAGKLTLGQPLTILTSHPVEALVRQPPNKWLSNARMTHYQAMLLDAERVHFGPTVSLNPATLLPLPSGGNHHDCLQILAETHGTRP DLTDQPLPDADLTWYTDGSSFIRNGEREAGAAVTTESEVIWAAPLPPGTSAQRAELIALTQALKMAEGKKLTVYTDSRYAFATTHVHGEIYRRRGWLTSE GKEIKNKNEILALLEALFLPKRLSIIHCPGHQKGDSPQAKGNRLADDTAKKAATETHSSLTVLPAGKRTADGSEFEKRTADGSEFESPKKKAKVE
1216	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPAPAPAPGGTLQLEEEY RLFEPESTQKQEMDIWLKNFPQAWAETGGMGTAHCQAPVLIQLKATATPISIRQYPMPHEAYQGIKPHIRRMLDQGILKPCQSPWNTPLLPVKKPGTEDY RPVQDLREVNKRVEDIHPTVPNPYNLLSTLPPSHPWYTVLDLKDAFFCLRLHSESQLLFAFEWRDPEIGLSGQLTWTRLPQGFKNSPTLFNEALHSDLAD FRVRYPALVLLQYVDDLLLAAATRTECLEGTKALLETLGNKGYRASAKKAQICLQEVTYLGYSLKDGQRWLTKARKEAILSIPVPKNSRQVREFLGKAGY CRLFIPGFAELAAPLYPLTRPGTLFQWGTEQQLAFEDIKKALLSSPALGLPDITKPFELFIDENSGFAKGVLVQKLGPWKRPVAYLSKKLDTVASGWPPC LRMVAAIAILVKDAGKLTLGQPLTILTSHPVEALVRQPPNKWLSNARMTHYQAMLLDAERVHFGPTVSLNPATLLPLPSGGNHHDCLQILAETHGTRPDL TDQPLPDADLTWYTDGSSFIRNGEREAGAAVTTESEVIWAAPLPPGTSAQRAELIALTQALKMAEGKKLTVYTDSRYAFATTHVHGEIYRRRGWLTSEGK EIKNKNEILALLEALFLPKRLSIIHCPGHQKGDSPQAKGNRLADDTAKKAATETHSSLTVLPAGKRTADGSEFEKRTADGSEFESPKKKAKVE
1219	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK

	VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPAPAPAPAPAPGGTLQL EEEYRLFEPESTQKQEMDIWLKNFPQAWAETGGMGTAHCQAPVLIQLKATATPISIRQYPMPHEAYQGIKPHIRRMLDQGILKPCQSPWNTPLLPVKKPG TEDYRPVQDLREVNKRVEDIHPTVPNPYNLLSTLPPSHPWYTVLDLKDAFFCLRLHSESQLLFAFEWRDPEIGLSGQLTWTRLPQGFKNSPTLFNEALHS DLADFRVRYPALVLLQYVDDLLLAAATRTECLEGTKALLETLGNKGYRASAKKAQICLQEVTYLGYSLKDGQRWLTKARKEAILSIPVPKNSRQVREFLG KAGYCRLFIPGFAELAAPLYPLTRPGTLFQWGTEQQLAFEDIKKALLSSPALGLPDITKPFELFIDENSGFAKGVLVQKLGPWKRPVAYLSKKLDTVASG WPPCLRMVAAIAILVKDAGKLTLGQPLTILTSHPVEALVRQPPNKWLSNARMTHYQAMLLDAERVHFGPTVSLNPATLLPLPSGGNHHDCLQILAETHGT RPDLTDQPLPDADLTWYTDGSSFIRNGEREAGAAVTTESEVIWAAPLPPGTSAQRAELIALTQALKMAEGKKLTVYTDSRYAFATTHVHGEIYRRRGWLT SEGKEIKNKNEILALLEALFLPKRLSIIHCPGHQKGDSPQAKGNRLADDTAKKAATETHSSLTVLPAGKRTADGSEFEKRTADGSEFESPKKKAKVE
1225	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSSPAPEAAAKGGTLQLEE EYRLFEPESTQKQEMDIWLKNFPQAWAETGGMGTAHCQAPVLIQLKATATPISIRQYPMPHEAYQGIKPHIRRMLDQGILKPCQSPWNTPLLPVKKPGTE DYRPVQDLREVNKRVEDIHPTVPNPYNLLSTLPPSHPWYTVLDLKDAFFCLRLHSESQLLFAFEWRDPEIGLSGQLTWTRLPQGFKNSPTLFNEALHSDL ADFRVRYPALVLLQYVDDLLLAAATRTECLEGTKALLETLGNKGYRASAKKAQICLQEVTYLGYSLKDGQRWLTKARKEAILSIPVPKNSRQVREFLGKA GYCRLFIPGFAELAAPLYPLTRPGTLFQWGTEQQLAFEDIKKALLSSPALGLPDITKPFELFIDENSGFAKGVLVQKLGPWKRPVAYLSKKLDTVASGWP PCLRMVAAIAILVKDAGKLTLGQPLTILTSHPVEALVRQPPNKWLSNARMTHYQAMLLDAERVHFGPTVSLNPATLLPLPSGGNHHDCLQILAETHGTRP DLTDQPLPDADLTWYTDGSSFIRNGEREAGAAVTTESEVIWAAPLPPGTSAQRAELIALTQALKMAEGKKLTVYTDSRYAFATTHVHGEIYRRRGWLTSE GKEIKNKNEILALLEALFLPKRLSIIHCPGHQKGDSPQAKGNRLADDTAKKAATETHSSLTVLPAGKRTADGSEFEKRTADGSEFESPKKKAKVE
1235	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE

	VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKGGGGGSGGTLQLEE EYRLFEPESTQKQEMDIWLKNFPQAWAETGGMGTAHCQAPVLIQLKATATPISIRQYPMPHEAYQGIKPHIRRMLDQGILKPCQSPWNTPLLPVKKPGTE DYRPVQDLREVNKRVEDIHPTVPNPYNLLSTLPPSHPWYTVLDLKDAFFCLRLHSESQLLFAFEWRDPEIGLSGQLTWTRLPQGFKNSPTLFNEALHSDL ADFRVRYPALVLLQYVDDLLLAAATRTECLEGTKALLETLGNKGYRASAKKAQICLQEVTYLGYSLKDGQRWLTKARKEAILSIPVPKNSRQVREFLGKA GYCRLFIPGFAELAAPLYPLTRPGTLFQWGTEQQLAFEDIKKALLSSPALGLPDITKPFELFIDENSGFAKGVLVQKLGPWKRPVAYLSKKLDTVASGWP PCLRMVAAIAILVKDAGKLTLGQPLTILTSHPVEALVRQPPNKWLSNARMTHYQAMLLDAERVHFGPTVSLNPATLLPLPSGGNHHDCLQILAETHGTRP DLTDQPLPDADLTWYTDGSSFIRNGEREAGAAVTTESEVIWAAPLPPGTSAQRAELIALTQALKMAEGKKLTVYTDSRYAFATTHVHGEIYRRRGWLTSE GKEIKNKNEILALLEALFLPKRLSIIHCPGHQKGDSPQAKGNRLADDTAKKAATETHSSLTVLPAGKRTADGSEFEKRTADGSEFESPKKKAKVE
1242	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSSGGSEAAAKGGTLQLEE EYRLFEPESTQKQEMDIWLKNFPQAWAETGGMGTAHCQAPVLIQLKATATPISIRQYPMPHEAYQGIKPHIRRMLDQGILKPCQSPWNTPLLPVKKPGTE DYRPVQDLREVNKRVEDIHPTVPNPYNLLSTLPPSHPWYTVLDLKDAFFCLRLHSESQLLFAFEWRDPEIGLSGQLTWTRLPQGFKNSPTLFNEALHSDL ADFRVRYPALVLLQYVDDLLLAAATRTECLEGTKALLETLGNKGYRASAKKAQICLQEVTYLGYSLKDGQRWLTKARKEAILSIPVPKNSRQVREFLGKA GYCRLFIPGFAELAAPLYPLTRPGTLFQWGTEQQLAFEDIKKALLSSPALGLPDITKPFELFIDENSGFAKGVLVQKLGPWKRPVAYLSKKLDTVASGWP PCLRMVAAIAILVKDAGKLTLGQPLTILTSHPVEALVRQPPNKWLSNARMTHYQAMLLDAERVHFGPTVSLNPATLLPLPSGGNHHDCLQILAETHGTRP DLTDQPLPDADLTWYTDGSSFIRNGEREAGAAVTTESEVIWAAPLPPGTSAQRAELIALTQALKMAEGKKLTVYTDSRYAFATTHVHGEIYRRRGWLTSE GKEIKNKNEILALLEALFLPKRLSIIHCPGHQKGDSPQAKGNRLADDTAKKAATETHSSLTVLPAGKRTADGSEFEKRTADGSEFESPKKKAKVE
1262	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM

	PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGGEAAAKPAPGGTLQLEE EYRLFEPESTQKQEMDIWLKNFPQAWAETGGMGTAHCQAPVLIQLKATATPISIRQYPMPHEAYQGIKPHIRRMLDQGILKPCQSPWNTPLLPVKKPGTE DYRPVQDLREVNKRVEDIHPTVPNPYNLLSTLPPSHPWYTVLDLKDAFFCLRLHSESQLLFAFEWRDPEIGLSGQLTWTRLPQGFKNSPTLFNEALHSDL ADFRVRYPALVLLQYVDDLLLAAATRTECLEGTKALLETLGNKGYRASAKKAQICLQEVTYLGYSLKDGQRWLTKARKEAILSIPVPKNSRQVREFLGKA GYCRLFIPGFAELAAPLYPLTRPGTLFQWGTEQQLAFEDIKKALLSSPALGLPDITKPFELFIDENSGFAKGVLVQKLGPWKRPVAYLSKKLDTVASGWP PCLRMVAAIAILVKDAGKLTLGQPLTILTSHPVEALVRQPPNKWLSNARMTHYQAMLLDAERVHFGPTVSLNPATLLPLPSGGNHHDCLQILAETHGTRP DLTDQPLPDADLTWYTDGSSFIRNGEREAGAAVTTESEVIWAAPLPPGTSAQRAELIALTQALKMAEGKKLTVYTDSRYAFATTHVHGEIYRRRGWLTSE GKEIKNKNEILALLEALFLPKRLSIIHCPGHQKGDSPQAKGNRLADDTAKKAATETHSSLTVLPAGKRTADGSEFEKRTADGSEFESPKKKAKVE
1371	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPGGSEAAAKGGTAPLEE EYRLFLEAPIQNVTLLEQWKREIPKVWAEINPPGLASTQAPIHVQLLSTALPVRVRQYPITLEAKRSLRETIRKFRAAGILRPVHSPWNTPLLPVRKSGT SEYRMVQDLREVNKRVETIHPTVPNPYTLLSLLPPDRIWYSVLDLKDAFFCIPLAPESQLIFAFEWADAEEGESGQLTWTRLPQGFKNSPTLFNEALNRD LQGFRLDHPSVSLLQYVDDLLIAADTQAACLSATRDLLMTLAELGYRVSGKKAQLCQEEVTYLGFKIHKGSRSLSNSRTQAILQIPVPKTKRQVREFLGK IGYCRLFIPGFAELAQPLYAATRPGNDPLVWGEKEEEAFQSLKLALTQPPALALPSLDKPFQLFVEETSGAAKGVLTQALGPWKRPVAYLSKRLDPVAAG WPRCLRAIAAAALLTREASKLTFGQDIEITSSHNLESLLRSPPDKWLTNARITQYQVLLLDPPRVRFKQTAALNPATLLPETDDTLPIHHCLDTLDSLTS TRPDLTDQPLAQAEATLFTDGSSYIRDGKRYAGAAVVTLDSVIWAEPLPIGTSAQKAELIALTKALEWSKDKSVNIYTDSRYAFATLHVHGMIYRERGWL TAGGKAIKNAPEILALLTAVWLPKRVAVMHCKGHQKDDAPTSTGNRRADEVAREVAIRPLSTQATISAGKRTADGSEFEKRTADGSEFESPKKKAKVE
1372	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL

	NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGAEAAAKEAAAKEAAAKEAA AKALEAEAAAKEAAAKEAAAKEAAAKAGGTAPLEEEYRLFLEAPIQNVTLLEQWKREIPKVWAEINPPGLASTQAPIHVQLLSTALPVRVRQYPITLEAK RSLRETIRKFRAAGILRPVHSPWNTPLLPVRKSGTSEYRMVQDLREVNKRVETIHPTVPNPYTLLSLLPPDRIWYSVLDLKDAFFCIPLAPESQLIFAFE WADAEEGESGQLTWTRLPQGFKNSPTLFNEALNRDLQGFRLDHPSVSLLQYVDDLLIAADTQAACLSATRDLLMTLAELGYRVSGKKAQLCQEEVTYLGF KIHKGSRSLSNSRTQAILQIPVPKTKRQVREFLGKIGYCRLFIPGFAELAQPLYAATRPGNDPLVWGEKEEEAFQSLKLALTQPPALALPSLDKPFQLFV EETSGAAKGVLTQALGPWKRPVAYLSKRLDPVAAGWPRCLRAIAAAALLTREASKLTFGQDIEITSSHNLESLLRSPPDKWLTNARITQYQVLLLDPPRV RFKQTAALNPATLLPETDDTLPIHHCLDTLDSLTSTRPDLTDQPLAQAEATLFTDGSSYIRDGKRYAGAAVVTLDSVIWAEPLPIGTSAQKAELIALTKA LEWSKDKSVNIYTDSRYAFATLHVHGMIYRERGWLTAGGKAIKNAPEILALLTAVWLPKRVAVMHCKGHQKDDAPTSTGNRRADEVAREVAIRPLSTQAT ISAGKRTADGSEFEKRTADGSEFESPKKKAKVE
1373	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGGSGGGGSGGGGSGGGG SGGGGSGGGGSGGTAPLEEEYRLFLEAPIQNVTLLEQWKREIPKVWAEINPPGLASTQAPIHVQLLSTALPVRVRQYPITLEAKRSLRETIRKFRAAGIL RPVHSPWNTPLLPVRKSGTSEYRMVQDLREVNKRVETIHPTVPNPYTLLSLLPPDRIWYSVLDLKDAFFCIPLAPESQLIFAFEWADAEEGESGQLTWTR LPQGFKNSPTLFNEALNRDLQGFRLDHPSVSLLQYVDDLLIAADTQAACLSATRDLLMTLAELGYRVSGKKAQLCQEEVTYLGFKIHKGSRSLSNSRTQA ILQIPVPKTKRQVREFLGKIGYCRLFIPGFAELAQPLYAATRPGNDPLVWGEKEEEAFQSLKLALTQPPALALPSLDKPFQLFVEETSGAAKGVLTQALG PWKRPVAYLSKRLDPVAAGWPRCLRAIAAAALLTREASKLTFGQDIEITSSHNLESLLRSPPDKWLTNARITQYQVLLLDPPRVRFKQTAALNPATLLPE TDDTLPIHHCLDTLDSLTSTRPDLTDQPLAQAEATLFTDGSSYIRDGKRYAGAAVVTLDSVIWAEPLPIGTSAQKAELIALTKALEWSKDKSVNIYTDSR YAFATLHVHGMIYRERGWLTAGGKAIKNAPEILALLTAVWLPKRVAVMHCKGHQKDDAPTSTGNRRADEVAREVAIRPLSTQATISAGKRTADGSEFEKR TADGSEFESPKKKAKVE
1374	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA

	NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGGSGGGGSGGGGSGGGG SGGTAPLEEEYRLFLEAPIQNVTLLEQWKREIPKVWAEINPPGLASTQAPIHVQLLSTALPVRVRQYPITLEAKRSLRETIRKFRAAGILRPVHSPWNTP LLPVRKSGTSEYRMVQDLREVNKRVETIHPTVPNPYTLLSLLPPDRIWYSVLDLKDAFFCIPLAPESQLIFAFEWADAEEGESGQLTWTRLPQGFKNSPT LFNEALNRDLQGFRLDHPSVSLLQYVDDLLIAADTQAACLSATRDLLMTLAELGYRVSGKKAQLCQEEVTYLGFKIHKGSRSLSNSRTQAILQIPVPKTK RQVREFLGKIGYCRLFIPGFAELAQPLYAATRPGNDPLVWGEKEEEAFQSLKLALTQPPALALPSLDKPFQLFVEETSGAAKGVLTQALGPWKRPVAYLS KRLDPVAAGWPRCLRAIAAAALLTREASKLTFGQDIEITSSHNLESLLRSPPDKWLTNARITQYQVLLLDPPRVRFKQTAALNPATLLPETDDTLPIHHC LDTLDSLTSTRPDLTDQPLAQAEATLFTDGSSYIRDGKRYAGAAVVTLDSVIWAEPLPIGTSAQKAELIALTKALEWSKDKSVNIYTDSRYAFATLHVHG MIYRERGWLTAGGKAIKNAPEILALLTAVWLPKRVAVMHCKGHQKDDAPTSTGNRRADEVAREVAIRPLSTQATISAGKRTADGSEFEKRTADGSEFESP KKKAKVE
1375	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSSPAPGGTAPLEEEYRLF LEAPIQNVTLLEQWKREIPKVWAEINPPGLASTQAPIHVQLLSTALPVRVRQYPITLEAKRSLRETIRKFRAAGILRPVHSPWNTPLLPVRKSGTSEYRM VQDLREVNKRVETIHPTVPNPYTLLSLLPPDRIWYSVLDLKDAFFCIPLAPESQLIFAFEWADAEEGESGQLTWTRLPQGFKNSPTLFNEALNRDLQGFR LDHPSVSLLQYVDDLLIAADTQAACLSATRDLLMTLAELGYRVSGKKAQLCQEEVTYLGFKIHKGSRSLSNSRTQAILQIPVPKTKRQVREFLGKIGYCR LFIPGFAELAQPLYAATRPGNDPLVWGEKEEEAFQSLKLALTQPPALALPSLDKPFQLFVEETSGAAKGVLTQALGPWKRPVAYLSKRLDPVAAGWPRCL RAIAAAALLTREASKLTFGQDIEITSSHNLESLLRSPPDKWLTNARITQYQVLLLDPPRVRFKQTAALNPATLLPETDDTLPIHHCLDTLDSLTSTRPDL TDQPLAQAEATLFTDGSSYIRDGKRYAGAAVVTLDSVIWAEPLPIGTSAQKAELIALTKALEWSKDKSVNIYTDSRYAFATLHVHGMIYRERGWLTAGGK AIKNAPEILALLTAVWLPKRVAVMHCKGHQKDDAPTSTGNRRADEVAREVAIRPLSTQATISAGKRTADGSEFEKRTADGSEFESPKKKAKVE
1376	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ

	SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGSGSETPGTSESATPESGGT APLEEEYRLFLEAPIQNVTLLEQWKREIPKVWAEINPPGLASTQAPIHVQLLSTALPVRVRQYPITLEAKRSLRETIRKFRAAGILRPVHSPWNTPLLPV RKSGTSEYRMVQDLREVNKRVETIHPTVPNPYTLLSLLPPDRIWYSVLDLKDAFFCIPLAPESQLIFAFEWADAEEGESGQLTWTRLPQGFKNSPTLFNE ALNRDLQGFRLDHPSVSLLQYVDDLLIAADTQAACLSATRDLLMTLAELGYRVSGKKAQLCQEEVTYLGFKIHKGSRSLSNSRTQAILQIPVPKTKRQVR EFLGKIGYCRLFIPGFAELAQPLYAATRPGNDPLVWGEKEEEAFQSLKLALTQPPALALPSLDKPFQLFVEETSGAAKGVLTQALGPWKRPVAYLSKRLD PVAAGWPRCLRAIAAAALLTREASKLTFGQDIEITSSHNLESLLRSPPDKWLTNARITQYQVLLLDPPRVRFKQTAALNPATLLPETDDTLPIHHCLDTL DSLTSTRPDLTDQPLAQAEATLFTDGSSYIRDGKRYAGAAVVTLDSVIWAEPLPIGTSAQKAELIALTKALEWSKDKSVNIYTDSRYAFATLHVHGMIYR ERGWLTAGGKAIKNAPEILALLTAVWLPKRVAVMHCKGHQKDDAPTSTGNRRADEVAREVAIRPLSTQATISAGKRTADGSEFEKRTADGSEFESPKKKA KVE
1377	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPEAAAKGGSGGTAPLEE EYRLFLEAPIQNVTLLEQWKREIPKVWAEINPPGLASTQAPIHVQLLSTALPVRVRQYPITLEAKRSLRETIRKFRAAGILRPVHSPWNTPLLPVRKSGT SEYRMVQDLREVNKRVETIHPTVPNPYTLLSLLPPDRIWYSVLDLKDAFFCIPLAPESQLIFAFEWADAEEGESGQLTWTRLPQGFKNSPTLFNEALNRD LQGFRLDHPSVSLLQYVDDLLIAADTQAACLSATRDLLMTLAELGYRVSGKKAQLCQEEVTYLGFKIHKGSRSLSNSRTQAILQIPVPKTKRQVREFLGK IGYCRLFIPGFAELAQPLYAATRPGNDPLVWGEKEEEAFQSLKLALTQPPALALPSLDKPFQLFVEETSGAAKGVLTQALGPWKRPVAYLSKRLDPVAAG WPRCLRAIAAAALLTREASKLTFGQDIEITSSHNLESLLRSPPDKWLTNARITQYQVLLLDPPRVRFKQTAALNPATLLPETDDTLPIHHCLDTLDSLTS TRPDLTDQPLAQAEATLFTDGSSYIRDGKRYAGAAVVTLDSVIWAEPLPIGTSAQKAELIALTKALEWSKDKSVNIYTDSRYAFATLHVHGMIYRERGWL TAGGKAIKNAPEILALLTAVWLPKRVAVMHCKGHQKDDAPTSTGNRRADEVAREVAIRPLSTQATISAGKRTADGSEFEKRTADGSEFESPKKKAKVE
1380	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL

	FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKGGTAPLEEEYRLFL EAPIQNVTLLEQWKREIPKVWAEINPPGLASTQAPIHVQLLSTALPVRVRQYPITLEAKRSLRETIRKFRAAGILRPVHSPWNTPLLPVRKSGTSEYRMV QDLREVNKRVETIHPTVPNPYTLLSLLPPDRIWYSVLDLKDAFFCIPLAPESQLIFAFEWADAEEGESGQLTWTRLPQGFKNSPTLFNEALNRDLQGFRL DHPSVSLLQYVDDLLIAADTQAACLSATRDLLMTLAELGYRVSGKKAQLCQEEVTYLGFKIHKGSRSLSNSRTQAILQIPVPKTKRQVREFLGKIGYCRL FIPGFAELAQPLYAATRPGNDPLVWGEKEEEAFQSLKLALTQPPALALPSLDKPFQLFVEETSGAAKGVLTQALGPWKRPVAYLSKRLDPVAAGWPRCLR AIAAAALLTREASKLTFGQDIEITSSHNLESLLRSPPDKWLTNARITQYQVLLLDPPRVRFKQTAALNPATLLPETDDTLPIHHCLDTLDSLTSTRPDLT DQPLAQAEATLFTDGSSYIRDGKRYAGAAVVTLDSVIWAEPLPIGTSAQKAELIALTKALEWSKDKSVNIYTDSRYAFATLHVHGMIYRERGWLTAGGKA IKNAPEILALLTAVWLPKRVAVMHCKGHQKDDAPTSTGNRRADEVAREVAIRPLSTQATISAGKRTADGSEFEKRTADGSEFESPKKKAKVE
1381	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSSEAAAKPAPGGTAPLEE EYRLFLEAPIQNVTLLEQWKREIPKVWAEINPPGLASTQAPIHVQLLSTALPVRVRQYPITLEAKRSLRETIRKFRAAGILRPVHSPWNTPLLPVRKSGT SEYRMVQDLREVNKRVETIHPTVPNPYTLLSLLPPDRIWYSVLDLKDAFFCIPLAPESQLIFAFEWADAEEGESGQLTWTRLPQGFKNSPTLFNEALNRD LQGFRLDHPSVSLLQYVDDLLIAADTQAACLSATRDLLMTLAELGYRVSGKKAQLCQEEVTYLGFKIHKGSRSLSNSRTQAILQIPVPKTKRQVREFLGK IGYCRLFIPGFAELAQPLYAATRPGNDPLVWGEKEEEAFQSLKLALTQPPALALPSLDKPFQLFVEETSGAAKGVLTQALGPWKRPVAYLSKRLDPVAAG WPRCLRAIAAAALLTREASKLTFGQDIEITSSHNLESLLRSPPDKWLTNARITQYQVLLLDPPRVRFKQTAALNPATLLPETDDTLPIHHCLDTLDSLTS TRPDLTDQPLAQAEATLFTDGSSYIRDGKRYAGAAVVTLDSVIWAEPLPIGTSAQKAELIALTKALEWSKDKSVNIYTDSRYAFATLHVHGMIYRERGWL TAGGKAIKNAPEILALLTAVWLPKRVAVMHCKGHQKDDAPTSTGNRRADEVAREVAIRPLSTQATISAGKRTADGSEFEKRTADGSEFESPKKKAKVE
1382	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV

	QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSSGSSGSSGSSGSSGSSG GTAPLEEEYRLFLEAPIQNVTLLEQWKREIPKVWAEINPPGLASTQAPIHVQLLSTALPVRVRQYPITLEAKRSLRETIRKFRAAGILRPVHSPWNTPLL PVRKSGTSEYRMVQDLREVNKRVETIHPTVPNPYTLLSLLPPDRIWYSVLDLKDAFFCIPLAPESQLIFAFEWADAEEGESGQLTWTRLPQGFKNSPTLF NEALNRDLQGFRLDHPSVSLLQYVDDLLIAADTQAACLSATRDLLMTLAELGYRVSGKKAQLCQEEVTYLGFKIHKGSRSLSNSRTQAILQIPVPKTKRQ VREFLGKIGYCRLFIPGFAELAQPLYAATRPGNDPLVWGEKEEEAFQSLKLALTQPPALALPSLDKPFQLFVEETSGAAKGVLTQALGPWKRPVAYLSKR LDPVAAGWPRCLRAIAAAALLTREASKLTFGQDIEITSSHNLESLLRSPPDKWLTNARITQYQVLLLDPPRVRFKQTAALNPATLLPETDDTLPIHHCLD TLDSLTSTRPDLTDQPLAQAEATLFTDGSSYIRDGKRYAGAAVVTLDSVIWAEPLPIGTSAQKAELIALTKALEWSKDKSVNIYTDSRYAFATLHVHGMI YRERGWLTAGGKAIKNAPEILALLTAVWLPKRVAVMHCKGHQKDDAPTSTGNRRADEVAREVAIRPLSTQATISAGKRTADGSEFEKRTADGSEFESPKK KAKVE
1383	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSPAPGGGGGTAPLEEEY RLFLEAPIQNVTLLEQWKREIPKVWAEINPPGLASTQAPIHVQLLSTALPVRVRQYPITLEAKRSLRETIRKFRAAGILRPVHSPWNTPLLPVRKSGTSE YRMVQDLREVNKRVETIHPTVPNPYTLLSLLPPDRIWYSVLDLKDAFFCIPLAPESQLIFAFEWADAEEGESGQLTWTRLPQGFKNSPTLFNEALNRDLQ GFRLDHPSVSLLQYVDDLLIAADTQAACLSATRDLLMTLAELGYRVSGKKAQLCQEEVTYLGFKIHKGSRSLSNSRTQAILQIPVPKTKRQVREFLGKIG YCRLFIPGFAELAQPLYAATRPGNDPLVWGEKEEEAFQSLKLALTQPPALALPSLDKPFQLFVEETSGAAKGVLTQALGPWKRPVAYLSKRLDPVAAGWP RCLRAIAAAALLTREASKLTFGQDIEITSSHNLESLLRSPPDKWLTNARITQYQVLLLDPPRVRFKQTAALNPATLLPETDDTLPIHHCLDTLDSLTSTR PDLTDQPLAQAEATLFTDGSSYIRDGKRYAGAAVVTLDSVIWAEPLPIGTSAQKAELIALTKALEWSKDKSVNIYTDSRYAFATLHVHGMIYRERGWLTA GGKAIKNAPEILALLTAVWLPKRVAVMHCKGHQKDDAPTSTGNRRADEVAREVAIRPLSTQATISAGKRTADGSEFEKRTADGSEFESPKKKAKVE

1384	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGGEAAAKPAPGGTAPLEE EYRLFLEAPIQNVTLLEQWKREIPKVWAEINPPGLASTQAPIHVQLLSTALPVRVRQYPITLEAKRSLRETIRKFRAAGILRPVHSPWNTPLLPVRKSGT SEYRMVQDLREVNKRVETIHPTVPNPYTLLSLLPPDRIWYSVLDLKDAFFCIPLAPESQLIFAFEWADAEEGESGQLTWTRLPQGFKNSPTLFNEALNRD LQGFRLDHPSVSLLQYVDDLLIAADTQAACLSATRDLLMTLAELGYRVSGKKAQLCQEEVTYLGFKIHKGSRSLSNSRTQAILQIPVPKTKRQVREFLGK IGYCRLFIPGFAELAQPLYAATRPGNDPLVWGEKEEEAFQSLKLALTQPPALALPSLDKPFQLFVEETSGAAKGVLTQALGPWKRPVAYLSKRLDPVAAG WPRCLRAIAAAALLTREASKLTFGQDIEITSSHNLESLLRSPPDKWLTNARITQYQVLLLDPPRVRFKQTAALNPATLLPETDDTLPIHHCLDTLDSLTS TRPDLTDQPLAQAEATLFTDGSSYIRDGKRYAGAAVVTLDSVIWAEPLPIGTSAQKAELIALTKALEWSKDKSVNIYTDSRYAFATLHVHGMIYRERGWL TAGGKAIKNAPEILALLTAVWLPKRVAVMHCKGHQKDDAPTSTGNRRADEVAREVAIRPLSTQATISAGKRTADGSEFEKRTADGSEFESPKKKAKVE
1385	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPGGSGSSGGTAPLEEEY RLFLEAPIQNVTLLEQWKREIPKVWAEINPPGLASTQAPIHVQLLSTALPVRVRQYPITLEAKRSLRETIRKFRAAGILRPVHSPWNTPLLPVRKSGTSE YRMVQDLREVNKRVETIHPTVPNPYTLLSLLPPDRIWYSVLDLKDAFFCIPLAPESQLIFAFEWADAEEGESGQLTWTRLPQGFKNSPTLFNEALNRDLQ GFRLDHPSVSLLQYVDDLLIAADTQAACLSATRDLLMTLAELGYRVSGKKAQLCQEEVTYLGFKIHKGSRSLSNSRTQAILQIPVPKTKRQVREFLGKIG YCRLFIPGFAELAQPLYAATRPGNDPLVWGEKEEEAFQSLKLALTQPPALALPSLDKPFQLFVEETSGAAKGVLTQALGPWKRPVAYLSKRLDPVAAGWP RCLRAIAAAALLTREASKLTFGQDIEITSSHNLESLLRSPPDKWLTNARITQYQVLLLDPPRVRFKQTAALNPATLLPETDDTLPIHHCLDTLDSLTSTR

	PDLTDQPLAQAEATLFTDGSSYIRDGKRYAGAAVVTLDSVIWAEPLPIGTSAQKAELIALTKALEWSKDKSVNIYTDSRYAFATLHVHGMIYRERGWLTA GGKAIKNAPEILALLTAVWLPKRVAVMHCKGHQKDDAPTSTGNRRADEVAREVAIRPLSTQATISAGKRTADGSEFEKRTADGSEFESPKKKAKVE
1389	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGGGGTAPLEEEYRLFLEA PIQNVTLLEQWKREIPKVWAEINPPGLASTQAPIHVQLLSTALPVRVRQYPITLEAKRSLRETIRKFRAAGILRPVHSPWNTPLLPVRKSGTSEYRMVQD LREVNKRVETIHPTVPNPYTLLSLLPPDRIWYSVLDLKDAFFCIPLAPESQLIFAFEWADAEEGESGQLTWTRLPQGFKNSPTLFNEALNRDLQGFRLDH PSVSLLQYVDDLLIAADTQAACLSATRDLLMTLAELGYRVSGKKAQLCQEEVTYLGFKIHKGSRSLSNSRTQAILQIPVPKTKRQVREFLGKIGYCRLFI PGFAELAQPLYAATRPGNDPLVWGEKEEEAFQSLKLALTQPPALALPSLDKPFQLFVEETSGAAKGVLTQALGPWKRPVAYLSKRLDPVAAGWPRCLRAI AAAALLTREASKLTFGQDIEITSSHNLESLLRSPPDKWLTNARITQYQVLLLDPPRVRFKQTAALNPATLLPETDDTLPIHHCLDTLDSLTSTRPDLTDQ PLAQAEATLFTDGSSYIRDGKRYAGAAVVTLDSVIWAEPLPIGTSAQKAELIALTKALEWSKDKSVNIYTDSRYAFATLHVHGMIYRERGWLTAGGKAIK NAPEILALLTAVWLPKRVAVMHCKGHQKDDAPTSTGNRRADEVAREVAIRPLSTQATISAGKRTADGSEFEKRTADGSEFESPKKKAKVE
1390	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKGGGGGSGGTAPLEE EYRLFLEAPIQNVTLLEQWKREIPKVWAEINPPGLASTQAPIHVQLLSTALPVRVRQYPITLEAKRSLRETIRKFRAAGILRPVHSPWNTPLLPVRKSGT SEYRMVQDLREVNKRVETIHPTVPNPYTLLSLLPPDRIWYSVLDLKDAFFCIPLAPESQLIFAFEWADAEEGESGQLTWTRLPQGFKNSPTLFNEALNRD LQGFRLDHPSVSLLQYVDDLLIAADTQAACLSATRDLLMTLAELGYRVSGKKAQLCQEEVTYLGFKIHKGSRSLSNSRTQAILQIPVPKTKRQVREFLGK IGYCRLFIPGFAELAQPLYAATRPGNDPLVWGEKEEEAFQSLKLALTQPPALALPSLDKPFQLFVEETSGAAKGVLTQALGPWKRPVAYLSKRLDPVAAG

	WPRCLRAIAAAALLTREASKLTFGQDIEITSSHNLESLLRSPPDKWLTNARITQYQVLLLDPPRVRFKQTAALNPATLLPETDDTLPIHHCLDTLDSLTS TRPDLTDQPLAQAEATLFTDGSSYIRDGKRYAGAAVVTLDSVIWAEPLPIGTSAQKAELIALTKALEWSKDKSVNIYTDSRYAFATLHVHGMIYRERGWL TAGGKAIKNAPEILALLTAVWLPKRVAVMHCKGHQKDDAPTSTGNRRADEVAREVAIRPLSTQATISAGKRTADGSEFEKRTADGSEFESPKKKAKVE
1394	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSSEAAAKGGGGGTAPLEE EYRLFLEAPIQNVTLLEQWKREIPKVWAEINPPGLASTQAPIHVQLLSTALPVRVRQYPITLEAKRSLRETIRKFRAAGILRPVHSPWNTPLLPVRKSGT SEYRMVQDLREVNKRVETIHPTVPNPYTLLSLLPPDRIWYSVLDLKDAFFCIPLAPESQLIFAFEWADAEEGESGQLTWTRLPQGFKNSPTLFNEALNRD LQGFRLDHPSVSLLQYVDDLLIAADTQAACLSATRDLLMTLAELGYRVSGKKAQLCQEEVTYLGFKIHKGSRSLSNSRTQAILQIPVPKTKRQVREFLGK IGYCRLFIPGFAELAQPLYAATRPGNDPLVWGEKEEEAFQSLKLALTQPPALALPSLDKPFQLFVEETSGAAKGVLTQALGPWKRPVAYLSKRLDPVAAG WPRCLRAIAAAALLTREASKLTFGQDIEITSSHNLESLLRSPPDKWLTNARITQYQVLLLDPPRVRFKQTAALNPATLLPETDDTLPIHHCLDTLDSLTS TRPDLTDQPLAQAEATLFTDGSSYIRDGKRYAGAAVVTLDSVIWAEPLPIGTSAQKAELIALTKALEWSKDKSVNIYTDSRYAFATLHVHGMIYRERGWL TAGGKAIKNAPEILALLTAVWLPKRVAVMHCKGHQKDDAPTSTGNRRADEVAREVAIRPLSTQATISAGKRTADGSEFEKRTADGSEFESPKKKAKVE
1397	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGPAPGGTAPLEEEYRLF LEAPIQNVTLLEQWKREIPKVWAEINPPGLASTQAPIHVQLLSTALPVRVRQYPITLEAKRSLRETIRKFRAAGILRPVHSPWNTPLLPVRKSGTSEYRM VQDLREVNKRVETIHPTVPNPYTLLSLLPPDRIWYSVLDLKDAFFCIPLAPESQLIFAFEWADAEEGESGQLTWTRLPQGFKNSPTLFNEALNRDLQGFR LDHPSVSLLQYVDDLLIAADTQAACLSATRDLLMTLAELGYRVSGKKAQLCQEEVTYLGFKIHKGSRSLSNSRTQAILQIPVPKTKRQVREFLGKIGYCR

	LFIPGFAELAQPLYAATRPGNDPLVWGEKEEEAFQSLKLALTQPPALALPSLDKPFQLFVEETSGAAKGVLTQALGPWKRPVAYLSKRLDPVAAGWPRCL RAIAAAALLTREASKLTFGQDIEITSSHNLESLLRSPPDKWLTNARITQYQVLLLDPPRVRFKQTAALNPATLLPETDDTLPIHHCLDTLDSLTSTRPDL TDQPLAQAEATLFTDGSSYIRDGKRYAGAAVVTLDSVIWAEPLPIGTSAQKAELIALTKALEWSKDKSVNIYTDSRYAFATLHVHGMIYRERGWLTAGGK AIKNAPEILALLTAVWLPKRVAVMHCKGHQKDDAPTSTGNRRADEVAREVAIRPLSTQATISAGKRTADGSEFEKRTADGSEFESPKKKAKVE
1399	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKGGGGSEAAAKGGTA PLEEEYRLFLEAPIQNVTLLEQWKREIPKVWAEINPPGLASTQAPIHVQLLSTALPVRVRQYPITLEAKRSLRETIRKFRAAGILRPVHSPWNTPLLPVR KSGTSEYRMVQDLREVNKRVETIHPTVPNPYTLLSLLPPDRIWYSVLDLKDAFFCIPLAPESQLIFAFEWADAEEGESGQLTWTRLPQGFKNSPTLFNEA LNRDLQGFRLDHPSVSLLQYVDDLLIAADTQAACLSATRDLLMTLAELGYRVSGKKAQLCQEEVTYLGFKIHKGSRSLSNSRTQAILQIPVPKTKRQVRE FLGKIGYCRLFIPGFAELAQPLYAATRPGNDPLVWGEKEEEAFQSLKLALTQPPALALPSLDKPFQLFVEETSGAAKGVLTQALGPWKRPVAYLSKRLDP VAAGWPRCLRAIAAAALLTREASKLTFGQDIEITSSHNLESLLRSPPDKWLTNARITQYQVLLLDPPRVRFKQTAALNPATLLPETDDTLPIHHCLDTLD SLTSTRPDLTDQPLAQAEATLFTDGSSYIRDGKRYAGAAVVTLDSVIWAEPLPIGTSAQKAELIALTKALEWSKDKSVNIYTDSRYAFATLHVHGMIYRE RGWLTAGGKAIKNAPEILALLTAVWLPKRVAVMHCKGHQKDDAPTSTGNRRADEVAREVAIRPLSTQATISAGKRTADGSEFEKRTADGSEFESPKKKAK VE
1400	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKEAAAKEAAAKEAAA KEAAAKGGTAPLEEEYRLFLEAPIQNVTLLEQWKREIPKVWAEINPPGLASTQAPIHVQLLSTALPVRVRQYPITLEAKRSLRETIRKFRAAGILRPVHS

	PWNTPLLPVRKSGTSEYRMVQDLREVNKRVETIHPTVPNPYTLLSLLPPDRIWYSVLDLKDAFFCIPLAPESQLIFAFEWADAEEGESGQLTWTRLPQGF KNSPTLFNEALNRDLQGFRLDHPSVSLLQYVDDLLIAADTQAACLSATRDLLMTLAELGYRVSGKKAQLCQEEVTYLGFKIHKGSRSLSNSRTQAILQIP VPKTKRQVREFLGKIGYCRLFIPGFAELAQPLYAATRPGNDPLVWGEKEEEAFQSLKLALTQPPALALPSLDKPFQLFVEETSGAAKGVLTQALGPWKRP VAYLSKRLDPVAAGWPRCLRAIAAAALLTREASKLTFGQDIEITSSHNLESLLRSPPDKWLTNARITQYQVLLLDPPRVRFKQTAALNPATLLPETDDTL PIHHCLDTLDSLTSTRPDLTDQPLAQAEATLFTDGSSYIRDGKRYAGAAVVTLDSVIWAEPLPIGTSAQKAELIALTKALEWSKDKSVNIYTDSRYAFAT LHVHGMIYRERGWLTAGGKAIKNAPEILALLTAVWLPKRVAVMHCKGHQKDDAPTSTGNRRADEVAREVAIRPLSTQATISAGKRTADGSEFEKRTADGS EFESPKKKAKVE
1401	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPGSSGGSGGTAPLEEEY RLFLEAPIQNVTLLEQWKREIPKVWAEINPPGLASTQAPIHVQLLSTALPVRVRQYPITLEAKRSLRETIRKFRAAGILRPVHSPWNTPLLPVRKSGTSE YRMVQDLREVNKRVETIHPTVPNPYTLLSLLPPDRIWYSVLDLKDAFFCIPLAPESQLIFAFEWADAEEGESGQLTWTRLPQGFKNSPTLFNEALNRDLQ GFRLDHPSVSLLQYVDDLLIAADTQAACLSATRDLLMTLAELGYRVSGKKAQLCQEEVTYLGFKIHKGSRSLSNSRTQAILQIPVPKTKRQVREFLGKIG YCRLFIPGFAELAQPLYAATRPGNDPLVWGEKEEEAFQSLKLALTQPPALALPSLDKPFQLFVEETSGAAKGVLTQALGPWKRPVAYLSKRLDPVAAGWP RCLRAIAAAALLTREASKLTFGQDIEITSSHNLESLLRSPPDKWLTNARITQYQVLLLDPPRVRFKQTAALNPATLLPETDDTLPIHHCLDTLDSLTSTR PDLTDQPLAQAEATLFTDGSSYIRDGKRYAGAAVVTLDSVIWAEPLPIGTSAQKAELIALTKALEWSKDKSVNIYTDSRYAFATLHVHGMIYRERGWLTA GGKAIKNAPEILALLTAVWLPKRVAVMHCKGHQKDDAPTSTGNRRADEVAREVAIRPLSTQATISAGKRTADGSEFEKRTADGSEFESPKKKAKVE
1402	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK

	VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGGPAPGGSGGTAPLEEEY RLFLEAPIQNVTLLEQWKREIPKVWAEINPPGLASTQAPIHVQLLSTALPVRVRQYPITLEAKRSLRETIRKFRAAGILRPVHSPWNTPLLPVRKSGTSE YRMVQDLREVNKRVETIHPTVPNPYTLLSLLPPDRIWYSVLDLKDAFFCIPLAPESQLIFAFEWADAEEGESGQLTWTRLPQGFKNSPTLFNEALNRDLQ GFRLDHPSVSLLQYVDDLLIAADTQAACLSATRDLLMTLAELGYRVSGKKAQLCQEEVTYLGFKIHKGSRSLSNSRTQAILQIPVPKTKRQVREFLGKIG YCRLFIPGFAELAQPLYAATRPGNDPLVWGEKEEEAFQSLKLALTQPPALALPSLDKPFQLFVEETSGAAKGVLTQALGPWKRPVAYLSKRLDPVAAGWP RCLRAIAAAALLTREASKLTFGQDIEITSSHNLESLLRSPPDKWLTNARITQYQVLLLDPPRVRFKQTAALNPATLLPETDDTLPIHHCLDTLDSLTSTR PDLTDQPLAQAEATLFTDGSSYIRDGKRYAGAAVVTLDSVIWAEPLPIGTSAQKAELIALTKALEWSKDKSVNIYTDSRYAFATLHVHGMIYRERGWLTA GGKAIKNAPEILALLTAVWLPKRVAVMHCKGHQKDDAPTSTGNRRADEVAREVAIRPLSTQATISAGKRTADGSEFEKRTADGSEFESPKKKAKVE
1404	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGGGSSEAAAKGGTAPLEE EYRLFLEAPIQNVTLLEQWKREIPKVWAEINPPGLASTQAPIHVQLLSTALPVRVRQYPITLEAKRSLRETIRKFRAAGILRPVHSPWNTPLLPVRKSGT SEYRMVQDLREVNKRVETIHPTVPNPYTLLSLLPPDRIWYSVLDLKDAFFCIPLAPESQLIFAFEWADAEEGESGQLTWTRLPQGFKNSPTLFNEALNRD LQGFRLDHPSVSLLQYVDDLLIAADTQAACLSATRDLLMTLAELGYRVSGKKAQLCQEEVTYLGFKIHKGSRSLSNSRTQAILQIPVPKTKRQVREFLGK IGYCRLFIPGFAELAQPLYAATRPGNDPLVWGEKEEEAFQSLKLALTQPPALALPSLDKPFQLFVEETSGAAKGVLTQALGPWKRPVAYLSKRLDPVAAG WPRCLRAIAAAALLTREASKLTFGQDIEITSSHNLESLLRSPPDKWLTNARITQYQVLLLDPPRVRFKQTAALNPATLLPETDDTLPIHHCLDTLDSLTS TRPDLTDQPLAQAEATLFTDGSSYIRDGKRYAGAAVVTLDSVIWAEPLPIGTSAQKAELIALTKALEWSKDKSVNIYTDSRYAFATLHVHGMIYRERGWL TAGGKAIKNAPEILALLTAVWLPKRVAVMHCKGHQKDDAPTSTGNRRADEVAREVAIRPLSTQATISAGKRTADGSEFEKRTADGSEFESPKKKAKVE
1405	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE

	VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSSEAAAKGGTAPLEEEYR LFLEAPIQNVTLLEQWKREIPKVWAEINPPGLASTQAPIHVQLLSTALPVRVRQYPITLEAKRSLRETIRKFRAAGILRPVHSPWNTPLLPVRKSGTSEY RMVQDLREVNKRVETIHPTVPNPYTLLSLLPPDRIWYSVLDLKDAFFCIPLAPESQLIFAFEWADAEEGESGQLTWTRLPQGFKNSPTLFNEALNRDLQG FRLDHPSVSLLQYVDDLLIAADTQAACLSATRDLLMTLAELGYRVSGKKAQLCQEEVTYLGFKIHKGSRSLSNSRTQAILQIPVPKTKRQVREFLGKIGY CRLFIPGFAELAQPLYAATRPGNDPLVWGEKEEEAFQSLKLALTQPPALALPSLDKPFQLFVEETSGAAKGVLTQALGPWKRPVAYLSKRLDPVAAGWPR CLRAIAAAALLTREASKLTFGQDIEITSSHNLESLLRSPPDKWLTNARITQYQVLLLDPPRVRFKQTAALNPATLLPETDDTLPIHHCLDTLDSLTSTRP DLTDQPLAQAEATLFTDGSSYIRDGKRYAGAAVVTLDSVIWAEPLPIGTSAQKAELIALTKALEWSKDKSVNIYTDSRYAFATLHVHGMIYRERGWLTAG GKAIKNAPEILALLTAVWLPKRVAVMHCKGHQKDDAPTSTGNRRADEVAREVAIRPLSTQATISAGKRTADGSEFEKRTADGSEFESPKKKAKVE
1406	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKGGSGSSGGTAPLEE EYRLFLEAPIQNVTLLEQWKREIPKVWAEINPPGLASTQAPIHVQLLSTALPVRVRQYPITLEAKRSLRETIRKFRAAGILRPVHSPWNTPLLPVRKSGT SEYRMVQDLREVNKRVETIHPTVPNPYTLLSLLPPDRIWYSVLDLKDAFFCIPLAPESQLIFAFEWADAEEGESGQLTWTRLPQGFKNSPTLFNEALNRD LQGFRLDHPSVSLLQYVDDLLIAADTQAACLSATRDLLMTLAELGYRVSGKKAQLCQEEVTYLGFKIHKGSRSLSNSRTQAILQIPVPKTKRQVREFLGK IGYCRLFIPGFAELAQPLYAATRPGNDPLVWGEKEEEAFQSLKLALTQPPALALPSLDKPFQLFVEETSGAAKGVLTQALGPWKRPVAYLSKRLDPVAAG WPRCLRAIAAAALLTREASKLTFGQDIEITSSHNLESLLRSPPDKWLTNARITQYQVLLLDPPRVRFKQTAALNPATLLPETDDTLPIHHCLDTLDSLTS TRPDLTDQPLAQAEATLFTDGSSYIRDGKRYAGAAVVTLDSVIWAEPLPIGTSAQKAELIALTKALEWSKDKSVNIYTDSRYAFATLHVHGMIYRERGWL TAGGKAIKNAPEILALLTAVWLPKRVAVMHCKGHQKDDAPTSTGNRRADEVAREVAIRPLSTQATISAGKRTADGSEFEKRTADGSEFESPKKKAKVE
1410	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM

	PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPGGGGGTAPLEEEYRLF LEAPIQNVTLLEQWKREIPKVWAEINPPGLASTQAPIHVQLLSTALPVRVRQYPITLEAKRSLRETIRKFRAAGILRPVHSPWNTPLLPVRKSGTSEYRM VQDLREVNKRVETIHPTVPNPYTLLSLLPPDRIWYSVLDLKDAFFCIPLAPESQLIFAFEWADAEEGESGQLTWTRLPQGFKNSPTLFNEALNRDLQGFR LDHPSVSLLQYVDDLLIAADTQAACLSATRDLLMTLAELGYRVSGKKAQLCQEEVTYLGFKIHKGSRSLSNSRTQAILQIPVPKTKRQVREFLGKIGYCR LFIPGFAELAQPLYAATRPGNDPLVWGEKEEEAFQSLKLALTQPPALALPSLDKPFQLFVEETSGAAKGVLTQALGPWKRPVAYLSKRLDPVAAGWPRCL RAIAAAALLTREASKLTFGQDIEITSSHNLESLLRSPPDKWLTNARITQYQVLLLDPPRVRFKQTAALNPATLLPETDDTLPIHHCLDTLDSLTSTRPDL TDQPLAQAEATLFTDGSSYIRDGKRYAGAAVVTLDSVIWAEPLPIGTSAQKAELIALTKALEWSKDKSVNIYTDSRYAFATLHVHGMIYRERGWLTAGGK AIKNAPEILALLTAVWLPKRVAVMHCKGHQKDDAPTSTGNRRADEVAREVAIRPLSTQATISAGKRTADGSEFEKRTADGSEFESPKKKAKVE
1415	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGPAPEAAAKGGTAPLEE EYRLFLEAPIQNVTLLEQWKREIPKVWAEINPPGLASTQAPIHVQLLSTALPVRVRQYPITLEAKRSLRETIRKFRAAGILRPVHSPWNTPLLPVRKSGT SEYRMVQDLREVNKRVETIHPTVPNPYTLLSLLPPDRIWYSVLDLKDAFFCIPLAPESQLIFAFEWADAEEGESGQLTWTRLPQGFKNSPTLFNEALNRD LQGFRLDHPSVSLLQYVDDLLIAADTQAACLSATRDLLMTLAELGYRVSGKKAQLCQEEVTYLGFKIHKGSRSLSNSRTQAILQIPVPKTKRQVREFLGK IGYCRLFIPGFAELAQPLYAATRPGNDPLVWGEKEEEAFQSLKLALTQPPALALPSLDKPFQLFVEETSGAAKGVLTQALGPWKRPVAYLSKRLDPVAAG WPRCLRAIAAAALLTREASKLTFGQDIEITSSHNLESLLRSPPDKWLTNARITQYQVLLLDPPRVRFKQTAALNPATLLPETDDTLPIHHCLDTLDSLTS TRPDLTDQPLAQAEATLFTDGSSYIRDGKRYAGAAVVTLDSVIWAEPLPIGTSAQKAELIALTKALEWSKDKSVNIYTDSRYAFATLHVHGMIYRERGWL TAGGKAIKNAPEILALLTAVWLPKRVAVMHCKGHQKDDAPTSTGNRRADEVAREVAIRPLSTQATISAGKRTADGSEFEKRTADGSEFESPKKKAKVE
1419	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL

	NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKGSSGGGGGTAPLEE EYRLFLEAPIQNVTLLEQWKREIPKVWAEINPPGLASTQAPIHVQLLSTALPVRVRQYPITLEAKRSLRETIRKFRAAGILRPVHSPWNTPLLPVRKSGT SEYRMVQDLREVNKRVETIHPTVPNPYTLLSLLPPDRIWYSVLDLKDAFFCIPLAPESQLIFAFEWADAEEGESGQLTWTRLPQGFKNSPTLFNEALNRD LQGFRLDHPSVSLLQYVDDLLIAADTQAACLSATRDLLMTLAELGYRVSGKKAQLCQEEVTYLGFKIHKGSRSLSNSRTQAILQIPVPKTKRQVREFLGK IGYCRLFIPGFAELAQPLYAATRPGNDPLVWGEKEEEAFQSLKLALTQPPALALPSLDKPFQLFVEETSGAAKGVLTQALGPWKRPVAYLSKRLDPVAAG WPRCLRAIAAAALLTREASKLTFGQDIEITSSHNLESLLRSPPDKWLTNARITQYQVLLLDPPRVRFKQTAALNPATLLPETDDTLPIHHCLDTLDSLTS TRPDLTDQPLAQAEATLFTDGSSYIRDGKRYAGAAVVTLDSVIWAEPLPIGTSAQKAELIALTKALEWSKDKSVNIYTDSRYAFATLHVHGMIYRERGWL TAGGKAIKNAPEILALLTAVWLPKRVAVMHCKGHQKDDAPTSTGNRRADEVAREVAIRPLSTQATISAGKRTADGSEFEKRTADGSEFESPKKKAKVE
1422	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKGGGGGTAPLEEEYR LFLEAPIQNVTLLEQWKREIPKVWAEINPPGLASTQAPIHVQLLSTALPVRVRQYPITLEAKRSLRETIRKFRAAGILRPVHSPWNTPLLPVRKSGTSEY RMVQDLREVNKRVETIHPTVPNPYTLLSLLPPDRIWYSVLDLKDAFFCIPLAPESQLIFAFEWADAEEGESGQLTWTRLPQGFKNSPTLFNEALNRDLQG FRLDHPSVSLLQYVDDLLIAADTQAACLSATRDLLMTLAELGYRVSGKKAQLCQEEVTYLGFKIHKGSRSLSNSRTQAILQIPVPKTKRQVREFLGKIGY CRLFIPGFAELAQPLYAATRPGNDPLVWGEKEEEAFQSLKLALTQPPALALPSLDKPFQLFVEETSGAAKGVLTQALGPWKRPVAYLSKRLDPVAAGWPR CLRAIAAAALLTREASKLTFGQDIEITSSHNLESLLRSPPDKWLTNARITQYQVLLLDPPRVRFKQTAALNPATLLPETDDTLPIHHCLDTLDSLTSTRP DLTDQPLAQAEATLFTDGSSYIRDGKRYAGAAVVTLDSVIWAEPLPIGTSAQKAELIALTKALEWSKDKSVNIYTDSRYAFATLHVHGMIYRERGWLTAG GKAIKNAPEILALLTAVWLPKRVAVMHCKGHQKDDAPTSTGNRRADEVAREVAIRPLSTQATISAGKRTADGSEFEKRTADGSEFESPKKKAKVE
1423	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA

	KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGGGSGGGGSGGTAPLEEE YRLFLEAPIQNVTLLEQWKREIPKVWAEINPPGLASTQAPIHVQLLSTALPVRVRQYPITLEAKRSLRETIRKFRAAGILRPVHSPWNTPLLPVRKSGTS EYRMVQDLREVNKRVETIHPTVPNPYTLLSLLPPDRIWYSVLDLKDAFFCIPLAPESQLIFAFEWADAEEGESGQLTWTRLPQGFKNSPTLFNEALNRDL QGFRLDHPSVSLLQYVDDLLIAADTQAACLSATRDLLMTLAELGYRVSGKKAQLCQEEVTYLGFKIHKGSRSLSNSRTQAILQIPVPKTKRQVREFLGKI GYCRLFIPGFAELAQPLYAATRPGNDPLVWGEKEEEAFQSLKLALTQPPALALPSLDKPFQLFVEETSGAAKGVLTQALGPWKRPVAYLSKRLDPVAAGW PRCLRAIAAAALLTREASKLTFGQDIEITSSHNLESLLRSPPDKWLTNARITQYQVLLLDPPRVRFKQTAALNPATLLPETDDTLPIHHCLDTLDSLTST RPDLTDQPLAQAEATLFTDGSSYIRDGKRYAGAAVVTLDSVIWAEPLPIGTSAQKAELIALTKALEWSKDKSVNIYTDSRYAFATLHVHGMIYRERGWLT AGGKAIKNAPEILALLTAVWLPKRVAVMHCKGHQKDDAPTSTGNRRADEVAREVAIRPLSTQATISAGKRTADGSEFEKRTADGSEFESPKKKAKVE
1424	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSSGGGEAAAKGGTAPLEE EYRLFLEAPIQNVTLLEQWKREIPKVWAEINPPGLASTQAPIHVQLLSTALPVRVRQYPITLEAKRSLRETIRKFRAAGILRPVHSPWNTPLLPVRKSGT SEYRMVQDLREVNKRVETIHPTVPNPYTLLSLLPPDRIWYSVLDLKDAFFCIPLAPESQLIFAFEWADAEEGESGQLTWTRLPQGFKNSPTLFNEALNRD LQGFRLDHPSVSLLQYVDDLLIAADTQAACLSATRDLLMTLAELGYRVSGKKAQLCQEEVTYLGFKIHKGSRSLSNSRTQAILQIPVPKTKRQVREFLGK IGYCRLFIPGFAELAQPLYAATRPGNDPLVWGEKEEEAFQSLKLALTQPPALALPSLDKPFQLFVEETSGAAKGVLTQALGPWKRPVAYLSKRLDPVAAG WPRCLRAIAAAALLTREASKLTFGQDIEITSSHNLESLLRSPPDKWLTNARITQYQVLLLDPPRVRFKQTAALNPATLLPETDDTLPIHHCLDTLDSLTS TRPDLTDQPLAQAEATLFTDGSSYIRDGKRYAGAAVVTLDSVIWAEPLPIGTSAQKAELIALTKALEWSKDKSVNIYTDSRYAFATLHVHGMIYRERGWL TAGGKAIKNAPEILALLTAVWLPKRVAVMHCKGHQKDDAPTSTGNRRADEVAREVAIRPLSTQATISAGKRTADGSEFEKRTADGSEFESPKKKAKVE
1441	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK

	ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKGGSGGGGGTAPLEE EYRLFLEAPIQNVTLLEQWKREIPKVWAEINPPGLASTQAPIHVQLLSTALPVRVRQYPITLEAKRSLRETIRKFRAAGILRPVHSPWNTPLLPVRKSGT SEYRMVQDLREVNKRVETIHPTVPNPYTLLSLLPPDRIWYSVLDLKDAFFCIPLAPESQLIFAFEWADAEEGESGQLTWTRLPQGFKNSPTLFNEALNRD LQGFRLDHPSVSLLQYVDDLLIAADTQAACLSATRDLLMTLAELGYRVSGKKAQLCQEEVTYLGFKIHKGSRSLSNSRTQAILQIPVPKTKRQVREFLGK IGYCRLFIPGFAELAQPLYAATRPGNDPLVWGEKEEEAFQSLKLALTQPPALALPSLDKPFQLFVEETSGAAKGVLTQALGPWKRPVAYLSKRLDPVAAG WPRCLRAIAAAALLTREASKLTFGQDIEITSSHNLESLLRSPPDKWLTNARITQYQVLLLDPPRVRFKQTAALNPATLLPETDDTLPIHHCLDTLDSLTS TRPDLTDQPLAQAEATLFTDGSSYIRDGKRYAGAAVVTLDSVIWAEPLPIGTSAQKAELIALTKALEWSKDKSVNIYTDSRYAFATLHVHGMIYRERGWL TAGGKAIKNAPEILALLTAVWLPKRVAVMHCKGHQKDDAPTSTGNRRADEVAREVAIRPLSTQATISAGKRTADGSEFEKRTADGSEFESPKKKAKVE
1540	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGGSSEAAAKGGTVSLQD EHRLFDIPVTTSLPDVWLQDFPQAWAETGGLGRAKCQAPIIIDLKPTAVPVSIKQYPMSLEAHMGIRQHIIKFLELGVLRPCRSPWNTPLLPVKKPGTQD YRPVQDLREINKRTVDIHPTVPNPYNLLSTLKPDYSWYTVLDLKDAFFCLPLAPQSQELFAFEWKDPERGISGQLTWTRLPQGFKNSPTLFNEALHRDLT DFRTQHPEVTLLQYVDDLLLAAPTKKACTQGTRHLLQELGEKGYRASAKKAQICQTKVTYLGYILSEGKRWLTPGRIETVARIPPPRNPREVREFLGTAG FCRLWIPGFAELAAPLYALTKPSTPFTWQTEHQLAFEALKKALLSAPALGLPDTSKPFTLFLDERQGIAKGVLTQKLGPWKRPVAYLSKKLDPVAAGWPP CLRIMAATAMLVKDSAKLTLGQPLTVITPHTLEAIVRQPPDRWITNARLTHYQALLLDTDRVQFGPPVTLNPATLLPVPENQPSPHDCRQVLAETHGTRE DLKDQELPDADHTWYTDGSSYLDSGTRRAGAAVVDGHNTIWAQSLPPGTSAQKAELIALTKALELSKGKKANIYTDSRYAFATAHTHGSIYERRGWLTSE GKEIKNKAEIIALLKALFLPQEVAIIHCPGHQKGQDPVAVGNRQADRVARQAAMAEVLTLATEPDNTSHITAGKRTADGSEFEKRTADGSEFESPKKKAK VE
1543	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA

	SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGGSGGGGSGGGGSGGGG SGGGGSGGTVSLQDEHRLFDIPVTTSLPDVWLQDFPQAWAETGGLGRAKCQAPIIIDLKPTAVPVSIKQYPMSLEAHMGIRQHIIKFLELGVLRPCRSPW NTPLLPVKKPGTQDYRPVQDLREINKRTVDIHPTVPNPYNLLSTLKPDYSWYTVLDLKDAFFCLPLAPQSQELFAFEWKDPERGISGQLTWTRLPQGFKN SPTLFNEALHRDLTDFRTQHPEVTLLQYVDDLLLAAPTKKACTQGTRHLLQELGEKGYRASAKKAQICQTKVTYLGYILSEGKRWLTPGRIETVARIPPP RNPREVREFLGTAGFCRLWIPGFAELAAPLYALTKPSTPFTWQTEHQLAFEALKKALLSAPALGLPDTSKPFTLFLDERQGIAKGVLTQKLGPWKRPVAY LSKKLDPVAAGWPPCLRIMAATAMLVKDSAKLTLGQPLTVITPHTLEAIVRQPPDRWITNARLTHYQALLLDTDRVQFGPPVTLNPATLLPVPENQPSPH DCRQVLAETHGTREDLKDQELPDADHTWYTDGSSYLDSGTRRAGAAVVDGHNTIWAQSLPPGTSAQKAELIALTKALELSKGKKANIYTDSRYAFATAHT HGSIYERRGWLTSEGKEIKNKAEIIALLKALFLPQEVAIIHCPGHQKGQDPVAVGNRQADRVARQAAMAEVLTLATEPDNTSHITAGKRTADGSEFEKRT ADGSEFESPKKKAKVE
1550	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGSGSSGGGGGTVSLQDEH RLFDIPVTTSLPDVWLQDFPQAWAETGGLGRAKCQAPIIIDLKPTAVPVSIKQYPMSLEAHMGIRQHIIKFLELGVLRPCRSPWNTPLLPVKKPGTQDYR PVQDLREINKRTVDIHPTVPNPYNLLSTLKPDYSWYTVLDLKDAFFCLPLAPQSQELFAFEWKDPERGISGQLTWTRLPQGFKNSPTLFNEALHRDLTDF RTQHPEVTLLQYVDDLLLAAPTKKACTQGTRHLLQELGEKGYRASAKKAQICQTKVTYLGYILSEGKRWLTPGRIETVARIPPPRNPREVREFLGTAGFC RLWIPGFAELAAPLYALTKPSTPFTWQTEHQLAFEALKKALLSAPALGLPDTSKPFTLFLDERQGIAKGVLTQKLGPWKRPVAYLSKKLDPVAAGWPPCL RIMAATAMLVKDSAKLTLGQPLTVITPHTLEAIVRQPPDRWITNARLTHYQALLLDTDRVQFGPPVTLNPATLLPVPENQPSPHDCRQVLAETHGTREDL KDQELPDADHTWYTDGSSYLDSGTRRAGAAVVDGHNTIWAQSLPPGTSAQKAELIALTKALELSKGKKANIYTDSRYAFATAHTHGSIYERRGWLTSEGK EIKNKAEIIALLKALFLPQEVAIIHCPGHQKGQDPVAVGNRQADRVARQAAMAEVLTLATEPDNTSHITAGKRTADGSEFEKRTADGSEFESPKKKAKVE
1553	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL

	LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSSGSSGSSGSSGSSGGTV SLQDEHRLFDIPVTTSLPDVWLQDFPQAWAETGGLGRAKCQAPIIIDLKPTAVPVSIKQYPMSLEAHMGIRQHIIKFLELGVLRPCRSPWNTPLLPVKKP GTQDYRPVQDLREINKRTVDIHPTVPNPYNLLSTLKPDYSWYTVLDLKDAFFCLPLAPQSQELFAFEWKDPERGISGQLTWTRLPQGFKNSPTLFNEALH RDLTDFRTQHPEVTLLQYVDDLLLAAPTKKACTQGTRHLLQELGEKGYRASAKKAQICQTKVTYLGYILSEGKRWLTPGRIETVARIPPPRNPREVREFL GTAGFCRLWIPGFAELAAPLYALTKPSTPFTWQTEHQLAFEALKKALLSAPALGLPDTSKPFTLFLDERQGIAKGVLTQKLGPWKRPVAYLSKKLDPVAA GWPPCLRIMAATAMLVKDSAKLTLGQPLTVITPHTLEAIVRQPPDRWITNARLTHYQALLLDTDRVQFGPPVTLNPATLLPVPENQPSPHDCRQVLAETH GTREDLKDQELPDADHTWYTDGSSYLDSGTRRAGAAVVDGHNTIWAQSLPPGTSAQKAELIALTKALELSKGKKANIYTDSRYAFATAHTHGSIYERRGW LTSEGKEIKNKAEIIALLKALFLPQEVAIIHCPGHQKGQDPVAVGNRQADRVARQAAMAEVLTLATEPDNTSHITAGKRTADGSEFEKRTADGSEFESPK KKAKVE
1616	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPAPAPGGLLGRDLLTKL KAQIQFSTEGPQVTWEDRPAMCLVLNLEEEYRLHEKPVPPSIDPSWLQLFPMVWAEKAGMGLANQVPPVVVELKSDASPVAVRQYPMSKEAREGIRPHIQ RFLDLGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVQDIHPTVPNPYNLLSSLPPSHTWYSVLDLKDAFFCLKLHPNSQPLFAFEWRDPEKGN TGQLTWTRLPQGFKNSPTLFNEALHRDLASFRALNPQVVMLQYVDDLLVAAPTYRDCKEGTRRLLQELSKLGYRVSAKKAQLCREEVTYLGYLLKGGKRW LTPARKATVMKIPTPTTPRQVREFLGTAGFCRLWIPGFASLAAPLYPLTRPKVPFTWTEAHQEAFGRIKEALLSAPALALPDLTKPFALYVDEKEGVARG VLTQTLGPWRRPVAYLSKKLDPVASGWPTCLKAIAAVALLLKDADKLTLGQNVLVIAPHNLESIVRQPPDRWMTNARMTHYQSLLLNERVSFAPPAILNP ATLLPVESDDTPIHICSEILAEETGTRPDLRDQPLPGVPAWYTDGSSFIMDGRRQAGAAIVDNKRTVWASNLPEGTSAQKAELIALTQALRLAEGKSINI YTDSRYAFATAHVHGAIYKQRGWLTSAGKDIKNKEEILALLEAIHLPKRVAIIHCPGHQRGTDPVATGNRKADEAAKQAAQSTRILTETTKNAGKRTADG SEFEKRTADGSEFESPKKKAKVE

1618	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKPAPGSSGGLLGRDL LTKLKAQIQFSTEGPQVTWEDRPAMCLVLNLEEEYRLHEKPVPPSIDPSWLQLFPMVWAEKAGMGLANQVPPVVVELKSDASPVAVRQYPMSKEAREGIR PHIQRFLDLGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVQDIHPTVPNPYNLLSSLPPSHTWYSVLDLKDAFFCLKLHPNSQPLFAFEWRDP EKGNTGQLTWTRLPQGFKNSPTLFNEALHRDLASFRALNPQVVMLQYVDDLLVAAPTYRDCKEGTRRLLQELSKLGYRVSAKKAQLCREEVTYLGYLLKG GKRWLTPARKATVMKIPTPTTPRQVREFLGTAGFCRLWIPGFASLAAPLYPLTRPKVPFTWTEAHQEAFGRIKEALLSAPALALPDLTKPFALYVDEKEG VARGVLTQTLGPWRRPVAYLSKKLDPVASGWPTCLKAIAAVALLLKDADKLTLGQNVLVIAPHNLESIVRQPPDRWMTNARMTHYQSLLLNERVSFAPPA ILNPATLLPVESDDTPIHICSEILAEETGTRPDLRDQPLPGVPAWYTDGSSFIMDGRRQAGAAIVDNKRTVWASNLPEGTSAQKAELIALTQALRLAEGK SINIYTDSRYAFATAHVHGAIYKQRGWLTSAGKDIKNKEEILALLEAIHLPKRVAIIHCPGHQRGTDPVATGNRKADEAAKQAAQSTRILTETTKNAGKR TADGSEFEKRTADGSEFESPKKKAKVE
1619	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPAPAPAPAPGGLLGRDL LTKLKAQIQFSTEGPQVTWEDRPAMCLVLNLEEEYRLHEKPVPPSIDPSWLQLFPMVWAEKAGMGLANQVPPVVVELKSDASPVAVRQYPMSKEAREGIR PHIQRFLDLGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVQDIHPTVPNPYNLLSSLPPSHTWYSVLDLKDAFFCLKLHPNSQPLFAFEWRDP EKGNTGQLTWTRLPQGFKNSPTLFNEALHRDLASFRALNPQVVMLQYVDDLLVAAPTYRDCKEGTRRLLQELSKLGYRVSAKKAQLCREEVTYLGYLLKG GKRWLTPARKATVMKIPTPTTPRQVREFLGTAGFCRLWIPGFASLAAPLYPLTRPKVPFTWTEAHQEAFGRIKEALLSAPALALPDLTKPFALYVDEKEG VARGVLTQTLGPWRRPVAYLSKKLDPVASGWPTCLKAIAAVALLLKDADKLTLGQNVLVIAPHNLESIVRQPPDRWMTNARMTHYQSLLLNERVSFAPPA

	ILNPATLLPVESDDTPIHICSEILAEETGTRPDLRDQPLPGVPAWYTDGSSFIMDGRRQAGAAIVDNKRTVWASNLPEGTSAQKAELIALTQALRLAEGK SINIYTDSRYAFATAHVHGAIYKQRGWLTSAGKDIKNKEEILALLEAIHLPKRVAIIHCPGHQRGTDPVATGNRKADEAAKQAAQSTRILTETTKNAGKR TADGSEFEKRTADGSEFESPKKKAKVE
1666	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGSPAPEAAAKGGLLGRDL LTKLKAQIQFSTEGPQVTWEDRPAMCLVLNLEEEYRLHEKPVPPSIDPSWLQLFPMVWAEKAGMGLANQVPPVVVELKSDASPVAVRQYPMSKEAREGIR PHIQRFLDLGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVQDIHPTVPNPYNLLSSLPPSHTWYSVLDLKDAFFCLKLHPNSQPLFAFEWRDP EKGNTGQLTWTRLPQGFKNSPTLFNEALHRDLASFRALNPQVVMLQYVDDLLVAAPTYRDCKEGTRRLLQELSKLGYRVSAKKAQLCREEVTYLGYLLKG GKRWLTPARKATVMKIPTPTTPRQVREFLGKAGFCRLFIPGFASLAAPLYPLTRPKVPFTWTEAHQEAFGRIKEALLSAPALALPDLTKPFALYVDEKEG VARGVLTQTLGPWRRPVAYLSKKLDPVASGWPTCLKAIAAVALLLKDADKLTLGQNVLVIAPHNLESIVRQPPDRWMTNARMTHYQSLLLNERVSFAPPA ILNPATLLPVESDDTPIHICSEILAEETGTRPDLRDQPLPGVPAWYTDGSSFIMDGRRQAGAAIVDNKRTVWASNLPEGTSAQKAELIALTQALRLAEGK SINIYTDSRYAFATAHVHGAIYKQRGWLTSAGKDIKNKEEILALLEAIHLPKRVAIIHCPGHQRGTDPVATGNRKADEAAKQAAQSTRILTETTKNAGKR TADGSEFEKRTADGSEFESPKKKAKVE
1668	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGSGGGGGLLGRDLLTKLK AQIQFSTEGPQVTWEDRPAMCLVLNLEEEYRLHEKPVPPSIDPSWLQLFPMVWAEKAGMGLANQVPPVVVELKSDASPVAVRQYPMSKEAREGIRPHIQR FLDLGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVQDIHPTVPNPYNLLSSLPPSHTWYSVLDLKDAFFCLKLHPNSQPLFAFEWRDPEKGNT

	GQLTWTRLPQGFKNSPTLFNEALHRDLASFRALNPQVVMLQYVDDLLVAAPTYRDCKEGTRRLLQELSKLGYRVSAKKAQLCREEVTYLGYLLKGGKRWL TPARKATVMKIPTPTTPRQVREFLGKAGFCRLFIPGFASLAAPLYPLTRPKVPFTWTEAHQEAFGRIKEALLSAPALALPDLTKPFALYVDEKEGVARGV LTQTLGPWRRPVAYLSKKLDPVASGWPTCLKAIAAVALLLKDADKLTLGQNVLVIAPHNLESIVRQPPDRWMTNARMTHYQSLLLNERVSFAPPAILNPA TLLPVESDDTPIHICSEILAEETGTRPDLRDQPLPGVPAWYTDGSSFIMDGRRQAGAAIVDNKRTVWASNLPEGTSAQKAELIALTQALRLAEGKSINIY TDSRYAFATAHVHGAIYKQRGWLTSAGKDIKNKEEILALLEAIHLPKRVAIIHCPGHQRGTDPVATGNRKADEAAKQAAQSTRILTETTKNAGKRTADGS EFEKRTADGSEFESPKKKAKVE
1672	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGGEAAAKPAPGGLLGRDL LTKLKAQIQFSTEGPQVTWEDRPAMCLVLNLEEEYRLHEKPVPPSIDPSWLQLFPMVWAEKAGMGLANQVPPVVVELKSDASPVAVRQYPMSKEAREGIR PHIQRFLDLGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVQDIHPTVPNPYNLLSSLPPSHTWYSVLDLKDAFFCLKLHPNSQPLFAFEWRDP EKGNTGQLTWTRLPQGFKNSPTLFNEALHRDLASFRALNPQVVMLQYVDDLLVAAPTYRDCKEGTRRLLQELSKLGYRVSAKKAQLCREEVTYLGYLLKG GKRWLTPARKATVMKIPTPTTPRQVREFLGKAGFCRLFIPGFASLAAPLYPLTRPKVPFTWTEAHQEAFGRIKEALLSAPALALPDLTKPFALYVDEKEG VARGVLTQTLGPWRRPVAYLSKKLDPVASGWPTCLKAIAAVALLLKDADKLTLGQNVLVIAPHNLESIVRQPPDRWMTNARMTHYQSLLLNERVSFAPPA ILNPATLLPVESDDTPIHICSEILAEETGTRPDLRDQPLPGVPAWYTDGSSFIMDGRRQAGAAIVDNKRTVWASNLPEGTSAQKAELIALTQALRLAEGK SINIYTDSRYAFATAHVHGAIYKQRGWLTSAGKDIKNKEEILALLEAIHLPKRVAIIHCPGHQRGTDPVATGNRKADEAAKQAAQSTRILTETTKNAGKR TADGSEFEKRTADGSEFESPKKKAKVE
1677	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK

	VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKGGGGSSGGLLGRDL LTKLKAQIQFSTEGPQVTWEDRPAMCLVLNLEEEYRLHEKPVPPSIDPSWLQLFPMVWAEKAGMGLANQVPPVVVELKSDASPVAVRQYPMSKEAREGIR PHIQRFLDLGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVQDIHPTVPNPYNLLSSLPPSHTWYSVLDLKDAFFCLKLHPNSQPLFAFEWRDP EKGNTGQLTWTRLPQGFKNSPTLFNEALHRDLASFRALNPQVVMLQYVDDLLVAAPTYRDCKEGTRRLLQELSKLGYRVSAKKAQLCREEVTYLGYLLKG GKRWLTPARKATVMKIPTPTTPRQVREFLGKAGFCRLFIPGFASLAAPLYPLTRPKVPFTWTEAHQEAFGRIKEALLSAPALALPDLTKPFALYVDEKEG VARGVLTQTLGPWRRPVAYLSKKLDPVASGWPTCLKAIAAVALLLKDADKLTLGQNVLVIAPHNLESIVRQPPDRWMTNARMTHYQSLLLNERVSFAPPA ILNPATLLPVESDDTPIHICSEILAEETGTRPDLRDQPLPGVPAWYTDGSSFIMDGRRQAGAAIVDNKRTVWASNLPEGTSAQKAELIALTQALRLAEGK SINIYTDSRYAFATAHVHGAIYKQRGWLTSAGKDIKNKEEILALLEAIHLPKRVAIIHCPGHQRGTDPVATGNRKADEAAKQAAQSTRILTETTKNAGKR TADGSEFEKRTADGSEFESPKKKAKVE
1679	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKGGSGGLLGRDLLTK LKAQIQFSTEGPQVTWEDRPAMCLVLNLEEEYRLHEKPVPPSIDPSWLQLFPMVWAEKAGMGLANQVPPVVVELKSDASPVAVRQYPMSKEAREGIRPHI QRFLDLGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVQDIHPTVPNPYNLLSSLPPSHTWYSVLDLKDAFFCLKLHPNSQPLFAFEWRDPEKG NTGQLTWTRLPQGFKNSPTLFNEALHRDLASFRALNPQVVMLQYVDDLLVAAPTYRDCKEGTRRLLQELSKLGYRVSAKKAQLCREEVTYLGYLLKGGKR WLTPARKATVMKIPTPTTPRQVREFLGKAGFCRLFIPGFASLAAPLYPLTRPKVPFTWTEAHQEAFGRIKEALLSAPALALPDLTKPFALYVDEKEGVAR GVLTQTLGPWRRPVAYLSKKLDPVASGWPTCLKAIAAVALLLKDADKLTLGQNVLVIAPHNLESIVRQPPDRWMTNARMTHYQSLLLNERVSFAPPAILN PATLLPVESDDTPIHICSEILAEETGTRPDLRDQPLPGVPAWYTDGSSFIMDGRRQAGAAIVDNKRTVWASNLPEGTSAQKAELIALTQALRLAEGKSIN IYTDSRYAFATAHVHGAIYKQRGWLTSAGKDIKNKEEILALLEAIHLPKRVAIIHCPGHQRGTDPVATGNRKADEAAKQAAQSTRILTETTKNAGKRTAD GSEFEKRTADGSEFESPKKKAKVE
1682	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL

	NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGGGGSEAAAKGGLLGRDL LTKLKAQIQFSTEGPQVTWEDRPAMCLVLNLEEEYRLHEKPVPPSIDPSWLQLFPMVWAEKAGMGLANQVPPVVVELKSDASPVAVRQYPMSKEAREGIR PHIQRFLDLGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVQDIHPTVPNPYNLLSSLPPSHTWYSVLDLKDAFFCLKLHPNSQPLFAFEWRDP EKGNTGQLTWTRLPQGFKNSPTLFNEALHRDLASFRALNPQVVMLQYVDDLLVAAPTYRDCKEGTRRLLQELSKLGYRVSAKKAQLCREEVTYLGYLLKG GKRWLTPARKATVMKIPTPTTPRQVREFLGKAGFCRLFIPGFASLAAPLYPLTRPKVPFTWTEAHQEAFGRIKEALLSAPALALPDLTKPFALYVDEKEG VARGVLTQTLGPWRRPVAYLSKKLDPVASGWPTCLKAIAAVALLLKDADKLTLGQNVLVIAPHNLESIVRQPPDRWMTNARMTHYQSLLLNERVSFAPPA ILNPATLLPVESDDTPIHICSEILAEETGTRPDLRDQPLPGVPAWYTDGSSFIMDGRRQAGAAIVDNKRTVWASNLPEGTSAQKAELIALTQALRLAEGK SINIYTDSRYAFATAHVHGAIYKQRGWLTSAGKDIKNKEEILALLEAIHLPKRVAIIHCPGHQRGTDPVATGNRKADEAAKQAAQSTRILTETTKNAGKR TADGSEFEKRTADGSEFESPKKKAKVE
1686	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGSGGSGGSGGLLGRDLLT KLKAQIQFSTEGPQVTWEDRPAMCLVLNLEEEYRLHEKPVPPSIDPSWLQLFPMVWAEKAGMGLANQVPPVVVELKSDASPVAVRQYPMSKEAREGIRPH IQRFLDLGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVQDIHPTVPNPYNLLSSLPPSHTWYSVLDLKDAFFCLKLHPNSQPLFAFEWRDPEK GNTGQLTWTRLPQGFKNSPTLFNEALHRDLASFRALNPQVVMLQYVDDLLVAAPTYRDCKEGTRRLLQELSKLGYRVSAKKAQLCREEVTYLGYLLKGGK RWLTPARKATVMKIPTPTTPRQVREFLGKAGFCRLFIPGFASLAAPLYPLTRPKVPFTWTEAHQEAFGRIKEALLSAPALALPDLTKPFALYVDEKEGVA RGVLTQTLGPWRRPVAYLSKKLDPVASGWPTCLKAIAAVALLLKDADKLTLGQNVLVIAPHNLESIVRQPPDRWMTNARMTHYQSLLLNERVSFAPPAIL NPATLLPVESDDTPIHICSEILAEETGTRPDLRDQPLPGVPAWYTDGSSFIMDGRRQAGAAIVDNKRTVWASNLPEGTSAQKAELIALTQALRLAEGKSI NIYTDSRYAFATAHVHGAIYKQRGWLTSAGKDIKNKEEILALLEAIHLPKRVAIIHCPGHQRGTDPVATGNRKADEAAKQAAQSTRILTETTKNAGKRTA DGSEFEKRTADGSEFESPKKKAKVE
1690	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA

	NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKGSSGGSGGLLGRDL LTKLKAQIQFSTEGPQVTWEDRPAMCLVLNLEEEYRLHEKPVPPSIDPSWLQLFPMVWAEKAGMGLANQVPPVVVELKSDASPVAVRQYPMSKEAREGIR PHIQRFLDLGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVQDIHPTVPNPYNLLSSLPPSHTWYSVLDLKDAFFCLKLHPNSQPLFAFEWRDP EKGNTGQLTWTRLPQGFKNSPTLFNEALHRDLASFRALNPQVVMLQYVDDLLVAAPTYRDCKEGTRRLLQELSKLGYRVSAKKAQLCREEVTYLGYLLKG GKRWLTPARKATVMKIPTPTTPRQVREFLGKAGFCRLFIPGFASLAAPLYPLTRPKVPFTWTEAHQEAFGRIKEALLSAPALALPDLTKPFALYVDEKEG VARGVLTQTLGPWRRPVAYLSKKLDPVASGWPTCLKAIAAVALLLKDADKLTLGQNVLVIAPHNLESIVRQPPDRWMTNARMTHYQSLLLNERVSFAPPA ILNPATLLPVESDDTPIHICSEILAEETGTRPDLRDQPLPGVPAWYTDGSSFIMDGRRQAGAAIVDNKRTVWASNLPEGTSAQKAELIALTQALRLAEGK SINIYTDSRYAFATAHVHGAIYKQRGWLTSAGKDIKNKEEILALLEAIHLPKRVAIIHCPGHQRGTDPVATGNRKADEAAKQAAQSTRILTETTKNAGKR TADGSEFEKRTADGSEFESPKKKAKVE
1691	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPGGGGSSGGLLGRDLLT KLKAQIQFSTEGPQVTWEDRPAMCLVLNLEEEYRLHEKPVPPSIDPSWLQLFPMVWAEKAGMGLANQVPPVVVELKSDASPVAVRQYPMSKEAREGIRPH IQRFLDLGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVQDIHPTVPNPYNLLSSLPPSHTWYSVLDLKDAFFCLKLHPNSQPLFAFEWRDPEK GNTGQLTWTRLPQGFKNSPTLFNEALHRDLASFRALNPQVVMLQYVDDLLVAAPTYRDCKEGTRRLLQELSKLGYRVSAKKAQLCREEVTYLGYLLKGGK RWLTPARKATVMKIPTPTTPRQVREFLGKAGFCRLFIPGFASLAAPLYPLTRPKVPFTWTEAHQEAFGRIKEALLSAPALALPDLTKPFALYVDEKEGVA RGVLTQTLGPWRRPVAYLSKKLDPVASGWPTCLKAIAAVALLLKDADKLTLGQNVLVIAPHNLESIVRQPPDRWMTNARMTHYQSLLLNERVSFAPPAIL NPATLLPVESDDTPIHICSEILAEETGTRPDLRDQPLPGVPAWYTDGSSFIMDGRRQAGAAIVDNKRTVWASNLPEGTSAQKAELIALTQALRLAEGKSI NIYTDSRYAFATAHVHGAIYKQRGWLTSAGKDIKNKEEILALLEAIHLPKRVAIIHCPGHQRGTDPVATGNRKADEAAKQAAQSTRILTETTKNAGKRTA DGSEFEKRTADGSEFESPKKKAKVE
1695	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL

	LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPGSSGGLLGRDLLTKLK AQIQFSTEGPQVTWEDRPAMCLVLNLEEEYRLHEKPVPPSIDPSWLQLFPMVWAEKAGMGLANQVPPVVVELKSDASPVAVRQYPMSKEAREGIRPHIQR FLDLGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVQDIHPTVPNPYNLLSSLPPSHTWYSVLDLKDAFFCLKLHPNSQPLFAFEWRDPEKGNT GQLTWTRLPQGFKNSPTLFNEALHRDLASFRALNPQVVMLQYVDDLLVAAPTYRDCKEGTRRLLQELSKLGYRVSAKKAQLCREEVTYLGYLLKGGKRWL TPARKATVMKIPTPTTPRQVREFLGKAGFCRLFIPGFASLAAPLYPLTRPKVPFTWTEAHQEAFGRIKEALLSAPALALPDLTKPFALYVDEKEGVARGV LTQTLGPWRRPVAYLSKKLDPVASGWPTCLKAIAAVALLLKDADKLTLGQNVLVIAPHNLESIVRQPPDRWMTNARMTHYQSLLLNERVSFAPPAILNPA TLLPVESDDTPIHICSEILAEETGTRPDLRDQPLPGVPAWYTDGSSFIMDGRRQAGAAIVDNKRTVWASNLPEGTSAQKAELIALTQALRLAEGKSINIY TDSRYAFATAHVHGAIYKQRGWLTSAGKDIKNKEEILALLEAIHLPKRVAIIHCPGHQRGTDPVATGNRKADEAAKQAAQSTRILTETTKNAGKRTADGS EFEKRTADGSEFESPKKKAKVE
1698	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSSGGGGGLLGRDLLTKLK AQIQFSTEGPQVTWEDRPAMCLVLNLEEEYRLHEKPVPPSIDPSWLQLFPMVWAEKAGMGLANQVPPVVVELKSDASPVAVRQYPMSKEAREGIRPHIQR FLDLGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVQDIHPTVPNPYNLLSSLPPSHTWYSVLDLKDAFFCLKLHPNSQPLFAFEWRDPEKGNT GQLTWTRLPQGFKNSPTLFNEALHRDLASFRALNPQVVMLQYVDDLLVAAPTYRDCKEGTRRLLQELSKLGYRVSAKKAQLCREEVTYLGYLLKGGKRWL TPARKATVMKIPTPTTPRQVREFLGKAGFCRLFIPGFASLAAPLYPLTRPKVPFTWTEAHQEAFGRIKEALLSAPALALPDLTKPFALYVDEKEGVARGV LTQTLGPWRRPVAYLSKKLDPVASGWPTCLKAIAAVALLLKDADKLTLGQNVLVIAPHNLESIVRQPPDRWMTNARMTHYQSLLLNERVSFAPPAILNPA TLLPVESDDTPIHICSEILAEETGTRPDLRDQPLPGVPAWYTDGSSFIMDGRRQAGAAIVDNKRTVWASNLPEGTSAQKAELIALTQALRLAEGKSINIY TDSRYAFATAHVHGAIYKQRGWLTSAGKDIKNKEEILALLEAIHLPKRVAIIHCPGHQRGTDPVATGNRKADEAAKQAAQSTRILTETTKNAGKRTADGS EFEKRTADGSEFESPKKKAKVE

1721	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSSPAPEAAAKGGLLGRDL LTKLKAQIQFSTEGPQVTWEDRPAMCLVLNLEEEYRLHEKPVPPSIDPSWLQLFPMVWAEKAGMGLANQVPPVVVELKSDASPVAVRQYPMSKEAREGIR PHIQRFLDLGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVQDIHPTVPNPYNLLSSLPPSHTWYSVLDLKDAFFCLKLHPNSQPLFAFEWRDP EKGNTGQLTWTRLPQGFKNSPTLFNEALHRDLASFRALNPQVVMLQYVDDLLVAAPTYRDCKEGTRRLLQELSKLGYRVSAKKAQLCREEVTYLGYLLKG GKRWLTPARKATVMKIPTPTTPRQVREFLGKAGFCRLFIPGFASLAAPLYPLTRPKVPFTWTEAHQEAFGRIKEALLSAPALALPDLTKPFALYVDEKEG VARGVLTQTLGPWRRPVAYLSKKLDPVASGWPTCLKAIAAVALLLKDADKLTLGQNVLVIAPHNLESIVRQPPDRWMTNARMTHYQSLLLNERVSFAPPA ILNPATLLPVESDDTPIHICSEILAEETGTRPDLRDQPLPGVPAWYTDGSSFIMDGRRQAGAAIVDNKRTVWASNLPEGTSAQKAELIALTQALRLAEGK SINIYTDSRYAFATAHVHGAIYKQRGWLTSAGKDIKNKEEILALLEAIHLPKRVAIIHCPGHQRGTDPVATGNRKADEAAKQAAQSTRILTETTKNAGKR TADGSEFEKRTADGSEFESPKKKAKVE
1754	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPGGSEAAAKGGTLGDQG SRGSDPLPEPRVTLTVEGIPTEFLVNTGAEHSVLTKPMGKMGSKRTVVAGATGSKVYPWTTKRLLKIGQKQVTHSFLVIPECPAPLLGRDLLTKLKAQIQ FSTEGPQVTWEDRPAMCLVLNLEEEYRLHEKPVPPSIDPSWLQLFPMVWAEKAGMGLANQVPPVVVELKSDASPVAVRQYPMSKEAREGIRPHIQRFLDL GILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVQDIHPTVPNPYNLLSSLPPSHTWYSVLDLKDAFFCLKLHPNSQPLFAFEWRDPEKGNTGQLT WTRLPQGFKNSPTLFNEALHRDLASFRALNPQVVMLQYVDDLLVAAPTYRDCKEGTRRLLQELSKLGYRVSAKKAQLCREEVTYLGYLLKGGKRWLTPAR KATVMKIPTPTTPRQVREFLGTAGFCRLWIPGFASLAAPLYPLTRPKVPFTWTEAHQEAFGRIKEALLSAPALALPDLTKPFALYVDEKEGVARGVLTQT

	LGPWRRPVAYLSKKLDPVASGWPTCLKAIAAVALLLKDADKLTLGQNVLVIAPHNLESIVRQPPDRWMTNARMTHYQSLLLNERVSFAPPAILNPATLLP VESDDTPIHICSEILAEETGTRPDLRDQPLPGVPAWYTDGSSFIMDGRRQAGAAIVDNKRTVWASNLPEGTSAQKAELIALTQALRLAEGKSINIYTDSR YAFATAHVHGAIYKQRGWLTSAGKDIKNKEEILALLEAIHLPKRVAIIHCPGHQRGTDPVATGNRKADEAAKQAAQSTRILTETTKNAGKRTADGSEFEK RTADGSEFESPKKKAKVE
1759	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSSGGGEAAAKGGTLGDQG SRGSDPLPEPRVTLTVEGIPTEFLVNTGAEHSVLTKPMGKMGSKRTVVAGATGSKVYPWTTKRLLKIGQKQVTHSFLVIPECPAPLLGRDLLTKLKAQIQ FSTEGPQVTWEDRPAMCLVLNLEEEYRLHEKPVPPSIDPSWLQLFPMVWAEKAGMGLANQVPPVVVELKSDASPVAVRQYPMSKEAREGIRPHIQRFLDL GILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVQDIHPTVPNPYNLLSSLPPSHTWYSVLDLKDAFFCLKLHPNSQPLFAFEWRDPEKGNTGQLT WTRLPQGFKNSPTLFNEALHRDLASFRALNPQVVMLQYVDDLLVAAPTYRDCKEGTRRLLQELSKLGYRVSAKKAQLCREEVTYLGYLLKGGKRWLTPAR KATVMKIPTPTTPRQVREFLGTAGFCRLWIPGFASLAAPLYPLTRPKVPFTWTEAHQEAFGRIKEALLSAPALALPDLTKPFALYVDEKEGVARGVLTQT LGPWRRPVAYLSKKLDPVASGWPTCLKAIAAVALLLKDADKLTLGQNVLVIAPHNLESIVRQPPDRWMTNARMTHYQSLLLNERVSFAPPAILNPATLLP VESDDTPIHICSEILAEETGTRPDLRDQPLPGVPAWYTDGSSFIMDGRRQAGAAIVDNKRTVWASNLPEGTSAQKAELIALTQALRLAEGKSINIYTDSR YAFATAHVHGAIYKQRGWLTSAGKDIKNKEEILALLEAIHLPKRVAIIHCPGHQRGTDPVATGNRKADEAAKQAAQSTRILTETTKNAGKRTADGSEFEK RTADGSEFESPKKKAKVE
1769	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSEAAAKGSSGGTLGDQG

	SRGSDPLPEPRVTLTVEGIPTEFLVNTGAEHSVLTKPMGKMGSKRTVVAGATGSKVYPWTTKRLLKIGQKQVTHSFLVIPECPAPLLGRDLLTKLKAQIQ FSTEGPQVTWEDRPAMCLVLNLEEEYRLHEKPVPPSIDPSWLQLFPMVWAEKAGMGLANQVPPVVVELKSDASPVAVRQYPMSKEAREGIRPHIQRFLDL GILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVQDIHPTVPNPYNLLSSLPPSHTWYSVLDLKDAFFCLKLHPNSQPLFAFEWRDPEKGNTGQLT WTRLPQGFKNSPTLFNEALHRDLASFRALNPQVVMLQYVDDLLVAAPTYRDCKEGTRRLLQELSKLGYRVSAKKAQLCREEVTYLGYLLKGGKRWLTPAR KATVMKIPTPTTPRQVREFLGKAGFCRLFIPGFASLAAPLYPLTRPKVPFTWTEAHQEAFGRIKEALLSAPALALPDLTKPFALYVDEKEGVARGVLTQT LGPWRRPVAYLSKKLDPVASGWPTCLKAIAAVALLLKDADKLTLGQNVLVIAPHNLESIVRQPPDRWMTNARMTHYQSLLLNERVSFAPPAILNPATLLP VESDDTPIHICSEILAEETGTRPDLRDQPLPGVPAWYTDGSSFIMDGRRQAGAAIVDNKRTVWASNLPEGTSAQKAELIALTQALRLAEGKSINIYTDSR YAFATAHVHGAIYKQRGWLTSAGKDIKNKEEILALLEAIHLPKRVAIIHCPGHQRGTDPVATGNRKADEAAKQAAQSTRILTETTKNAGKRTADGSEFEK RTADGSEFESPKKKAKVE
1770	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKGGGPAPGGTLGDQG SRGSDPLPEPRVTLTVEGIPTEFLVNTGAEHSVLTKPMGKMGSKRTVVAGATGSKVYPWTTKRLLKIGQKQVTHSFLVIPECPAPLLGRDLLTKLKAQIQ FSTEGPQVTWEDRPAMCLVLNLEEEYRLHEKPVPPSIDPSWLQLFPMVWAEKAGMGLANQVPPVVVELKSDASPVAVRQYPMSKEAREGIRPHIQRFLDL GILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVQDIHPTVPNPYNLLSSLPPSHTWYSVLDLKDAFFCLKLHPNSQPLFAFEWRDPEKGNTGQLT WTRLPQGFKNSPTLFNEALHRDLASFRALNPQVVMLQYVDDLLVAAPTYRDCKEGTRRLLQELSKLGYRVSAKKAQLCREEVTYLGYLLKGGKRWLTPAR KATVMKIPTPTTPRQVREFLGKAGFCRLFIPGFASLAAPLYPLTRPKVPFTWTEAHQEAFGRIKEALLSAPALALPDLTKPFALYVDEKEGVARGVLTQT LGPWRRPVAYLSKKLDPVASGWPTCLKAIAAVALLLKDADKLTLGQNVLVIAPHNLESIVRQPPDRWMTNARMTHYQSLLLNERVSFAPPAILNPATLLP VESDDTPIHICSEILAEETGTRPDLRDQPLPGVPAWYTDGSSFIMDGRRQAGAAIVDNKRTVWASNLPEGTSAQKAELIALTQALRLAEGKSINIYTDSR YAFATAHVHGAIYKQRGWLTSAGKDIKNKEEILALLEAIHLPKRVAIIHCPGHQRGTDPVATGNRKADEAAKQAAQSTRILTETTKNAGKRTADGSEFEK RTADGSEFESPKKKAKVE
1772	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA

	KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGGGSSGGTLGDQGSRGSD PLPEPRVTLTVEGIPTEFLVNTGAEHSVLTKPMGKMGSKRTVVAGATGSKVYPWTTKRLLKIGQKQVTHSFLVIPECPAPLLGRDLLTKLKAQIQFSTEG PQVTWEDRPAMCLVLNLEEEYRLHEKPVPPSIDPSWLQLFPMVWAEKAGMGLANQVPPVVVELKSDASPVAVRQYPMSKEAREGIRPHIQRFLDLGILVP CQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVQDIHPTVPNPYNLLSSLPPSHTWYSVLDLKDAFFCLKLHPNSQPLFAFEWRDPEKGNTGQLTWTRLP QGFKNSPTLFNEALHRDLASFRALNPQVVMLQYVDDLLVAAPTYRDCKEGTRRLLQELSKLGYRVSAKKAQLCREEVTYLGYLLKGGKRWLTPARKATVM KIPTPTTPRQVREFLGKAGFCRLFIPGFASLAAPLYPLTRPKVPFTWTEAHQEAFGRIKEALLSAPALALPDLTKPFALYVDEKEGVARGVLTQTLGPWR RPVAYLSKKLDPVASGWPTCLKAIAAVALLLKDADKLTLGQNVLVIAPHNLESIVRQPPDRWMTNARMTHYQSLLLNERVSFAPPAILNPATLLPVESDD TPIHICSEILAEETGTRPDLRDQPLPGVPAWYTDGSSFIMDGRRQAGAAIVDNKRTVWASNLPEGTSAQKAELIALTQALRLAEGKSINIYTDSRYAFAT AHVHGAIYKQRGWLTSAGKDIKNKEEILALLEAIHLPKRVAIIHCPGHQRGTDPVATGNRKADEAAKQAAQSTRILTETTKNAGKRTADGSEFEKRTADG SEFESPKKKAKVE
1773	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKEAAAKGGTLGDQGS RGSDPLPEPRVTLTVEGIPTEFLVNTGAEHSVLTKPMGKMGSKRTVVAGATGSKVYPWTTKRLLKIGQKQVTHSFLVIPECPAPLLGRDLLTKLKAQIQF STEGPQVTWEDRPAMCLVLNLEEEYRLHEKPVPPSIDPSWLQLFPMVWAEKAGMGLANQVPPVVVELKSDASPVAVRQYPMSKEAREGIRPHIQRFLDLG ILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVQDIHPTVPNPYNLLSSLPPSHTWYSVLDLKDAFFCLKLHPNSQPLFAFEWRDPEKGNTGQLTW TRLPQGFKNSPTLFNEALHRDLASFRALNPQVVMLQYVDDLLVAAPTYRDCKEGTRRLLQELSKLGYRVSAKKAQLCREEVTYLGYLLKGGKRWLTPARK ATVMKIPTPTTPRQVREFLGKAGFCRLFIPGFASLAAPLYPLTRPKVPFTWTEAHQEAFGRIKEALLSAPALALPDLTKPFALYVDEKEGVARGVLTQTL GPWRRPVAYLSKKLDPVASGWPTCLKAIAAVALLLKDADKLTLGQNVLVIAPHNLESIVRQPPDRWMTNARMTHYQSLLLNERVSFAPPAILNPATLLPV ESDDTPIHICSEILAEETGTRPDLRDQPLPGVPAWYTDGSSFIMDGRRQAGAAIVDNKRTVWASNLPEGTSAQKAELIALTQALRLAEGKSINIYTDSRY AFATAHVHGAIYKQRGWLTSAGKDIKNKEEILALLEAIHLPKRVAIIHCPGHQRGTDPVATGNRKADEAAKQAAQSTRILTETTKNAGKRTADGSEFEKR TADGSEFESPKKKAKVE
1856	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL

	LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPGGGEAAAKGGTLNLED EYRLYETSAEPEVSPGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEAKLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGT NDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHRWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGMGISGQLTWTRLPQGFKNSPTLFNEALHRD LADFRIQHPDLILLQYVDDILLAATSELDCQQGTRALLLTLGNLGYRASAKKAQLCQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGK AGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGW PPCLRMVAAIAVLRKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEEGAPHDCLEILAETHGTR PDLTDQPIPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKRLNVYTDSRYAFATAHIHGEIYRRRGWLTS EGREIKNKSEILALLKALFLPKRLSIIHCLGHQKGDSAEARGNRLADQAAREAAIKTPPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
1857	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGPAPGSSGGTLNLEDEY RLYETSAEPEVSPGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEAKLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTND YRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHRWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGMGISGQLTWTRLPQGFKNSPTLFNEALHRDLA DFRIQHPDLILLQYVDDILLAATSELDCQQGTRALLLTLGNLGYRASAKKAQLCQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAG FCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPP CLRMVAAIAVLRKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEEGAPHDCLEILAETHGTRPD LTDQPIPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKRLNVYTDSRYAFATAHIHGEIYRRRGWLTSEG REIKNKSEILALLKALFLPKRLSIIHCLGHQKGDSAEARGNRLADQAAREAAIKTPPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
1860	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL

	FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKGGGGSEAAAKGGTL NLEDEYRLYETSAEPEVSPGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEAKLGIKPHIQRLLDQGILVPCQSPWNTPLLPVK KPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHRWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGMGISGQLTWTRLPQGFKNSPTLFNEA LHRDLADFRIQHPDLILLQYVDDILLAATSELDCQQGTRALLLTLGNLGYRASAKKAQLCQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLRE FLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPV AAGWPPCLRMVAAIAVLRKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEEGAPHDCLEILAET HGTRPDLTDQPIPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKRLNVYTDSRYAFATAHIHGEIYRRRG WLTSEGREIKNKSEILALLKALFLPKRLSIIHCLGHQKGDSAEARGNRLADQAAREAAIKTPPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
1861	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSSEAAAKGGGGGTLNLED EYRLYETSAEPEVSPGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEAKLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGT NDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHRWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGMGISGQLTWTRLPQGFKNSPTLFNEALHRD LADFRIQHPDLILLQYVDDILLAATSELDCQQGTRALLLTLGNLGYRASAKKAQLCQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGK AGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGW PPCLRMVAAIAVLRKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEEGAPHDCLEILAETHGTR PDLTDQPIPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKRLNVYTDSRYAFATAHIHGEIYRRRGWLTS EGREIKNKSEILALLKALFLPKRLSIIHCLGHQKGDSAEARGNRLADQAAREAAIKTPPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
1863	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV

	QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPAPAPAPAPAPGGTLNL EDEYRLYETSAEPEVSPGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEAKLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKP GTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHRWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGMGISGQLTWTRLPQGFKNSPTLFNEALH RDLADFRIQHPDLILLQYVDDILLAATSELDCQQGTRALLLTLGNLGYRASAKKAQLCQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFL GKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAA GWPPCLRMVAAIAVLRKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEEGAPHDCLEILAETHG TRPDLTDQPIPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKRLNVYTDSRYAFATAHIHGEIYRRRGWL TSEGREIKNKSEILALLKALFLPKRLSIIHCLGHQKGDSAEARGNRLADQAAREAAIKTPPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
1864	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPEAAAKGGGGGTLNLED EYRLYETSAEPEVSPGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEAKLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGT NDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHRWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGMGISGQLTWTRLPQGFKNSPTLFNEALHRD LADFRIQHPDLILLQYVDDILLAATSELDCQQGTRALLLTLGNLGYRASAKKAQLCQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGK AGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGW PPCLRMVAAIAVLRKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEEGAPHDCLEILAETHGTR PDLTDQPIPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKRLNVYTDSRYAFATAHIHGEIYRRRGWLTS EGREIKNKSEILALLKALFLPKRLSIIHCLGHQKGDSAEARGNRLADQAAREAAIKTPPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE

1865	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKEAAAKEAAAKEAAA KGGTLNLEDEYRLYETSAEPEVSPGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEAKLGIKPHIQRLLDQGILVPCQSPWNTP LLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHRWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGMGISGQLTWTRLPQGFKNSPT LFNEALHRDLADFRIQHPDLILLQYVDDILLAATSELDCQQGTRALLLTLGNLGYRASAKKAQLCQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTP RQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSK KLDPVAAGWPPCLRMVAAIAVLRKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEEGAPHDCLE ILAETHGTRPDLTDQPIPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKRLNVYTDSRYAFATAHIHGEI YRRRGWLTSEGREIKNKSEILALLKALFLPKRLSIIHCLGHQKGDSAEARGNRLADQAAREAAIKTPPDTSTLLAGKRTADGSEFEKRTADGSEFESPKK KAKVE
1867	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKGGGPAPGGTLNLED EYRLYETSAEPEVSPGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEAKLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGT NDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHRWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGMGISGQLTWTRLPQGFKNSPTLFNEALHRD LADFRIQHPDLILLQYVDDILLAATSELDCQQGTRALLLTLGNLGYRASAKKAQLCQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGK AGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGW PPCLRMVAAIAVLRKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEEGAPHDCLEILAETHGTR

	PDLTDQPIPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKRLNVYTDSRYAFATAHIHGEIYRRRGWLTS EGREIKNKSEILALLKALFLPKRLSIIHCLGHQKGDSAEARGNRLADQAAREAAIKTPPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
1868	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKGGTLNLEDEYRLYE TSAEPEVSPGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEAKLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPV QDLREVNKRVEDIHPTVPNPYNLLSGLPPSHRWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRI QHPDLILLQYVDDILLAATSELDCQQGTRALLLTLGNLGYRASAKKAQLCQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRL FIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRM VAAIAVLRKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEEGAPHDCLEILAETHGTRPDLTDQ PIPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKRLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGREIK NKSEILALLKALFLPKRLSIIHCLGHQKGDSAEARGNRLADQAAREAAIKTPPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
1870	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSAGSAAGSGEFGGTLNLE DEYRLYETSAEPEVSPGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEAKLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPG TNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHRWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGMGISGQLTWTRLPQGFKNSPTLFNEALHR DLADFRIQHPDLILLQYVDDILLAATSELDCQQGTRALLLTLGNLGYRASAKKAQLCQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLG KAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAG

	WPPCLRMVAAIAVLRKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEEGAPHDCLEILAETHGT RPDLTDQPIPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKRLNVYTDSRYAFATAHIHGEIYRRRGWLT SEGREIKNKSEILALLKALFLPKRLSIIHCLGHQKGDSAEARGNRLADQAAREAAIKTPPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
1871	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKPAPGGSGGTLNLED EYRLYETSAEPEVSPGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEAKLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGT NDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHRWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGMGISGQLTWTRLPQGFKNSPTLFNEALHRD LADFRIQHPDLILLQYVDDILLAATSELDCQQGTRALLLTLGNLGYRASAKKAQLCQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGK AGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGW PPCLRMVAAIAVLRKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEEGAPHDCLEILAETHGTR PDLTDQPIPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKRLNVYTDSRYAFATAHIHGEIYRRRGWLTS EGREIKNKSEILALLKALFLPKRLSIIHCLGHQKGDSAEARGNRLADQAAREAAIKTPPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
1874	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSSPAPGGGGGTLNLEDEY RLYETSAEPEVSPGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEAKLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTND YRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHRWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGMGISGQLTWTRLPQGFKNSPTLFNEALHRDLA DFRIQHPDLILLQYVDDILLAATSELDCQQGTRALLLTLGNLGYRASAKKAQLCQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAG

	FCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPP CLRMVAAIAVLRKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEEGAPHDCLEILAETHGTRPD LTDQPIPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKRLNVYTDSRYAFATAHIHGEIYRRRGWLTSEG REIKNKSEILALLKALFLPKRLSIIHCLGHQKGDSAEARGNRLADQAAREAAIKTPPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
1875	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSSGGGEAAAKGGTLNLED EYRLYETSAEPEVSPGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEAKLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGT NDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHRWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGMGISGQLTWTRLPQGFKNSPTLFNEALHRD LADFRIQHPDLILLQYVDDILLAATSELDCQQGTRALLLTLGNLGYRASAKKAQLCQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGK AGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGW PPCLRMVAAIAVLRKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEEGAPHDCLEILAETHGTR PDLTDQPIPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKRLNVYTDSRYAFATAHIHGEIYRRRGWLTS EGREIKNKSEILALLKALFLPKRLSIIHCLGHQKGDSAEARGNRLADQAAREAAIKTPPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
1876	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGGSGGGGSGGGGSGGGG SGGTLNLEDEYRLYETSAEPEVSPGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEAKLGIKPHIQRLLDQGILVPCQSPWNTP LLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHRWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGMGISGQLTWTRLPQGFKNSPT

	LFNEALHRDLADFRIQHPDLILLQYVDDILLAATSELDCQQGTRALLLTLGNLGYRASAKKAQLCQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTP RQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSK KLDPVAAGWPPCLRMVAAIAVLRKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEEGAPHDCLE ILAETHGTRPDLTDQPIPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKRLNVYTDSRYAFATAHIHGEI YRRRGWLTSEGREIKNKSEILALLKALFLPKRLSIIHCLGHQKGDSAEARGNRLADQAAREAAIKTPPDTSTLLAGKRTADGSEFEKRTADGSEFESPKK KAKVE
1877	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGSSGSSGSSGSSGGTLNLE DEYRLYETSAEPEVSPGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEAKLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPG TNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHRWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGMGISGQLTWTRLPQGFKNSPTLFNEALHR DLADFRIQHPDLILLQYVDDILLAATSELDCQQGTRALLLTLGNLGYRASAKKAQLCQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLG KAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAG WPPCLRMVAAIAVLRKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEEGAPHDCLEILAETHGT RPDLTDQPIPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKRLNVYTDSRYAFATAHIHGEIYRRRGWLT SEGREIKNKSEILALLKALFLPKRLSIIHCLGHQKGDSAEARGNRLADQAAREAAIKTPPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
1881	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPAPAPAPGGTLNLEDEY

	RLYETSAEPEVSPGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEAKLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTND YRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHRWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGMGISGQLTWTRLPQGFKNSPTLFNEALHRDLA DFRIQHPDLILLQYVDDILLAATSELDCQQGTRALLLTLGNLGYRASAKKAQLCQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAG FCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPP CLRMVAAIAVLRKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEEGAPHDCLEILAETHGTRPD LTDQPIPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKRLNVYTDSRYAFATAHIHGEIYRRRGWLTSEG REIKNKSEILALLKALFLPKRLSIIHCLGHQKGDSAEARGNRLADQAAREAAIKTPPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
1883	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPGSSGGSGGTLNLEDEY RLYETSAEPEVSPGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEAKLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTND YRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHRWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGMGISGQLTWTRLPQGFKNSPTLFNEALHRDLA DFRIQHPDLILLQYVDDILLAATSELDCQQGTRALLLTLGNLGYRASAKKAQLCQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAG FCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPP CLRMVAAIAVLRKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEEGAPHDCLEILAETHGTRPD LTDQPIPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKRLNVYTDSRYAFATAHIHGEIYRRRGWLTSEG REIKNKSEILALLKALFLPKRLSIIHCLGHQKGDSAEARGNRLADQAAREAAIKTPPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
1889	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK

	VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGSGSSEAAAKGGTLNLED EYRLYETSAEPEVSPGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEAKLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGT NDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHRWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGMGISGQLTWTRLPQGFKNSPTLFNEALHRD LADFRIQHPDLILLQYVDDILLAATSELDCQQGTRALLLTLGNLGYRASAKKAQLCQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGK AGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGW PPCLRMVAAIAVLRKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEEGAPHDCLEILAETHGTR PDLTDQPIPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKRLNVYTDSRYAFATAHIHGEIYRRRGWLTS EGREIKNKSEILALLKALFLPKRLSIIHCLGHQKGDSAEARGNRLADQAAREAAIKTPPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
1899	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGSPAPGGGGGTLNLEDEY RLYETSAEPEVSPGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEAKLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTND YRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHRWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGMGISGQLTWTRLPQGFKNSPTLFNEALHRDLA DFRIQHPDLILLQYVDDILLAATSELDCQQGTRALLLTLGNLGYRASAKKAQLCQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAG FCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPP CLRMVAAIAVLRKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEEGAPHDCLEILAETHGTRPD LTDQPIPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKRLNVYTDSRYAFATAHIHGEIYRRRGWLTSEG REIKNKSEILALLKALFLPKRLSIIHCLGHQKGDSAEARGNRLADQAAREAAIKTPPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
1937	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE

	VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGGGGSEAAAKGGTVSLQD EHRLFDIPVTTSLPDVWLQDFPQAWAETGGLGRAKCQAPIIIDLKPTAVPVSIKQYPMSLEAHMGIRQHIIKFLELGVLRPCRSPWNTPLLPVKKPGTQD YRPVQDLREINKRTVDIHPTVPNPYNLLSTLKPDYSWYTVLDLKDAFFCLPLAPQSQELFAFEWKDPERGISGQLTWTRLPQGFKNSPTLFNEALHRDLT DFRTQHPEVTLLQYVDDLLLAAPTKKACTQGTRHLLQELGEKGYRASAKKAQICQTKVTYLGYILSEGKRWLTPGRIETVARIPPPRNPREVREFLGKAG FCRLFIPGFAELAAPLYALTKPSTPFTWQTEHQLAFEALKKALLSAPALGLPDTSKPFTLFLDERQGIAKGVLTQKLGPWKRPVAYLSKKLDPVAAGWPP CLRIMAATAMLVKDSAKLTLGQPLTVITPHTLEAIVRQPPDRWITNARLTHYQALLLDTDRVQFGPPVTLNPATLLPVPENQPSPHDCRQVLAETHGTRE DLKDQELPDADHTWYTDGSSYLDSGTRRAGAAVVDGHNTIWAQSLPPGTSAQKAELIALTKALELSKGKKANIYTDSRYAFATAHTHGSIYERRGWLTSE GKEIKNKAEIIALLKALFLPQEVAIIHCPGHQKGQDPVAVGNRQADRVARQAAMAEVLTLATEPDNTSHITAGKRTADGSEFEKRTADGSEFESPKKKAK VE
1938	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGGPAPEAAAKGGTVSLQD EHRLFDIPVTTSLPDVWLQDFPQAWAETGGLGRAKCQAPIIIDLKPTAVPVSIKQYPMSLEAHMGIRQHIIKFLELGVLRPCRSPWNTPLLPVKKPGTQD YRPVQDLREINKRTVDIHPTVPNPYNLLSTLKPDYSWYTVLDLKDAFFCLPLAPQSQELFAFEWKDPERGISGQLTWTRLPQGFKNSPTLFNEALHRDLT DFRTQHPEVTLLQYVDDLLLAAPTKKACTQGTRHLLQELGEKGYRASAKKAQICQTKVTYLGYILSEGKRWLTPGRIETVARIPPPRNPREVREFLGKAG FCRLFIPGFAELAAPLYALTKPSTPFTWQTEHQLAFEALKKALLSAPALGLPDTSKPFTLFLDERQGIAKGVLTQKLGPWKRPVAYLSKKLDPVAAGWPP CLRIMAATAMLVKDSAKLTLGQPLTVITPHTLEAIVRQPPDRWITNARLTHYQALLLDTDRVQFGPPVTLNPATLLPVPENQPSPHDCRQVLAETHGTRE DLKDQELPDADHTWYTDGSSYLDSGTRRAGAAVVDGHNTIWAQSLPPGTSAQKAELIALTKALELSKGKKANIYTDSRYAFATAHTHGSIYERRGWLTSE GKEIKNKAEIIALLKALFLPQEVAIIHCPGHQKGQDPVAVGNRQADRVARQAAMAEVLTLATEPDNTSHITAGKRTADGSEFEKRTADGSEFESPKKKAK VE
1939	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA

	KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPGGSEAAAKGGTVSLQD EHRLFDIPVTTSLPDVWLQDFPQAWAETGGLGRAKCQAPIIIDLKPTAVPVSIKQYPMSLEAHMGIRQHIIKFLELGVLRPCRSPWNTPLLPVKKPGTQD YRPVQDLREINKRTVDIHPTVPNPYNLLSTLKPDYSWYTVLDLKDAFFCLPLAPQSQELFAFEWKDPERGISGQLTWTRLPQGFKNSPTLFNEALHRDLT DFRTQHPEVTLLQYVDDLLLAAPTKKACTQGTRHLLQELGEKGYRASAKKAQICQTKVTYLGYILSEGKRWLTPGRIETVARIPPPRNPREVREFLGKAG FCRLFIPGFAELAAPLYALTKPSTPFTWQTEHQLAFEALKKALLSAPALGLPDTSKPFTLFLDERQGIAKGVLTQKLGPWKRPVAYLSKKLDPVAAGWPP CLRIMAATAMLVKDSAKLTLGQPLTVITPHTLEAIVRQPPDRWITNARLTHYQALLLDTDRVQFGPPVTLNPATLLPVPENQPSPHDCRQVLAETHGTRE DLKDQELPDADHTWYTDGSSYLDSGTRRAGAAVVDGHNTIWAQSLPPGTSAQKAELIALTKALELSKGKKANIYTDSRYAFATAHTHGSIYERRGWLTSE GKEIKNKAEIIALLKALFLPQEVAIIHCPGHQKGQDPVAVGNRQADRVARQAAMAEVLTLATEPDNTSHITAGKRTADGSEFEKRTADGSEFESPKKKAK VE
1940	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGSGGGGGTVSLQDEHRLF DIPVTTSLPDVWLQDFPQAWAETGGLGRAKCQAPIIIDLKPTAVPVSIKQYPMSLEAHMGIRQHIIKFLELGVLRPCRSPWNTPLLPVKKPGTQDYRPVQ DLREINKRTVDIHPTVPNPYNLLSTLKPDYSWYTVLDLKDAFFCLPLAPQSQELFAFEWKDPERGISGQLTWTRLPQGFKNSPTLFNEALHRDLTDFRTQ HPEVTLLQYVDDLLLAAPTKKACTQGTRHLLQELGEKGYRASAKKAQICQTKVTYLGYILSEGKRWLTPGRIETVARIPPPRNPREVREFLGKAGFCRLF IPGFAELAAPLYALTKPSTPFTWQTEHQLAFEALKKALLSAPALGLPDTSKPFTLFLDERQGIAKGVLTQKLGPWKRPVAYLSKKLDPVAAGWPPCLRIM AATAMLVKDSAKLTLGQPLTVITPHTLEAIVRQPPDRWITNARLTHYQALLLDTDRVQFGPPVTLNPATLLPVPENQPSPHDCRQVLAETHGTREDLKDQ ELPDADHTWYTDGSSYLDSGTRRAGAAVVDGHNTIWAQSLPPGTSAQKAELIALTKALELSKGKKANIYTDSRYAFATAHTHGSIYERRGWLTSEGKEIK NKAEIIALLKALFLPQEVAIIHCPGHQKGQDPVAVGNRQADRVARQAAMAEVLTLATEPDNTSHITAGKRTADGSEFEKRTADGSEFESPKKKAKVE
1942	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA

	NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGSGGGPAPGGTVSLQDEH RLFDIPVTTSLPDVWLQDFPQAWAETGGLGRAKCQAPIIIDLKPTAVPVSIKQYPMSLEAHMGIRQHIIKFLELGVLRPCRSPWNTPLLPVKKPGTQDYR PVQDLREINKRTVDIHPTVPNPYNLLSTLKPDYSWYTVLDLKDAFFCLPLAPQSQELFAFEWKDPERGISGQLTWTRLPQGFKNSPTLFNEALHRDLTDF RTQHPEVTLLQYVDDLLLAAPTKKACTQGTRHLLQELGEKGYRASAKKAQICQTKVTYLGYILSEGKRWLTPGRIETVARIPPPRNPREVREFLGKAGFC RLFIPGFAELAAPLYALTKPSTPFTWQTEHQLAFEALKKALLSAPALGLPDTSKPFTLFLDERQGIAKGVLTQKLGPWKRPVAYLSKKLDPVAAGWPPCL RIMAATAMLVKDSAKLTLGQPLTVITPHTLEAIVRQPPDRWITNARLTHYQALLLDTDRVQFGPPVTLNPATLLPVPENQPSPHDCRQVLAETHGTREDL KDQELPDADHTWYTDGSSYLDSGTRRAGAAVVDGHNTIWAQSLPPGTSAQKAELIALTKALELSKGKKANIYTDSRYAFATAHTHGSIYERRGWLTSEGK EIKNKAEIIALLKALFLPQEVAIIHCPGHQKGQDPVAVGNRQADRVARQAAMAEVLTLATEPDNTSHITAGKRTADGSEFEKRTADGSEFESPKKKAKVE
1943	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGEAAAKGGSGGTVSLQD EHRLFDIPVTTSLPDVWLQDFPQAWAETGGLGRAKCQAPIIIDLKPTAVPVSIKQYPMSLEAHMGIRQHIIKFLELGVLRPCRSPWNTPLLPVKKPGTQD YRPVQDLREINKRTVDIHPTVPNPYNLLSTLKPDYSWYTVLDLKDAFFCLPLAPQSQELFAFEWKDPERGISGQLTWTRLPQGFKNSPTLFNEALHRDLT DFRTQHPEVTLLQYVDDLLLAAPTKKACTQGTRHLLQELGEKGYRASAKKAQICQTKVTYLGYILSEGKRWLTPGRIETVARIPPPRNPREVREFLGKAG FCRLFIPGFAELAAPLYALTKPSTPFTWQTEHQLAFEALKKALLSAPALGLPDTSKPFTLFLDERQGIAKGVLTQKLGPWKRPVAYLSKKLDPVAAGWPP CLRIMAATAMLVKDSAKLTLGQPLTVITPHTLEAIVRQPPDRWITNARLTHYQALLLDTDRVQFGPPVTLNPATLLPVPENQPSPHDCRQVLAETHGTRE DLKDQELPDADHTWYTDGSSYLDSGTRRAGAAVVDGHNTIWAQSLPPGTSAQKAELIALTKALELSKGKKANIYTDSRYAFATAHTHGSIYERRGWLTSE GKEIKNKAEIIALLKALFLPQEVAIIHCPGHQKGQDPVAVGNRQADRVARQAAMAEVLTLATEPDNTSHITAGKRTADGSEFEKRTADGSEFESPKKKAK VE
1945	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ

	SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPAPGGTVSLQDEHRLFD IPVTTSLPDVWLQDFPQAWAETGGLGRAKCQAPIIIDLKPTAVPVSIKQYPMSLEAHMGIRQHIIKFLELGVLRPCRSPWNTPLLPVKKPGTQDYRPVQD LREINKRTVDIHPTVPNPYNLLSTLKPDYSWYTVLDLKDAFFCLPLAPQSQELFAFEWKDPERGISGQLTWTRLPQGFKNSPTLFNEALHRDLTDFRTQH PEVTLLQYVDDLLLAAPTKKACTQGTRHLLQELGEKGYRASAKKAQICQTKVTYLGYILSEGKRWLTPGRIETVARIPPPRNPREVREFLGKAGFCRLFI PGFAELAAPLYALTKPSTPFTWQTEHQLAFEALKKALLSAPALGLPDTSKPFTLFLDERQGIAKGVLTQKLGPWKRPVAYLSKKLDPVAAGWPPCLRIMA ATAMLVKDSAKLTLGQPLTVITPHTLEAIVRQPPDRWITNARLTHYQALLLDTDRVQFGPPVTLNPATLLPVPENQPSPHDCRQVLAETHGTREDLKDQE LPDADHTWYTDGSSYLDSGTRRAGAAVVDGHNTIWAQSLPPGTSAQKAELIALTKALELSKGKKANIYTDSRYAFATAHTHGSIYERRGWLTSEGKEIKN KAEIIALLKALFLPQEVAIIHCPGHQKGQDPVAVGNRQADRVARQAAMAEVLTLATEPDNTSHITAGKRTADGSEFEKRTADGSEFESPKKKAKVE
1949	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGGGSEAAAKGGGGSGGTV SLQDEHRLFDIPVTTSLPDVWLQDFPQAWAETGGLGRAKCQAPIIIDLKPTAVPVSIKQYPMSLEAHMGIRQHIIKFLELGVLRPCRSPWNTPLLPVKKP GTQDYRPVQDLREINKRTVDIHPTVPNPYNLLSTLKPDYSWYTVLDLKDAFFCLPLAPQSQELFAFEWKDPERGISGQLTWTRLPQGFKNSPTLFNEALH RDLTDFRTQHPEVTLLQYVDDLLLAAPTKKACTQGTRHLLQELGEKGYRASAKKAQICQTKVTYLGYILSEGKRWLTPGRIETVARIPPPRNPREVREFL GKAGFCRLFIPGFAELAAPLYALTKPSTPFTWQTEHQLAFEALKKALLSAPALGLPDTSKPFTLFLDERQGIAKGVLTQKLGPWKRPVAYLSKKLDPVAA GWPPCLRIMAATAMLVKDSAKLTLGQPLTVITPHTLEAIVRQPPDRWITNARLTHYQALLLDTDRVQFGPPVTLNPATLLPVPENQPSPHDCRQVLAETH GTREDLKDQELPDADHTWYTDGSSYLDSGTRRAGAAVVDGHNTIWAQSLPPGTSAQKAELIALTKALELSKGKKANIYTDSRYAFATAHTHGSIYERRGW LTSEGKEIKNKAEIIALLKALFLPQEVAIIHCPGHQKGQDPVAVGNRQADRVARQAAMAEVLTLATEPDNTSHITAGKRTADGSEFEKRTADGSEFESPK KKAKVE
1951	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL

	FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGSGSSEAAAKGGTVSLQD EHRLFDIPVTTSLPDVWLQDFPQAWAETGGLGRAKCQAPIIIDLKPTAVPVSIKQYPMSLEAHMGIRQHIIKFLELGVLRPCRSPWNTPLLPVKKPGTQD YRPVQDLREINKRTVDIHPTVPNPYNLLSTLKPDYSWYTVLDLKDAFFCLPLAPQSQELFAFEWKDPERGISGQLTWTRLPQGFKNSPTLFNEALHRDLT DFRTQHPEVTLLQYVDDLLLAAPTKKACTQGTRHLLQELGEKGYRASAKKAQICQTKVTYLGYILSEGKRWLTPGRIETVARIPPPRNPREVREFLGKAG FCRLFIPGFAELAAPLYALTKPSTPFTWQTEHQLAFEALKKALLSAPALGLPDTSKPFTLFLDERQGIAKGVLTQKLGPWKRPVAYLSKKLDPVAAGWPP CLRIMAATAMLVKDSAKLTLGQPLTVITPHTLEAIVRQPPDRWITNARLTHYQALLLDTDRVQFGPPVTLNPATLLPVPENQPSPHDCRQVLAETHGTRE DLKDQELPDADHTWYTDGSSYLDSGTRRAGAAVVDGHNTIWAQSLPPGTSAQKAELIALTKALELSKGKKANIYTDSRYAFATAHTHGSIYERRGWLTSE GKEIKNKAEIIALLKALFLPQEVAIIHCPGHQKGQDPVAVGNRQADRVARQAAMAEVLTLATEPDNTSHITAGKRTADGSEFEKRTADGSEFESPKKKAK VE
1953	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPAPAPGGTVSLQDEHRL FDIPVTTSLPDVWLQDFPQAWAETGGLGRAKCQAPIIIDLKPTAVPVSIKQYPMSLEAHMGIRQHIIKFLELGVLRPCRSPWNTPLLPVKKPGTQDYRPV QDLREINKRTVDIHPTVPNPYNLLSTLKPDYSWYTVLDLKDAFFCLPLAPQSQELFAFEWKDPERGISGQLTWTRLPQGFKNSPTLFNEALHRDLTDFRT QHPEVTLLQYVDDLLLAAPTKKACTQGTRHLLQELGEKGYRASAKKAQICQTKVTYLGYILSEGKRWLTPGRIETVARIPPPRNPREVREFLGKAGFCRL FIPGFAELAAPLYALTKPSTPFTWQTEHQLAFEALKKALLSAPALGLPDTSKPFTLFLDERQGIAKGVLTQKLGPWKRPVAYLSKKLDPVAAGWPPCLRI MAATAMLVKDSAKLTLGQPLTVITPHTLEAIVRQPPDRWITNARLTHYQALLLDTDRVQFGPPVTLNPATLLPVPENQPSPHDCRQVLAETHGTREDLKD QELPDADHTWYTDGSSYLDSGTRRAGAAVVDGHNTIWAQSLPPGTSAQKAELIALTKALELSKGKKANIYTDSRYAFATAHTHGSIYERRGWLTSEGKEI KNKAEIIALLKALFLPQEVAIIHCPGHQKGQDPVAVGNRQADRVARQAAMAEVLTLATEPDNTSHITAGKRTADGSEFEKRTADGSEFESPKKKAKVE

1961	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPGSSGGSGGTVSLQDEH RLFDIPVTTSLPDVWLQDFPQAWAETGGLGRAKCQAPIIIDLKPTAVPVSIKQYPMSLEAHMGIRQHIIKFLELGVLRPCRSPWNTPLLPVKKPGTQDYR PVQDLREINKRTVDIHPTVPNPYNLLSTLKPDYSWYTVLDLKDAFFCLPLAPQSQELFAFEWKDPERGISGQLTWTRLPQGFKNSPTLFNEALHRDLTDF RTQHPEVTLLQYVDDLLLAAPTKKACTQGTRHLLQELGEKGYRASAKKAQICQTKVTYLGYILSEGKRWLTPGRIETVARIPPPRNPREVREFLGKAGFC RLFIPGFAELAAPLYALTKPSTPFTWQTEHQLAFEALKKALLSAPALGLPDTSKPFTLFLDERQGIAKGVLTQKLGPWKRPVAYLSKKLDPVAAGWPPCL RIMAATAMLVKDSAKLTLGQPLTVITPHTLEAIVRQPPDRWITNARLTHYQALLLDTDRVQFGPPVTLNPATLLPVPENQPSPHDCRQVLAETHGTREDL KDQELPDADHTWYTDGSSYLDSGTRRAGAAVVDGHNTIWAQSLPPGTSAQKAELIALTKALELSKGKKANIYTDSRYAFATAHTHGSIYERRGWLTSEGK EIKNKAEIIALLKALFLPQEVAIIHCPGHQKGQDPVAVGNRQADRVARQAAMAEVLTLATEPDNTSHITAGKRTADGSEFEKRTADGSEFESPKKKAKVE
1967	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGAEAAAKEAAAKEAAAKEAA AKALEAEAAAKEAAAKEAAAKEAAAKAGGTVSLQDEHRLFDIPVTTSLPDVWLQDFPQAWAETGGLGRAKCQAPIIIDLKPTAVPVSIKQYPMSLEAHMG IRQHIIKFLELGVLRPCRSPWNTPLLPVKKPGTQDYRPVQDLREINKRTVDIHPTVPNPYNLLSTLKPDYSWYTVLDLKDAFFCLPLAPQSQELFAFEWK DPERGISGQLTWTRLPQGFKNSPTLFNEALHRDLTDFRTQHPEVTLLQYVDDLLLAAPTKKACTQGTRHLLQELGEKGYRASAKKAQICQTKVTYLGYIL SEGKRWLTPGRIETVARIPPPRNPREVREFLGKAGFCRLFIPGFAELAAPLYALTKPSTPFTWQTEHQLAFEALKKALLSAPALGLPDTSKPFTLFLDER QGIAKGVLTQKLGPWKRPVAYLSKKLDPVAAGWPPCLRIMAATAMLVKDSAKLTLGQPLTVITPHTLEAIVRQPPDRWITNARLTHYQALLLDTDRVQFG PPVTLNPATLLPVPENQPSPHDCRQVLAETHGTREDLKDQELPDADHTWYTDGSSYLDSGTRRAGAAVVDGHNTIWAQSLPPGTSAQKAELIALTKALEL

	SKGKKANIYTDSRYAFATAHTHGSIYERRGWLTSEGKEIKNKAEIIALLKALFLPQEVAIIHCPGHQKGQDPVAVGNRQADRVARQAAMAEVLTLATEPD NTSHITAGKRTADGSEFEKRTADGSEFESPKKKAKVE
1968	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPGSSEAAAKGGTVSLQD EHRLFDIPVTTSLPDVWLQDFPQAWAETGGLGRAKCQAPIIIDLKPTAVPVSIKQYPMSLEAHMGIRQHIIKFLELGVLRPCRSPWNTPLLPVKKPGTQD YRPVQDLREINKRTVDIHPTVPNPYNLLSTLKPDYSWYTVLDLKDAFFCLPLAPQSQELFAFEWKDPERGISGQLTWTRLPQGFKNSPTLFNEALHRDLT DFRTQHPEVTLLQYVDDLLLAAPTKKACTQGTRHLLQELGEKGYRASAKKAQICQTKVTYLGYILSEGKRWLTPGRIETVARIPPPRNPREVREFLGKAG FCRLFIPGFAELAAPLYALTKPSTPFTWQTEHQLAFEALKKALLSAPALGLPDTSKPFTLFLDERQGIAKGVLTQKLGPWKRPVAYLSKKLDPVAAGWPP CLRIMAATAMLVKDSAKLTLGQPLTVITPHTLEAIVRQPPDRWITNARLTHYQALLLDTDRVQFGPPVTLNPATLLPVPENQPSPHDCRQVLAETHGTRE DLKDQELPDADHTWYTDGSSYLDSGTRRAGAAVVDGHNTIWAQSLPPGTSAQKAELIALTKALELSKGKKANIYTDSRYAFATAHTHGSIYERRGWLTSE GKEIKNKAEIIALLKALFLPQEVAIIHCPGHQKGQDPVAVGNRQADRVARQAAMAEVLTLATEPDNTSHITAGKRTADGSEFEKRTADGSEFESPKKKAK VE
1970	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSSGSSGGTVSLQDEHRLF DIPVTTSLPDVWLQDFPQAWAETGGLGRAKCQAPIIIDLKPTAVPVSIKQYPMSLEAHMGIRQHIIKFLELGVLRPCRSPWNTPLLPVKKPGTQDYRPVQ DLREINKRTVDIHPTVPNPYNLLSTLKPDYSWYTVLDLKDAFFCLPLAPQSQELFAFEWKDPERGISGQLTWTRLPQGFKNSPTLFNEALHRDLTDFRTQ HPEVTLLQYVDDLLLAAPTKKACTQGTRHLLQELGEKGYRASAKKAQICQTKVTYLGYILSEGKRWLTPGRIETVARIPPPRNPREVREFLGKAGFCRLF

	IPGFAELAAPLYALTKPSTPFTWQTEHQLAFEALKKALLSAPALGLPDTSKPFTLFLDERQGIAKGVLTQKLGPWKRPVAYLSKKLDPVAAGWPPCLRIM AATAMLVKDSAKLTLGQPLTVITPHTLEAIVRQPPDRWITNARLTHYQALLLDTDRVQFGPPVTLNPATLLPVPENQPSPHDCRQVLAETHGTREDLKDQ ELPDADHTWYTDGSSYLDSGTRRAGAAVVDGHNTIWAQSLPPGTSAQKAELIALTKALELSKGKKANIYTDSRYAFATAHTHGSIYERRGWLTSEGKEIK NKAEIIALLKALFLPQEVAIIHCPGHQKGQDPVAVGNRQADRVARQAAMAEVLTLATEPDNTSHITAGKRTADGSEFEKRTADGSEFESPKKKAKVE
1976	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSPAPGGGGGTVSLQDEH RLFDIPVTTSLPDVWLQDFPQAWAETGGLGRAKCQAPIIIDLKPTAVPVSIKQYPMSLEAHMGIRQHIIKFLELGVLRPCRSPWNTPLLPVKKPGTQDYR PVQDLREINKRTVDIHPTVPNPYNLLSTLKPDYSWYTVLDLKDAFFCLPLAPQSQELFAFEWKDPERGISGQLTWTRLPQGFKNSPTLFNEALHRDLTDF RTQHPEVTLLQYVDDLLLAAPTKKACTQGTRHLLQELGEKGYRASAKKAQICQTKVTYLGYILSEGKRWLTPGRIETVARIPPPRNPREVREFLGKAGFC RLFIPGFAELAAPLYALTKPSTPFTWQTEHQLAFEALKKALLSAPALGLPDTSKPFTLFLDERQGIAKGVLTQKLGPWKRPVAYLSKKLDPVAAGWPPCL RIMAATAMLVKDSAKLTLGQPLTVITPHTLEAIVRQPPDRWITNARLTHYQALLLDTDRVQFGPPVTLNPATLLPVPENQPSPHDCRQVLAETHGTREDL KDQELPDADHTWYTDGSSYLDSGTRRAGAAVVDGHNTIWAQSLPPGTSAQKAELIALTKALELSKGKKANIYTDSRYAFATAHTHGSIYERRGWLTSEGK EIKNKAEIIALLKALFLPQEVAIIHCPGHQKGQDPVAVGNRQADRVARQAAMAEVLTLATEPDNTSHITAGKRTADGSEFEKRTADGSEFESPKKKAKVE
1978	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPAPAPAPGGTVSLQDEH RLFDIPVTTSLPDVWLQDFPQAWAETGGLGRAKCQAPIIIDLKPTAVPVSIKQYPMSLEAHMGIRQHIIKFLELGVLRPCRSPWNTPLLPVKKPGTQDYR PVQDLREINKRTVDIHPTVPNPYNLLSTLKPDYSWYTVLDLKDAFFCLPLAPQSQELFAFEWKDPERGISGQLTWTRLPQGFKNSPTLFNEALHRDLTDF

	RTQHPEVTLLQYVDDLLLAAPTKKACTQGTRHLLQELGEKGYRASAKKAQICQTKVTYLGYILSEGKRWLTPGRIETVARIPPPRNPREVREFLGKAGFC RLFIPGFAELAAPLYALTKPSTPFTWQTEHQLAFEALKKALLSAPALGLPDTSKPFTLFLDERQGIAKGVLTQKLGPWKRPVAYLSKKLDPVAAGWPPCL RIMAATAMLVKDSAKLTLGQPLTVITPHTLEAIVRQPPDRWITNARLTHYQALLLDTDRVQFGPPVTLNPATLLPVPENQPSPHDCRQVLAETHGTREDL KDQELPDADHTWYTDGSSYLDSGTRRAGAAVVDGHNTIWAQSLPPGTSAQKAELIALTKALELSKGKKANIYTDSRYAFATAHTHGSIYERRGWLTSEGK EIKNKAEIIALLKALFLPQEVAIIHCPGHQKGQDPVAVGNRQADRVARQAAMAEVLTLATEPDNTSHITAGKRTADGSEFEKRTADGSEFESPKKKAKVE
1991	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGGGSSGGSGGTVSLQDEH RLFDIPVTTSLPDVWLQDFPQAWAETGGLGRAKCQAPIIIDLKPTAVPVSIKQYPMSLEAHMGIRQHIIKFLELGVLRPCRSPWNTPLLPVKKPGTQDYR PVQDLREINKRTVDIHPTVPNPYNLLSTLKPDYSWYTVLDLKDAFFCLPLAPQSQELFAFEWKDPERGISGQLTWTRLPQGFKNSPTLFNEALHRDLTDF RTQHPEVTLLQYVDDLLLAAPTKKACTQGTRHLLQELGEKGYRASAKKAQICQTKVTYLGYILSEGKRWLTPGRIETVARIPPPRNPREVREFLGKAGFC RLFIPGFAELAAPLYALTKPSTPFTWQTEHQLAFEALKKALLSAPALGLPDTSKPFTLFLDERQGIAKGVLTQKLGPWKRPVAYLSKKLDPVAAGWPPCL RIMAATAMLVKDSAKLTLGQPLTVITPHTLEAIVRQPPDRWITNARLTHYQALLLDTDRVQFGPPVTLNPATLLPVPENQPSPHDCRQVLAETHGTREDL KDQELPDADHTWYTDGSSYLDSGTRRAGAAVVDGHNTIWAQSLPPGTSAQKAELIALTKALELSKGKKANIYTDSRYAFATAHTHGSIYERRGWLTSEGK EIKNKAEIIALLKALFLPQEVAIIHCPGHQKGQDPVAVGNRQADRVARQAAMAEVLTLATEPDNTSHITAGKRTADGSEFEKRTADGSEFESPKKKAKVE
1992	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGSGGSGGSGGSGGTV SLQDEHRLFDIPVTTSLPDVWLQDFPQAWAETGGLGRAKCQAPIIIDLKPTAVPVSIKQYPMSLEAHMGIRQHIIKFLELGVLRPCRSPWNTPLLPVKKP

	GTQDYRPVQDLREINKRTVDIHPTVPNPYNLLSTLKPDYSWYTVLDLKDAFFCLPLAPQSQELFAFEWKDPERGISGQLTWTRLPQGFKNSPTLFNEALH RDLTDFRTQHPEVTLLQYVDDLLLAAPTKKACTQGTRHLLQELGEKGYRASAKKAQICQTKVTYLGYILSEGKRWLTPGRIETVARIPPPRNPREVREFL GKAGFCRLFIPGFAELAAPLYALTKPSTPFTWQTEHQLAFEALKKALLSAPALGLPDTSKPFTLFLDERQGIAKGVLTQKLGPWKRPVAYLSKKLDPVAA GWPPCLRIMAATAMLVKDSAKLTLGQPLTVITPHTLEAIVRQPPDRWITNARLTHYQALLLDTDRVQFGPPVTLNPATLLPVPENQPSPHDCRQVLAETH GTREDLKDQELPDADHTWYTDGSSYLDSGTRRAGAAVVDGHNTIWAQSLPPGTSAQKAELIALTKALELSKGKKANIYTDSRYAFATAHTHGSIYERRGW LTSEGKEIKNKAEIIALLKALFLPQEVAIIHCPGHQKGQDPVAVGNRQADRVARQAAMAEVLTLATEPDNTSHITAGKRTADGSEFEKRTADGSEFESPK KKAKVE
2048	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPGGSEAAAKGGLGIEDE YRLHETSTEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIQQYPMSHEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTN DYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGMGISGQLTWTRLPQGFKNSPTLFNEALHRDL ADFRIQHPDLILLQYVDDILLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLREGQRWLTEARKETVMGQPVPKTPRQLREFLGKA GFCRLFIPGFAEMAAPLYPLTKPGTLFSWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWP PCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEEGAPHDCLEILAETHGTRP DLTDQPIPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVIWAGALPAGTSAQRAELIALTQALKMAEGKRLNVYTDSRYAFATAHIHGEIYRRRGWLTSE GREIKNKSEILALLKALFLPKRLSIIHCLGHQKGDSAEARGNRLADQAAREAAIKTPPDTSTLLIAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2048	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK

	VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPGGSEAAAKGGLGIEDE YRLHETSTEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIQQYPMSHEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTN DYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGMGISGQLTWTRLPQGFKNSPTLFNEALHRDL ADFRIQHPDLILLQYVDDILLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLREGQRWLTEARKETVMGQPVPKTPRQLREFLGKA GFCRLFIPGFAEMAAPLYPLTKPGTLFSWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWP PCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEEGAPHDCLEILAETHGTRP DLTDQPIPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVIWAGALPAGTSAQRAELIALTQALKMAEGKRLNVYTDSRYAFATAHIHGEIYRRRGWLTSE GREIKNKSEILALLKALFLPKRLSIIHCLGHQKGDSAEARGNRLADQAAREAAIKTPPDTSTLLIAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2049	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKGGGGSEAAAKGGLG IEDEYRLHETSTEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIQQYPMSHEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKK PGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGMGISGQLTWTRLPQGFKNSPTLFNEAL HRDLADFRIQHPDLILLQYVDDILLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLREGQRWLTEARKETVMGQPVPKTPRQLREF LGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFSWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVA AGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEEGAPHDCLEILAETH GTRPDLTDQPIPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVIWAGALPAGTSAQRAELIALTQALKMAEGKRLNVYTDSRYAFATAHIHGEIYRRRGW LTSEGREIKNKSEILALLKALFLPKRLSIIHCLGHQKGDSAEARGNRLADQAAREAAIKTPPDTSTLLIAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2050	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE

	VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPGSSEAAAKGGLGIEDE YRLHETSTEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIQQYPMSHEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTN DYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGMGISGQLTWTRLPQGFKNSPTLFNEALHRDL ADFRIQHPDLILLQYVDDILLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLREGQRWLTEARKETVMGQPVPKTPRQLREFLGKA GFCRLFIPGFAEMAAPLYPLTKPGTLFSWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWP PCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEEGAPHDCLEILAETHGTRP DLTDQPIPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVIWAGALPAGTSAQRAELIALTQALKMAEGKRLNVYTDSRYAFATAHIHGEIYRRRGWLTSE GREIKNKSEILALLKALFLPKRLSIIHCLGHQKGDSAEARGNRLADQAAREAAIKTPPDTSTLLIAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2054	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKGGGPAPGGLGIEDE YRLHETSTEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIQQYPMSHEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTN DYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGMGISGQLTWTRLPQGFKNSPTLFNEALHRDL ADFRIQHPDLILLQYVDDILLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLREGQRWLTEARKETVMGQPVPKTPRQLREFLGKA GFCRLFIPGFAEMAAPLYPLTKPGTLFSWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWP PCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEEGAPHDCLEILAETHGTRP DLTDQPIPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVIWAGALPAGTSAQRAELIALTQALKMAEGKRLNVYTDSRYAFATAHIHGEIYRRRGWLTSE GREIKNKSEILALLKALFLPKRLSIIHCLGHQKGDSAEARGNRLADQAAREAAIKTPPDTSTLLIAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2055	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM

	PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKGGSGSSGGLGIEDE YRLHETSTEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIQQYPMSHEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTN DYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGMGISGQLTWTRLPQGFKNSPTLFNEALHRDL ADFRIQHPDLILLQYVDDILLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLREGQRWLTEARKETVMGQPVPKTPRQLREFLGKA GFCRLFIPGFAEMAAPLYPLTKPGTLFSWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWP PCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEEGAPHDCLEILAETHGTRP DLTDQPIPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVIWAGALPAGTSAQRAELIALTQALKMAEGKRLNVYTDSRYAFATAHIHGEIYRRRGWLTSE GREIKNKSEILALLKALFLPKRLSIIHCLGHQKGDSAEARGNRLADQAAREAAIKTPPDTSTLLIAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2058	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGSPAPGGGGGLGIEDEYR LHETSTEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIQQYPMSHEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDY RPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGMGISGQLTWTRLPQGFKNSPTLFNEALHRDLAD FRIQHPDLILLQYVDDILLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLREGQRWLTEARKETVMGQPVPKTPRQLREFLGKAGF CRLFIPGFAEMAAPLYPLTKPGTLFSWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPC LRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEEGAPHDCLEILAETHGTRPDL TDQPIPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVIWAGALPAGTSAQRAELIALTQALKMAEGKRLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGR EIKNKSEILALLKALFLPKRLSIIHCLGHQKGDSAEARGNRLADQAAREAAIKTPPDTSTLLIAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2060	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL

	NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSSPAPGGGGGLGIEDEYR LHETSTEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIQQYPMSHEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDY RPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGMGISGQLTWTRLPQGFKNSPTLFNEALHRDLAD FRIQHPDLILLQYVDDILLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLREGQRWLTEARKETVMGQPVPKTPRQLREFLGKAGF CRLFIPGFAEMAAPLYPLTKPGTLFSWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPC LRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEEGAPHDCLEILAETHGTRPDL TDQPIPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVIWAGALPAGTSAQRAELIALTQALKMAEGKRLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGR EIKNKSEILALLKALFLPKRLSIIHCLGHQKGDSAEARGNRLADQAAREAAIKTPPDTSTLLIAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2085	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGGSGGGGSGGGGSGGGG SGGLGIEDEYRLHETSTEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIQQYPMSHEARLGIKPHIQRLLDQGILVPCQSPWNTPL LPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGMGISGQLTWTRLPQGFKNSPTL FNEALHRDLADFRIQHPDLILLQYVDDILLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLREGQRWLTEARKETVMGQPVPKTPR QLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFSWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKK LDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEEGAPHDCLEI LAETHGTRPDLTDQPIPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVIWAGALPAGTSAQRAELIALTQALKMAEGKRLNVYTDSRYAFATAHIHGEIY RRRGWLTSEGREIKNKSEILALLKALFLPKRLSIIHCLGHQKGDSAEARGNRLADQAAREAAIKTPPDTSTLLIAGKRTADGSEFEKRTADGSEFESPKK KAKVE
2086	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK

	ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKEAAAKEAAAKEAAA KEAAAKGGLGIEDEYRLHETSTEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIQQYPMSHEARLGIKPHIQRLLDQGILVPCQSP WNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGMGISGQLTWTRLPQGFK NSPTLFNEALHRDLADFRIQHPDLILLQYVDDILLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLREGQRWLTEARKETVMGQPV PKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFSWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVA YLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEEGAPH DCLEILAETHGTRPDLTDQPIPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVIWAGALPAGTSAQRAELIALTQALKMAEGKRLNVYTDSRYAFATAHI HGEIYRRRGWLTSEGREIKNKSEILALLKALFLPKRLSIIHCLGHQKGDSAEARGNRLADQAAREAAIKTPPDTSTLLIAGKRTADGSEFEKRTADGSEF ESPKKKAKVE
2087	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPAPAPAPAPGGLGIE DEYRLHETSTEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIQQYPMSHEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPG TNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGMGISGQLTWTRLPQGFKNSPTLFNEALHR DLADFRIQHPDLILLQYVDDILLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLREGQRWLTEARKETVMGQPVPKTPRQLREFLG KAGFCRLFIPGFAEMAAPLYPLTKPGTLFSWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAG WPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEEGAPHDCLEILAETHGT RPDLTDQPIPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVIWAGALPAGTSAQRAELIALTQALKMAEGKRLNVYTDSRYAFATAHIHGEIYRRRGWLT SEGREIKNKSEILALLKALFLPKRLSIIHCLGHQKGDSAEARGNRLADQAAREAAIKTPPDTSTLLIAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2089	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA

	SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPGSSEAAAKGGLGIEDE YRLHETSTEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIQQYPMSHEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTN DYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGMGISGQLTWTRLPQGFKNSPTLFNEALHRDL ADFRIQHPDLILLQYVDDILLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLREGQRWLTEARKETVMGQPVPKTPRQLREFLGKA GFCRLFIPGFAEMAAPLYPLTKPGTLFSWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWP PCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEEGAPHDCLEILAETHGTRP DLTDQPIPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVIWAGALPAGTSAQRAELIALTQALKMAEGKRLNVYTDSRYAFATAHIHGEIYRRRGWLTSE GREIKNKSEILALLKALFLPKRLSIIHCLGHQKGDSAEARGNRLADQAAREAAIKTPPDTSTLLIAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2090	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKGGGGSEAAAKGGLG IEDEYRLHETSTEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIQQYPMSHEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKK PGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGMGISGQLTWTRLPQGFKNSPTLFNEAL HRDLADFRIQHPDLILLQYVDDILLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLREGQRWLTEARKETVMGQPVPKTPRQLREF LGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFSWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVA AGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEEGAPHDCLEILAETH GTRPDLTDQPIPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVIWAGALPAGTSAQRAELIALTQALKMAEGKRLNVYTDSRYAFATAHIHGEIYRRRGW LTSEGREIKNKSEILALLKALFLPKRLSIIHCLGHQKGDSAEARGNRLADQAAREAAIKTPPDTSTLLIAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2091	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ

	SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPGSSGGGGGLGIEDEYR LHETSTEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIQQYPMSHEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDY RPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGMGISGQLTWTRLPQGFKNSPTLFNEALHRDLAD FRIQHPDLILLQYVDDILLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLREGQRWLTEARKETVMGQPVPKTPRQLREFLGKAGF CRLFIPGFAEMAAPLYPLTKPGTLFSWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPC LRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEEGAPHDCLEILAETHGTRPDL TDQPIPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVIWAGALPAGTSAQRAELIALTQALKMAEGKRLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGR EIKNKSEILALLKALFLPKRLSIIHCLGHQKGDSAEARGNRLADQAAREAAIKTPPDTSTLLIAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2092	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKEAAAKEAAAKEAAA KGGLGIEDEYRLHETSTEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIQQYPMSHEARLGIKPHIQRLLDQGILVPCQSPWNTPL LPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGMGISGQLTWTRLPQGFKNSPTL FNEALHRDLADFRIQHPDLILLQYVDDILLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLREGQRWLTEARKETVMGQPVPKTPR QLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFSWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKK LDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEEGAPHDCLEI LAETHGTRPDLTDQPIPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVIWAGALPAGTSAQRAELIALTQALKMAEGKRLNVYTDSRYAFATAHIHGEIY RRRGWLTSEGREIKNKSEILALLKALFLPKRLSIIHCLGHQKGDSAEARGNRLADQAAREAAIKTPPDTSTLLIAGKRTADGSEFEKRTADGSEFESPKK KAKVE
2093	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL

	FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPGGSEAAAKGGLGIEDE YRLHETSTEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIQQYPMSHEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTN DYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGMGISGQLTWTRLPQGFKNSPTLFNEALHRDL ADFRIQHPDLILLQYVDDILLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLREGQRWLTEARKETVMGQPVPKTPRQLREFLGKA GFCRLFIPGFAEMAAPLYPLTKPGTLFSWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWP PCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEEGAPHDCLEILAETHGTRP DLTDQPIPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVIWAGALPAGTSAQRAELIALTQALKMAEGKRLNVYTDSRYAFATAHIHGEIYRRRGWLTSE GREIKNKSEILALLKALFLPKRLSIIHCLGHQKGDSAEARGNRLADQAAREAAIKTPPDTSTLLIAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2093	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPGGSEAAAKGGLGIEDE YRLHETSTEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIQQYPMSHEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTN DYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGMGISGQLTWTRLPQGFKNSPTLFNEALHRDL ADFRIQHPDLILLQYVDDILLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLREGQRWLTEARKETVMGQPVPKTPRQLREFLGKA GFCRLFIPGFAEMAAPLYPLTKPGTLFSWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWP PCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEEGAPHDCLEILAETHGTRP DLTDQPIPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVIWAGALPAGTSAQRAELIALTQALKMAEGKRLNVYTDSRYAFATAHIHGEIYRRRGWLTSE GREIKNKSEILALLKALFLPKRLSIIHCLGHQKGDSAEARGNRLADQAAREAAIKTPPDTSTLLIAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2094	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV

	QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGGSGGGGSGGGGSGGGG SGGGGSGGGGSGGLGIEDEYRLHETSTEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIQQYPMSHEARLGIKPHIQRLLDQGILV PCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGMGISGQLTWTRL PQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDILLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLREGQRWLTEARKETV MGQPVPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFSWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPW RRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPE EGAPHDCLEILAETHGTRPDLTDQPIPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVIWAGALPAGTSAQRAELIALTQALKMAEGKRLNVYTDSRYAF ATAHIHGEIYRRRGWLTSEGREIKNKSEILALLKALFLPKRLSIIHCLGHQKGDSAEARGNRLADQAAREAAIKTPPDTSTLLIAGKRTADGSEFEKRTA DGSEFESPKKKAKVE
2095	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPEAAAKGSSGGLGIEDE YRLHETSTEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIQQYPMSHEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTN DYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGMGISGQLTWTRLPQGFKNSPTLFNEALHRDL ADFRIQHPDLILLQYVDDILLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLREGQRWLTEARKETVMGQPVPKTPRQLREFLGKA GFCRLFIPGFAEMAAPLYPLTKPGTLFSWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWP PCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEEGAPHDCLEILAETHGTRP DLTDQPIPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVIWAGALPAGTSAQRAELIALTQALKMAEGKRLNVYTDSRYAFATAHIHGEIYRRRGWLTSE GREIKNKSEILALLKALFLPKRLSIIHCLGHQKGDSAEARGNRLADQAAREAAIKTPPDTSTLLIAGKRTADGSEFEKRTADGSEFESPKKKAKVE

2097	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPEAAAKGGSGGLGIEDE YRLHETSTEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIQQYPMSHEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTN DYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGMGISGQLTWTRLPQGFKNSPTLFNEALHRDL ADFRIQHPDLILLQYVDDILLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLREGQRWLTEARKETVMGQPVPKTPRQLREFLGKA GFCRLFIPGFAEMAAPLYPLTKPGTLFSWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWP PCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEEGAPHDCLEILAETHGTRP DLTDQPIPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVIWAGALPAGTSAQRAELIALTQALKMAEGKRLNVYTDSRYAFATAHIHGEIYRRRGWLTSE GREIKNKSEILALLKALFLPKRLSIIHCLGHQKGDSAEARGNRLADQAAREAAIKTPPDTSTLLIAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2098	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKEAAAKEAAAKEAAA KEAAAKEAAAKGGLGIEDEYRLHETSTEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIQQYPMSHEARLGIKPHIQRLLDQGILV PCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGMGISGQLTWTRL PQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDILLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLREGQRWLTEARKETV MGQPVPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFSWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPW RRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPE EGAPHDCLEILAETHGTRPDLTDQPIPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVIWAGALPAGTSAQRAELIALTQALKMAEGKRLNVYTDSRYAF

	ATAHIHGEIYRRRGWLTSEGREIKNKSEILALLKALFLPKRLSIIHCLGHQKGDSAEARGNRLADQAAREAAIKTPPDTSTLLIAGKRTADGSEFEKRTA DGSEFESPKKKAKVE
2099	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKPAPGGSGGLGIEDE YRLHETSTEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIQQYPMSHEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTN DYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGMGISGQLTWTRLPQGFKNSPTLFNEALHRDL ADFRIQHPDLILLQYVDDILLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLREGQRWLTEARKETVMGQPVPKTPRQLREFLGKA GFCRLFIPGFAEMAAPLYPLTKPGTLFSWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWP PCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEEGAPHDCLEILAETHGTRP DLTDQPIPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVIWAGALPAGTSAQRAELIALTQALKMAEGKRLNVYTDSRYAFATAHIHGEIYRRRGWLTSE GREIKNKSEILALLKALFLPKRLSIIHCLGHQKGDSAEARGNRLADQAAREAAIKTPPDTSTLLIAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2100	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGSGSSEAAAKGGLGIEDE YRLHETSTEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIQQYPMSHEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTN DYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGMGISGQLTWTRLPQGFKNSPTLFNEALHRDL ADFRIQHPDLILLQYVDDILLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLREGQRWLTEARKETVMGQPVPKTPRQLREFLGKA GFCRLFIPGFAEMAAPLYPLTKPGTLFSWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWP

	PCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEEGAPHDCLEILAETHGTRP DLTDQPIPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVIWAGALPAGTSAQRAELIALTQALKMAEGKRLNVYTDSRYAFATAHIHGEIYRRRGWLTSE GREIKNKSEILALLKALFLPKRLSIIHCLGHQKGDSAEARGNRLADQAAREAAIKTPPDTSTLLIAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2101	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPGGGGSSGGLGIEDEYR LHETSTEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIQQYPMSHEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDY RPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGMGISGQLTWTRLPQGFKNSPTLFNEALHRDLAD FRIQHPDLILLQYVDDILLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLREGQRWLTEARKETVMGQPVPKTPRQLREFLGKAGF CRLFIPGFAEMAAPLYPLTKPGTLFSWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPC LRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEEGAPHDCLEILAETHGTRPDL TDQPIPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVIWAGALPAGTSAQRAELIALTQALKMAEGKRLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGR EIKNKSEILALLKALFLPKRLSIIHCLGHQKGDSAEARGNRLADQAAREAAIKTPPDTSTLLIAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2102	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGSEAAAKGGGGGLGIEDE YRLHETSTEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIQQYPMSHEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTN DYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGMGISGQLTWTRLPQGFKNSPTLFNEALHRDL ADFRIQHPDLILLQYVDDILLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLREGQRWLTEARKETVMGQPVPKTPRQLREFLGKA

	GFCRLFIPGFAEMAAPLYPLTKPGTLFSWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWP PCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEEGAPHDCLEILAETHGTRP DLTDQPIPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVIWAGALPAGTSAQRAELIALTQALKMAEGKRLNVYTDSRYAFATAHIHGEIYRRRGWLTSE GREIKNKSEILALLKALFLPKRLSIIHCLGHQKGDSAEARGNRLADQAAREAAIKTPPDTSTLLIAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2104	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKGGSGGLGIEDEYRL HETSTEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIQQYPMSHEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYR PVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADF RIQHPDLILLQYVDDILLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLREGQRWLTEARKETVMGQPVPKTPRQLREFLGKAGFC RLFIPGFAEMAAPLYPLTKPGTLFSWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCL RMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEEGAPHDCLEILAETHGTRPDLT DQPIPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVIWAGALPAGTSAQRAELIALTQALKMAEGKRLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGRE IKNKSEILALLKALFLPKRLSIIHCLGHQKGDSAEARGNRLADQAAREAAIKTPPDTSTLLIAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2105	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGSEAAAKGGLGIEDEYRL HETSTEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIQQYPMSHEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYR PVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADF

	RIQHPDLILLQYVDDILLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLREGQRWLTEARKETVMGQPVPKTPRQLREFLGKAGFC RLFIPGFAEMAAPLYPLTKPGTLFSWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCL RMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEEGAPHDCLEILAETHGTRPDLT DQPIPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVIWAGALPAGTSAQRAELIALTQALKMAEGKRLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGRE IKNKSEILALLKALFLPKRLSIIHCLGHQKGDSAEARGNRLADQAAREAAIKTPPDTSTLLIAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2106	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGGGSEAAAKGGGGSGGLG IEDEYRLHETSTEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIQQYPMSHEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKK PGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGMGISGQLTWTRLPQGFKNSPTLFNEAL HRDLADFRIQHPDLILLQYVDDILLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLREGQRWLTEARKETVMGQPVPKTPRQLREF LGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFSWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVA AGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEEGAPHDCLEILAETH GTRPDLTDQPIPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVIWAGALPAGTSAQRAELIALTQALKMAEGKRLNVYTDSRYAFATAHIHGEIYRRRGW LTSEGREIKNKSEILALLKALFLPKRLSIIHCLGHQKGDSAEARGNRLADQAAREAAIKTPPDTSTLLIAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2109	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSSEAAAKPAPGGLGIEDE YRLHETSTEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIQQYPMSHEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTN

	DYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGMGISGQLTWTRLPQGFKNSPTLFNEALHRDL ADFRIQHPDLILLQYVDDILLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLREGQRWLTEARKETVMGQPVPKTPRQLREFLGKA GFCRLFIPGFAEMAAPLYPLTKPGTLFSWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWP PCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEEGAPHDCLEILAETHGTRP DLTDQPIPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVIWAGALPAGTSAQRAELIALTQALKMAEGKRLNVYTDSRYAFATAHIHGEIYRRRGWLTSE GREIKNKSEILALLKALFLPKRLSIIHCLGHQKGDSAEARGNRLADQAAREAAIKTPPDTSTLLIAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2110	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGGGGGGGLGIEDEYRLH ETSTEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIQQYPMSHEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRP VQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFR IQHPDLILLQYVDDILLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLREGQRWLTEARKETVMGQPVPKTPRQLREFLGKAGFCR LFIPGFAEMAAPLYPLTKPGTLFSWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLR MVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEEGAPHDCLEILAETHGTRPDLTD QPIPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVIWAGALPAGTSAQRAELIALTQALKMAEGKRLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGREI KNKSEILALLKALFLPKRLSIIHCLGHQKGDSAEARGNRLADQAAREAAIKTPPDTSTLLIAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2112	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKGGSPAPGGLGIEDE

	YRLHETSTEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIQQYPMSHEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTN DYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGMGISGQLTWTRLPQGFKNSPTLFNEALHRDL ADFRIQHPDLILLQYVDDILLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLREGQRWLTEARKETVMGQPVPKTPRQLREFLGKA GFCRLFIPGFAEMAAPLYPLTKPGTLFSWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWP PCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEEGAPHDCLEILAETHGTRP DLTDQPIPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVIWAGALPAGTSAQRAELIALTQALKMAEGKRLNVYTDSRYAFATAHIHGEIYRRRGWLTSE GREIKNKSEILALLKALFLPKRLSIIHCLGHQKGDSAEARGNRLADQAAREAAIKTPPDTSTLLIAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2114	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSSPAPGGGGGLGIEDEYR LHETSTEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIQQYPMSHEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDY RPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGMGISGQLTWTRLPQGFKNSPTLFNEALHRDLAD FRIQHPDLILLQYVDDILLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLREGQRWLTEARKETVMGQPVPKTPRQLREFLGKAGF CRLFIPGFAEMAAPLYPLTKPGTLFSWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPC LRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEEGAPHDCLEILAETHGTRPDL TDQPIPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVIWAGALPAGTSAQRAELIALTQALKMAEGKRLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGR EIKNKSEILALLKALFLPKRLSIIHCLGHQKGDSAEARGNRLADQAAREAAIKTPPDTSTLLIAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2115	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK

	VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSSEAAAKGGLGIEDEYRL HETSTEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIQQYPMSHEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYR PVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADF RIQHPDLILLQYVDDILLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLREGQRWLTEARKETVMGQPVPKTPRQLREFLGKAGFC RLFIPGFAEMAAPLYPLTKPGTLFSWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCL RMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEEGAPHDCLEILAETHGTRPDLT DQPIPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVIWAGALPAGTSAQRAELIALTQALKMAEGKRLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGRE IKNKSEILALLKALFLPKRLSIIHCLGHQKGDSAEARGNRLADQAAREAAIKTPPDTSTLLIAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2116	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGGSGGGGSGGGGSGGLG IEDEYRLHETSTEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIQQYPMSHEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKK PGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGMGISGQLTWTRLPQGFKNSPTLFNEAL HRDLADFRIQHPDLILLQYVDDILLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLREGQRWLTEARKETVMGQPVPKTPRQLREF LGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFSWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVA AGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEEGAPHDCLEILAETH GTRPDLTDQPIPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVIWAGALPAGTSAQRAELIALTQALKMAEGKRLNVYTDSRYAFATAHIHGEIYRRRGW LTSEGREIKNKSEILALLKALFLPKRLSIIHCLGHQKGDSAEARGNRLADQAAREAAIKTPPDTSTLLIAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2117	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE

	VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSSGGSEAAAKGGLGIEDE YRLHETSTEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIQQYPMSHEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTN DYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGMGISGQLTWTRLPQGFKNSPTLFNEALHRDL ADFRIQHPDLILLQYVDDILLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLREGQRWLTEARKETVMGQPVPKTPRQLREFLGKA GFCRLFIPGFAEMAAPLYPLTKPGTLFSWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWP PCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEEGAPHDCLEILAETHGTRP DLTDQPIPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVIWAGALPAGTSAQRAELIALTQALKMAEGKRLNVYTDSRYAFATAHIHGEIYRRRGWLTSE GREIKNKSEILALLKALFLPKRLSIIHCLGHQKGDSAEARGNRLADQAAREAAIKTPPDTSTLLIAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2120	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPEAAAKGGGGGLGIEDE YRLHETSTEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIQQYPMSHEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTN DYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGMGISGQLTWTRLPQGFKNSPTLFNEALHRDL ADFRIQHPDLILLQYVDDILLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLREGQRWLTEARKETVMGQPVPKTPRQLREFLGKA GFCRLFIPGFAEMAAPLYPLTKPGTLFSWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWP PCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEEGAPHDCLEILAETHGTRP DLTDQPIPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVIWAGALPAGTSAQRAELIALTQALKMAEGKRLNVYTDSRYAFATAHIHGEIYRRRGWLTSE GREIKNKSEILALLKALFLPKRLSIIHCLGHQKGDSAEARGNRLADQAAREAAIKTPPDTSTLLIAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2122	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM

	PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGSPAPGGGGGLGIEDEYR LHETSTEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIQQYPMSHEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDY RPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGMGISGQLTWTRLPQGFKNSPTLFNEALHRDLAD FRIQHPDLILLQYVDDILLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLREGQRWLTEARKETVMGQPVPKTPRQLREFLGKAGF CRLFIPGFAEMAAPLYPLTKPGTLFSWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPC LRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEEGAPHDCLEILAETHGTRPDL TDQPIPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVIWAGALPAGTSAQRAELIALTQALKMAEGKRLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGR EIKNKSEILALLKALFLPKRLSIIHCLGHQKGDSAEARGNRLADQAAREAAIKTPPDTSTLLIAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2123	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKGGGPAPGGLGIEDE YRLHETSTEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIQQYPMSHEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTN DYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGMGISGQLTWTRLPQGFKNSPTLFNEALHRDL ADFRIQHPDLILLQYVDDILLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLREGQRWLTEARKETVMGQPVPKTPRQLREFLGKA GFCRLFIPGFAEMAAPLYPLTKPGTLFSWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWP PCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEEGAPHDCLEILAETHGTRP DLTDQPIPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVIWAGALPAGTSAQRAELIALTQALKMAEGKRLNVYTDSRYAFATAHIHGEIYRRRGWLTSE GREIKNKSEILALLKALFLPKRLSIIHCLGHQKGDSAEARGNRLADQAAREAAIKTPPDTSTLLIAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2131	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL

	NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGSGGLGIEDEYRLHETST EPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIQQYPMSHEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDL REVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHP DLILLQYVDDILLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLREGQRWLTEARKETVMGQPVPKTPRQLREFLGKAGFCRLFIP GFAEMAAPLYPLTKPGTLFSWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAA IAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEEGAPHDCLEILAETHGTRPDLTDQPIP DADHTWYTDGSSFLQEGQRKAGAAVTTETEVIWAGALPAGTSAQRAELIALTQALKMAEGKRLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGREIKNKS EILALLKALFLPKRLSIIHCLGHQKGDSAEARGNRLADQAAREAAIKTPPDTSTLLIAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2132	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGGEAAAKGGSGGLGIEDE YRLHETSTEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIQQYPMSHEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTN DYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGMGISGQLTWTRLPQGFKNSPTLFNEALHRDL ADFRIQHPDLILLQYVDDILLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLREGQRWLTEARKETVMGQPVPKTPRQLREFLGKA GFCRLFIPGFAEMAAPLYPLTKPGTLFSWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWP PCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEEGAPHDCLEILAETHGTRP DLTDQPIPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVIWAGALPAGTSAQRAELIALTQALKMAEGKRLNVYTDSRYAFATAHIHGEIYRRRGWLTSE GREIKNKSEILALLKALFLPKRLSIIHCLGHQKGDSAEARGNRLADQAAREAAIKTPPDTSTLLIAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2133	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA

	KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGGGGSPAPGGLGIEDEYR LHETSTEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIQQYPMSHEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDY RPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGMGISGQLTWTRLPQGFKNSPTLFNEALHRDLAD FRIQHPDLILLQYVDDILLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLREGQRWLTEARKETVMGQPVPKTPRQLREFLGKAGF CRLFIPGFAEMAAPLYPLTKPGTLFSWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPC LRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEEGAPHDCLEILAETHGTRPDL TDQPIPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVIWAGALPAGTSAQRAELIALTQALKMAEGKRLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGR EIKNKSEILALLKALFLPKRLSIIHCLGHQKGDSAEARGNRLADQAAREAAIKTPPDTSTLLIAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2137	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSGGSGGSGGSGGLGIED EYRLHETSTEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIQQYPMSHEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGT NDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGMGISGQLTWTRLPQGFKNSPTLFNEALHRD LADFRIQHPDLILLQYVDDILLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLREGQRWLTEARKETVMGQPVPKTPRQLREFLGK AGFCRLFIPGFAEMAAPLYPLTKPGTLFSWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGW PPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEEGAPHDCLEILAETHGTR PDLTDQPIPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVIWAGALPAGTSAQRAELIALTQALKMAEGKRLNVYTDSRYAFATAHIHGEIYRRRGWLTS EGREIKNKSEILALLKALFLPKRLSIIHCLGHQKGDSAEARGNRLADQAAREAAIKTPPDTSTLLIAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2140	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK

	ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSSGSSGSSGSSGSSG GLGIEDEYRLHETSTEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIQQYPMSHEARLGIKPHIQRLLDQGILVPCQSPWNTPLLP VKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGMGISGQLTWTRLPQGFKNSPTLFN EALHRDLADFRIQHPDLILLQYVDDILLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLREGQRWLTEARKETVMGQPVPKTPRQL REFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFSWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLD PVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEEGAPHDCLEILA ETHGTRPDLTDQPIPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVIWAGALPAGTSAQRAELIALTQALKMAEGKRLNVYTDSRYAFATAHIHGEIYRR RGWLTSEGREIKNKSEILALLKALFLPKRLSIIHCLGHQKGDSAEARGNRLADQAAREAAIKTPPDTSTLLIAGKRTADGSEFEKRTADGSEFESPKKKA KVE
2142	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSSGSSGSSGGLGIEDEYR LHETSTEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIQQYPMSHEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDY RPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGMGISGQLTWTRLPQGFKNSPTLFNEALHRDLAD FRIQHPDLILLQYVDDILLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLREGQRWLTEARKETVMGQPVPKTPRQLREFLGKAGF CRLFIPGFAEMAAPLYPLTKPGTLFSWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPC LRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEEGAPHDCLEILAETHGTRPDL TDQPIPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVIWAGALPAGTSAQRAELIALTQALKMAEGKRLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGR EIKNKSEILALLKALFLPKRLSIIHCLGHQKGDSAEARGNRLADQAAREAAIKTPPDTSTLLIAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2144	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA

	SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPAPGGLGIEDEYRLHET STEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIQQYPMSHEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQ DLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQ HPDLILLQYVDDILLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLREGQRWLTEARKETVMGQPVPKTPRQLREFLGKAGFCRLF IPGFAEMAAPLYPLTKPGTLFSWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMV AAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEEGAPHDCLEILAETHGTRPDLTDQP IPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVIWAGALPAGTSAQRAELIALTQALKMAEGKRLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGREIKN KSEILALLKALFLPKRLSIIHCLGHQKGDSAEARGNRLADQAAREAAIKTPPDTSTLLIAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2145	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGGGSSEAAAKGGLGIEDE YRLHETSTEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIQQYPMSHEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTN DYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGMGISGQLTWTRLPQGFKNSPTLFNEALHRDL ADFRIQHPDLILLQYVDDILLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLREGQRWLTEARKETVMGQPVPKTPRQLREFLGKA GFCRLFIPGFAEMAAPLYPLTKPGTLFSWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWP PCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEEGAPHDCLEILAETHGTRP DLTDQPIPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVIWAGALPAGTSAQRAELIALTQALKMAEGKRLNVYTDSRYAFATAHIHGEIYRRRGWLTSE GREIKNKSEILALLKALFLPKRLSIIHCLGHQKGDSAEARGNRLADQAAREAAIKTPPDTSTLLIAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2146	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ

	SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGSEAAAKPAPGGLGIEDE YRLHETSTEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIQQYPMSHEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTN DYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGMGISGQLTWTRLPQGFKNSPTLFNEALHRDL ADFRIQHPDLILLQYVDDILLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLREGQRWLTEARKETVMGQPVPKTPRQLREFLGKA GFCRLFIPGFAEMAAPLYPLTKPGTLFSWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWP PCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEEGAPHDCLEILAETHGTRP DLTDQPIPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVIWAGALPAGTSAQRAELIALTQALKMAEGKRLNVYTDSRYAFATAHIHGEIYRRRGWLTSE GREIKNKSEILALLKALFLPKRLSIIHCLGHQKGDSAEARGNRLADQAAREAAIKTPPDTSTLLIAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2148	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGSGGGGGLGIEDEYRLHE TSTEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIQQYPMSHEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPV QDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRI QHPDLILLQYVDDILLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLREGQRWLTEARKETVMGQPVPKTPRQLREFLGKAGFCRL FIPGFAEMAAPLYPLTKPGTLFSWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRM VAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEEGAPHDCLEILAETHGTRPDLTDQ PIPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVIWAGALPAGTSAQRAELIALTQALKMAEGKRLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGREIK NKSEILALLKALFLPKRLSIIHCLGHQKGDSAEARGNRLADQAAREAAIKTPPDTSTLLIAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2149	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL

	LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSSPAPEAAAKGGLGIEDE YRLHETSTEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIQQYPMSHEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTN DYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGMGISGQLTWTRLPQGFKNSPTLFNEALHRDL ADFRIQHPDLILLQYVDDILLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLREGQRWLTEARKETVMGQPVPKTPRQLREFLGKA GFCRLFIPGFAEMAAPLYPLTKPGTLFSWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWP PCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEEGAPHDCLEILAETHGTRP DLTDQPIPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVIWAGALPAGTSAQRAELIALTQALKMAEGKRLNVYTDSRYAFATAHIHGEIYRRRGWLTSE GREIKNKSEILALLKALFLPKRLSIIHCLGHQKGDSAEARGNRLADQAAREAAIKTPPDTSTLLIAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2151	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPGGGGGSGGLGIEDEYR LHETSTEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIQQYPMSHEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDY RPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGMGISGQLTWTRLPQGFKNSPTLFNEALHRDLAD FRIQHPDLILLQYVDDILLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLREGQRWLTEARKETVMGQPVPKTPRQLREFLGKAGF CRLFIPGFAEMAAPLYPLTKPGTLFSWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPC LRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEEGAPHDCLEILAETHGTRPDL TDQPIPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVIWAGALPAGTSAQRAELIALTQALKMAEGKRLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGR EIKNKSEILALLKALFLPKRLSIIHCLGHQKGDSAEARGNRLADQAAREAAIKTPPDTSTLLIAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2154	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL

	FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGGPAPGGSGGLGIEDEYR LHETSTEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIQQYPMSHEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDY RPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGMGISGQLTWTRLPQGFKNSPTLFNEALHRDLAD FRIQHPDLILLQYVDDILLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLREGQRWLTEARKETVMGQPVPKTPRQLREFLGKAGF CRLFIPGFAEMAAPLYPLTKPGTLFSWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPC LRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEEGAPHDCLEILAETHGTRPDL TDQPIPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVIWAGALPAGTSAQRAELIALTQALKMAEGKRLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGR EIKNKSEILALLKALFLPKRLSIIHCLGHQKGDSAEARGNRLADQAAREAAIKTPPDTSTLLIAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2158	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGSGSSGGLGIEDEYRLHE TSTEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIQQYPMSHEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPV QDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRI QHPDLILLQYVDDILLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLREGQRWLTEARKETVMGQPVPKTPRQLREFLGKAGFCRL FIPGFAEMAAPLYPLTKPGTLFSWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRM VAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEEGAPHDCLEILAETHGTRPDLTDQ PIPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVIWAGALPAGTSAQRAELIALTQALKMAEGKRLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGREIK NKSEILALLKALFLPKRLSIIHCLGHQKGDSAEARGNRLADQAAREAAIKTPPDTSTLLIAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2159	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV

	QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKGGSGSSGGLGIEDE YRLHETSTEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIQQYPMSHEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTN DYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGMGISGQLTWTRLPQGFKNSPTLFNEALHRDL ADFRIQHPDLILLQYVDDILLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLREGQRWLTEARKETVMGQPVPKTPRQLREFLGKA GFCRLFIPGFAEMAAPLYPLTKPGTLFSWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWP PCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEEGAPHDCLEILAETHGTRP DLTDQPIPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVIWAGALPAGTSAQRAELIALTQALKMAEGKRLNVYTDSRYAFATAHIHGEIYRRRGWLTSE GREIKNKSEILALLKALFLPKRLSIIHCLGHQKGDSAEARGNRLADQAAREAAIKTPPDTSTLLIAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2161	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKGGGGGSGGLGIEDE YRLHETSTEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIQQYPMSHEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTN DYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGMGISGQLTWTRLPQGFKNSPTLFNEALHRDL ADFRIQHPDLILLQYVDDILLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLREGQRWLTEARKETVMGQPVPKTPRQLREFLGKA GFCRLFIPGFAEMAAPLYPLTKPGTLFSWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWP PCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEEGAPHDCLEILAETHGTRP DLTDQPIPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVIWAGALPAGTSAQRAELIALTQALKMAEGKRLNVYTDSRYAFATAHIHGEIYRRRGWLTSE GREIKNKSEILALLKALFLPKRLSIIHCLGHQKGDSAEARGNRLADQAAREAAIKTPPDTSTLLIAGKRTADGSEFEKRTADGSEFESPKKKAKVE

2165	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSSGGSGGGGGLGIEDEYR LHETSTEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIQQYPMSHEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDY RPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGMGISGQLTWTRLPQGFKNSPTLFNEALHRDLAD FRIQHPDLILLQYVDDILLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLREGQRWLTEARKETVMGQPVPKTPRQLREFLGKAGF CRLFIPGFAEMAAPLYPLTKPGTLFSWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPC LRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEEGAPHDCLEILAETHGTRPDL TDQPIPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVIWAGALPAGTSAQRAELIALTQALKMAEGKRLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGR EIKNKSEILALLKALFLPKRLSIIHCLGHQKGDSAEARGNRLADQAAREAAIKTPPDTSTLLIAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2172	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSGGGGSSGGLGIEDEYR LHETSTEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIQQYPMSHEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDY RPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGMGISGQLTWTRLPQGFKNSPTLFNEALHRDLAD FRIQHPDLILLQYVDDILLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLREGQRWLTEARKETVMGQPVPKTPRQLREFLGKAGF CRLFIPGFAEMAAPLYPLTKPGTLFSWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPC LRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEEGAPHDCLEILAETHGTRPDL

	TDQPIPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVIWAGALPAGTSAQRAELIALTQALKMAEGKRLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGR EIKNKSEILALLKALFLPKRLSIIHCLGHQKGDSAEARGNRLADQAAREAAIKTPPDTSTLLIAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2174	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGGEAAAKGSSGGLGIEDE YRLHETSTEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIQQYPMSHEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTN DYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGMGISGQLTWTRLPQGFKNSPTLFNEALHRDL ADFRIQHPDLILLQYVDDILLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLREGQRWLTEARKETVMGQPVPKTPRQLREFLGKA GFCRLFIPGFAEMAAPLYPLTKPGTLFSWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWP PCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEEGAPHDCLEILAETHGTRP DLTDQPIPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVIWAGALPAGTSAQRAELIALTQALKMAEGKRLNVYTDSRYAFATAHIHGEIYRRRGWLTSE GREIKNKSEILALLKALFLPKRLSIIHCLGHQKGDSAEARGNRLADQAAREAAIKTPPDTSTLLIAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2187	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPAPAPAPAPGGTLGIED EYRLHETSTEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIQQYPMSHEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGT NDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGMGISGQLTWTRLPQGFKNSPTLFNEALHRD LADFRIQHPDLILLQYVDDILLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLREGQRWLTEARKETVMGQPVPKTPRQLREFLGT AGFCRLWIPGFAEMAAPLYPLTKPGTLFSWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGW

	PPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEEGAPHDCLEILAETHGTR PDLTDQPIPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVIWAGALPAGTSAQRAELIALTQALKMAEGKRLNVYTDSRYAFATAHIHGEIYRRRGWLTS EGREIKNKSEILALLKALFLPKRLSIIHCLGHQKGDSAEARGNRLADQAAREAAIKTPPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2188	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKEAAAKEAAAKEAAA KEAAAKGGTLGIEDEYRLHETSTEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIQQYPMSHEARLGIKPHIQRLLDQGILVPCQS PWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGMGISGQLTWTRLPQGF KNSPTLFNEALHRDLADFRIQHPDLILLQYVDDILLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLREGQRWLTEARKETVMGQP VPKTPRQLREFLGTAGFCRLWIPGFAEMAAPLYPLTKPGTLFSWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPV AYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEEGAP HDCLEILAETHGTRPDLTDQPIPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVIWAGALPAGTSAQRAELIALTQALKMAEGKRLNVYTDSRYAFATAH IHGEIYRRRGWLTSEGREIKNKSEILALLKALFLPKRLSIIHCLGHQKGDSAEARGNRLADQAAREAAIKTPPDTSTLLAGKRTADGSEFEKRTADGSEF ESPKKKAKVE
2190	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKGSSGGSGGTLGIED EYRLHETSTEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIQQYPMSHEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGT NDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGMGISGQLTWTRLPQGFKNSPTLFNEALHRD

	LADFRIQHPDLILLQYVDDILLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLREGQRWLTEARKETVMGQPVPKTPRQLREFLGT AGFCRLWIPGFAEMAAPLYPLTKPGTLFSWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGW PPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEEGAPHDCLEILAETHGTR PDLTDQPIPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVIWAGALPAGTSAQRAELIALTQALKMAEGKRLNVYTDSRYAFATAHIHGEIYRRRGWLTS EGREIKNKSEILALLKALFLPKRLSIIHCLGHQKGDSAEARGNRLADQAAREAAIKTPPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2192	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGSPAPEAAAKGGTLGIED EYRLHETSTEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIQQYPMSHEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGT NDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGMGISGQLTWTRLPQGFKNSPTLFNEALHRD LADFRIQHPDLILLQYVDDILLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLREGQRWLTEARKETVMGQPVPKTPRQLREFLGT AGFCRLWIPGFAEMAAPLYPLTKPGTLFSWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGW PPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEEGAPHDCLEILAETHGTR PDLTDQPIPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVIWAGALPAGTSAQRAELIALTQALKMAEGKRLNVYTDSRYAFATAHIHGEIYRRRGWLTS EGREIKNKSEILALLKALFLPKRLSIIHCLGHQKGDSAEARGNRLADQAAREAAIKTPPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2196	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGGSSEAAAKGGTLGIED EYRLHETSTEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIQQYPMSHEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGT

	NDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGMGISGQLTWTRLPQGFKNSPTLFNEALHRD LADFRIQHPDLILLQYVDDILLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLREGQRWLTEARKETVMGQPVPKTPRQLREFLGT AGFCRLWIPGFAEMAAPLYPLTKPGTLFSWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGW PPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEEGAPHDCLEILAETHGTR PDLTDQPIPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVIWAGALPAGTSAQRAELIALTQALKMAEGKRLNVYTDSRYAFATAHIHGEIYRRRGWLTS EGREIKNKSEILALLKALFLPKRLSIIHCLGHQKGDSAEARGNRLADQAAREAAIKTPPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2225	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPGSSEAAAKGGTLNIED EYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGT NDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRD LAGFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPIPKTPRQLREFLGT AGFCRLWIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAFQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGW PPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHDCLDILAEAHGTR SDLMDQPLPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTS EGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGNSAEARGNRMADQAAREVATRETPETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2226	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKGGGGSEAAAKGGTL

	NIEDEYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVK KPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEA LHRDLAGFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPIPKTPRQLRE FLGTAGFCRLWIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAFQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPV AAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHDCLDILAEA HGTRSDLMDQPLPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRG WLTSEGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGNSAEARGNRMADQAAREVATRETPETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2227	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSSGSSGGTLNIEDEYRLH ETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRP VQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLAGFR IQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPIPKTPRQLREFLGTAGFCR LWIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAFQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLR MVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHDCLDILAEAHGTRSDLMD QPLPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEI KNKDEILALLKALFLPKRLSIIHCPGHQKGNSAEARGNRMADQAAREVATRETPETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2231	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK

	VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGGGGSGSSGGTLNIEDEY RLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTND YRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLA GFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPIPKTPRQLREFLGTAG FCRLWIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAFQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPP CLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHDCLDILAEAHGTRSD LMDQPLPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEG KEIKNKDEILALLKALFLPKRLSIIHCPGHQKGNSAEARGNRMADQAAREVATRETPETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2235	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKGSSPAPGGTLNIED EYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGT NDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRD LAGFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPIPKTPRQLREFLGT AGFCRLWIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAFQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGW PPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHDCLDILAEAHGTR SDLMDQPLPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTS EGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGNSAEARGNRMADQAAREVATRETPETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2236	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE

	VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKEAAAKGGTLNIEDE YRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTN DYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDL AGFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPIPKTPRQLREFLGTA GFCRLWIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAFQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWP PCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHDCLDILAEAHGTRS DLMDQPLPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSE GKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGNSAEARGNRMADQAAREVATRETPETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2249	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKEAAAKEAAAKEAAA KEAAAKEAAAKGGTLNIEDEYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGIL VPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTR LPQGFKNSPTLFNEALHRDLAGFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKET VMGQPIPKTPRQLREFLGTAGFCRLWIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAFQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGP WRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLP EEGLQHDCLDILAEAHGTRSDLMDQPLPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYA FATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGNSAEARGNRMADQAAREVATRETPETSTLLAGKRTADGSEFEKRTA DGSEFESPKKKAKVE
2280	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL

	NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSSGSSGSSGSSGSSGGTL NIEDEYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVK KPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEA LHRDLAGFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPIPKTPRQLRE FLGTAGFCRLWIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAFQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPV AAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHDCLDILAEA HGTRSDLMDQPLPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRG WLTSEGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGNSAEARGNRMADQAAREVATRETPETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2299	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPGGTLNIEDEYRLHETS KEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQD LREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLAGFRIQH PDLILLQYVDDLLLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPIPKTPRQLREFLGKAGFCRLFI PGFAEMAAPLYPLTKPGTLFNWGPDQQKAFQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVA AIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHDCLDILAEAHGTRSDLMDQPL PDADHTWYTDGSSFLQEGQRKAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNK DEILALLKALFLPKRLSIIHCPGHQKGNSAEARGNRMADQAAREVATRETPETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2300	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA

	KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGSGGSGGSGGSGGSG GTLNIEDEYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLL PVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLF NEALHRDLAGFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPIPKTPRQ LREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAFQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKL DPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHDCLDIL AEAHGTRSDLMDQPLPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYR RRGWLTSEGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGNSAEARGNRMADQAARFVATRETPETSTLLAGKRTADGSEFEKRTADGSEFESPKKKA KVE
2301	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPAPAPAPAPGGTLNIED EYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGT NDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRD LAGFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPIPKTPRQLREFLGK AGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAFQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGW PPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHDCLDILAEAHGTR SDLMDQPLPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTS EGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGNSAEARGNRMADQAARFVATRETPETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2302	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA

	NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGGPAPGGTLNIEDEYRLH ETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRP VQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLAGFR IQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPIPKTPRQLREFLGKAGFCR LFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAFQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLR MVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHDCLDILAEAHGTRSDLMD QPLPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEI KNKDEILALLKALFLPKRLSIIHCPGHQKGNSAEARGNRMADQAAREVATRETPETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2303	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGGSGGGGSGGGGSGGGG SGGGGSGGGGSGGTLNIEDEYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGIL VPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTR LPQGFKNSPTLFNEALHRDLAGFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKET VMGQPIPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAFQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGP WRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLP EEGLQHDCLDILAEAHGTRSDLMDQPLPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYA FATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGNSAEARGNRMADQAAREVATRETPETSTLLAGKRTADGSEFEKRTA DGSEFESPKKKAKVE
2304	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ

	SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGSSGSSGSSGSSGSSGSSG GTLNIEDEYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLL PVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLF NEALHRDLAGFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPIPKTPRQ LREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAFQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKL DPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHDCLDIL AEAHGTRSDLMDQPLPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYR RRGWLTSEGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGNSAEARGNRMADQAARFVATRETPETSTLLAGKRTADGSEFEKRTADGSEFESPKKKA KVE
2305	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKGGGGSEAAAKGGTL NIEDEYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVK KPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEA LHRDLAGFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPIPKTPRQLRE FLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAFQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPV AAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHDCLDILAEA HGTRSDLMDQPLPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRG WLTSEGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGNSAEARGNRMADQAARFVATRETPETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2308	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL

	FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPGGGGSSGGTLNIEDEY RLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTND YRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLA GFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPIPKTPRQLREFLGKAG FCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAFQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPP CLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHDCLDILAEAHGTRSD LMDQPLPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEG KEIKNKDEILALLKALFLPKRLSIIHCPGHQKGNSAEARGNRMADQAAREVATRETPETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2309	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPAPAPAPAPGGTLNI EDEYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKP GTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALH RDLAGFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPIPKTPRQLREFL GKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAFQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAA GWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHDCLDILAEAHG TRSDLMDQPLPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWL TSEGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGNSAEARGNRMADQAAREVATRETPETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2311	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV

	QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGGGSGGGGSGGGGSGGGG SGGTLNIEDEYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTP LLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPT LFNEALHRDLAGFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPIPKTP RQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAFQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSK KLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHDCLD ILAEAHGTRSDLMDQPLPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEI YRRRGWLTSEGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGNSAEARGNRMADQAAREVATRETPETSTLLAGKRTADGSEFEKRTADGSEFESPKK KAKVE
2312	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGGGSGSSGGTLNIEDEY RLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTND YRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLA GFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPIPKTPRQLREFLGKAG FCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAFQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPP CLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHDCLDILAEAHGTRSD LMDQPLPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEG KEIKNKDEILALLKALFLPKRLSIIHCPGHQKGNSAEARGNRMADQAAREVATRETPETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE

2313	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGSAGSAAGSGEFGGTLNIE DEYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPG TNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHR DLAGFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPIPKTPRQLREFLG KAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAFQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAG WPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHDCLDILAEAHGT RSDLMDQPLPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLT SEGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGNSAEARGNRMADQAARFVATRETPETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2314	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPEAAAKGGSGGTLNIED EYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGT NDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRD LAGFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPIPKTPRQLREFLGK AGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAFQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGW PPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHDCLDILAEAHGTR

	SDLMDQPLPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTS EGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGNSAEARGNRMADQAARELVATRETPETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2315	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKPAPGGSGGTLNIED EYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGT NDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRD LAGFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPIPKTPRQLREFLGK AGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAFQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGW PPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHDCLDILAEAHGTR SDLMDQPLPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTS EGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGNSAEARGNRMADQAARELVATRETPETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2316	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGGEAAAKGSSGGTLNIED EYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGT NDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRD LAGFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPIPKTPRQLREFLGK AGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAFQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGW

	PPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHDCLDILAEAHGTR SDLMDQPLPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTS EGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGNSAEARGNRMADQAARE VATRETPETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2317	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGSGGGPAPGGTLNIEDEY RLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTND YRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLA GFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPIPKTPRQLREFLGKAG FCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAFQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPP CLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHDCLDILAEAHGTRSD LMDQPLPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEG KEIKNKDEILALLKALFLPKRLSIIHCPGHQKGNSAEARGNRMADQAAREVATRETPETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2319	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGSGGSGGSGGSGGTLNIE DEYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPG TNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHR DLAGFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPIPKTPRQLREFLG

	KAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAFQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAG WPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHDCLDILAEAHGT RSDLMDQPLPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLT SEGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGNSAEARGNRMADQAAREVATRETPETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2320	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGPAPGGSGGTLNIEDEY RLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTND YRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLA GFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPIPKTPRQLREFLGKAG FCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAFQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPP CLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHDCLDILAEAHGTRSD LMDQPLPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEG KEIKNKDEILALLKALFLPKRLSIIHCPGHQKGNSAEARGNRMADQAAREVATRETPETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2322	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKEAAAKEAAAKEAAA KEAAAKEAAAKGGTLNIEDEYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGIL VPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTR

	LPQGFKNSPTLFNEALHRDLAGFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKET VMGQPIPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAFQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGP WRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLP EEGLQHDCLDILAEAHGTRSDLMDQPLPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYA FATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGNSAEARGNRMADQAAREVATRETPETSTLLAGKRTADGSEFEKRTA DGSEFESPKKKAKVE
2323	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGSGGTLNIEDEYRLHETS KEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQD LREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLAGFRIQH PDLILLQYVDDLLLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPIPKTPRQLREFLGKAGFCRLFI PGFAEMAAPLYPLTKPGTLFNWGPDQQKAFQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVA AIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHDCLDILAEAHGTRSDLMDQPL PDADHTWYTDGSSFLQEGQRKAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNK DEILALLKALFLPKRLSIIHCPGHQKGNSAEARGNRMADQAAREVATRETPETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2324	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKEAAAKEAAAKEAAA

	KEAAAKGGTLNIEDEYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQS PWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGF KNSPTLFNEALHRDLAGFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQP IPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAFQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPV AYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQ HDCLDILAEAHGTRSDLMDQPLPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAH IHGEIYRRRGWLTSEGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGNSAEARGNRMADQAAREVATRETPETSTLLAGKRTADGSEFEKRTADGSEF ESPKKKAKVE
2325	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKEAAAKEAAAKEAAA KGGTLNIEDEYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTP LLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPT LFNEALHRDLAGFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPIPKTP RQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAFQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSK KLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHDCLD ILAEAHGTRSDLMDQPLPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEI YRRRGWLTSEGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGNSAEARGNRMADQAAREVATRETPETSTLLAGKRTADGSEFEKRTADGSEFESPKK KAKVE
2326	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM

	PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGSEAAAKPAPGGTLNIED EYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGT NDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRD LAGFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPIPKTPRQLREFLGK AGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAFQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGW PPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHDCLDILAEAHGTR SDLMDQPLPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTS EGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGNSAEARGNRMADQAARE VATRETPETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2327	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGGSSEAAAKGGTLNIED EYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGT NDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRD LAGFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPIPKTPRQLREFLGK AGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAFQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGW PPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHDCLDILAEAHGTR SDLMDQPLPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTS EGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGNSAEARGNRMADQAARE VATRETPETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2328	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL

	NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKGGTLNIEDEYRLHE TSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPV QDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLAGFRI QHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPIPKTPRQLREFLGKAGFCRL FIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAFQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRM VAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHDCLDILAEAHGTRSDLMDQ PLPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIK NKDEILALLKALFLPKRLSIIHCPGHQKGNSAEARGNRMADQAARE VATRETPETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2329	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSSPAPGGGGGTLNIEDEY RLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTND YRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLA GFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPIPKTPRQLREFLGKAG FCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAFQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPP CLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHDCLDILAEAHGTRSD LMDQPLPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEG KEIKNKDEILALLKALFLPKRLSIIHCPGHQKGNSAEARGNRMADQAARE VATRETPETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2331	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA

	KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGSGSSGGGGGTLNIEDEY RLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTND YRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLA GFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPIPKTPRQLREFLGKAG FCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAFQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPP CLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHDCLDILAEAHGTRSD LMDQPLPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEG KEIKNKDEILALLKALFLPKRLSIIHCPGHQKGNSAEARGNRMADQAAREVATRETPETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2332	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPGGSEAAAKGGTLNIED EYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGT NDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRD LAGFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPIPKTPRQLREFLGK AGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAFQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGW PPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHDCLDILAEAHGTR SDLMDQPLPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTS EGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGNSAEARGNRMADQAAREVATRETPETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2333	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK

	ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGGSGGGGSGGGGSGGTL NIEDEYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVK KPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEA LHRDLAGFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPIPKTPRQLRE FLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAFQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPV AAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHDCLDILAEA HGTRSDLMDQPLPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRG WLTSEGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGNSAEARGNRMADQAAREVATRETPETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2335	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGSGGGGGTLNIEDEYRLH ETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRP VQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLAGFR IQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPIPKTPRQLREFLGKAGFCR LFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAFQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLR MVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHDCLDILAEAHGTRSDLMD QPLPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEI KNKDEILALLKALFLPKRLSIIHCPGHQKGNSAEARGNRMADQAAREVATRETPETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2338	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA

	NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGSPAPEAAAKGGTLNIED EYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGT NDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRD LAGFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPIPKTPRQLREFLGK AGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAFQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGW PPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHDCLDILAEAHGTR SDLMDQPLPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTS EGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGNSAEARGNRMADQAAREVATRETPETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2342	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGEAAAKGGTLNIEDEYR LHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDY RPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLAG FRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPIPKTPRQLREFLGKAGF CRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAFQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPC LRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHDCLDILAEAHGTRSDL MDQPLPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGK EIKNKDEILALLKALFLPKRLSIIHCPGHQKGNSAEARGNRMADQAAREVATRETPETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2343	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA

	SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGAEAAAKEAAAKEAAAKEAA AKALEAEAAAKEAAAKEAAAKEAAAKAGGTLNIEDEYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEAR LGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFE WRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLAGFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGY LLKEGQRWLTEARKETVMGQPIPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAFQEIKQALLTAPALGLPDLTKPFELFVD EKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQ FGPVVALNPATLLPLPEEGLQHDCLDILAEAHGTRSDLMDQPLPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVIWARALPAGTSAQRAELIALTQALK MAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGNSAEARGNRMADQAARFVATRETPETSTLL AGKRTADGSEFEKRTADGSEFESPKKKAKVE
2345	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSSPAPEAAAKGGTLNIED EYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGT NDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRD LAGFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPIPKTPRQLREFLGK AGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAFQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGW PPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHDCLDILAEAHGTR SDLMDQPLPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTS EGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGNSAEARGNRMADQAAREVATRETPETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2346	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL

	LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGGGSSPAPGGTLNIEDEY RLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTND YRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLA GFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPIPKTPRQLREFLGKAG FCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAFQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPP CLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHDCLDILAEAHGTRSD LMDQPLPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEG KEIKNKDEILALLKALFLPKRLSIIHCPGHQKGNSAEARGNRMADQAARFVATRETPETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2347	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPEAAAKGSSGGTLNIED EYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGT NDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRD LAGFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPIPKTPRQLREFLGK AGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAFQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGW PPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHDCLDILAEAHGTR SDLMDQPLPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTS EGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGNSAEARGNRMADQAARFVATRETPETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2353	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL

	FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGSGSSGGTLNIEDEYRLH ETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRP VQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLAGFR IQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPIPKTPRQLREFLGKAGFCR LFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAFQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLR MVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHDCLDILAEAHGTRSDLMD QPLPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEI KNKDEILALLKALFLPKRLSIIHCPGHQKGNSAEARGNRMADQAAREVATRETPETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2359	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSSEAAAKPAPGGTLNIED EYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGT NDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRD LAGFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPIPKTPRQLREFLGK AGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAFQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGW PPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHDCLDILAEAHGTR SDLMDQPLPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTS EGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGNSAEARGNRMADQAAREVATRETPETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2360	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV

	QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGSGGSGGSGGTLNIEDEY RLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTND YRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLA GFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPIPKTPRQLREFLGKAG FCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAFQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPP CLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHDCLDILAEAHGTRSD LMDQPLPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEG KEIKNKDEILALLKALFLPKRLSIIHCPGHQKGNSAEARGNRMADQAAREVATRETPETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2363	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGSEAAAKGGTLNIEDEYR LHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDY RPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLAG FRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPIPKTPRQLREFLGKAGF CRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAFQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPC LRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHDCLDILAEAHGTRSDL MDQPLPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGK EIKNKDEILALLKALFLPKRLSIIHCPGHQKGNSAEARGNRMADQAAREVATRETPETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE

2364	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPAPGGTLNIEDEYRLHE TSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPV QDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLAGFRI QHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPIPKTPRQLREFLGKAGFCRL FIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAFQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRM VAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHDCLDILAEAHGTRSDLMDQ PLPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIK NKDEILALLKALFLPKRLSIIHCPGHQKGNSAEARGNRMADQAARFVATRETPETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2365	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGSPAPGGGGGTLNIEDEY RLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTND YRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLA GFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPIPKTPRQLREFLGKAG FCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAFQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPP CLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHDCLDILAEAHGTRSD

	LMDQPLPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEG KEIKNKDEILALLKALFLPKRLSIIHCPGHQKGNSAEARGNRMADQAARAVATRETPETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2370	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKGGSGSSGGTLNIED EYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGT NDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRD LAGFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPIPKTPRQLREFLGK AGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAFQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGW PPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHDCLDILAEAHGTR SDLMDQPLPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTS EGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGNSAEARGNRMADQAARAVATRETPETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2371	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGSGGGGSSGGTLNIEDEY RLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTND YRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLA GFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPIPKTPRQLREFLGKAG FCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAFQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPP

	CLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHDCLDILAEAHGTRSD LMDQPLPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEG KEIKNKDEILALLKALFLPKRLSIIHCPGHQKGNSAEARGNRMADQAAREVATRETPETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2382	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSSEAAAKGGTLNIEDEYR LHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDY RPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLAG FRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPIPKTPRQLREFLGKAGF CRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAFQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPC LRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHDCLDILAEAHGTRSDL MDQPLPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGK EIKNKDEILALLKALFLPKRLSIIHCPGHQKGNSAEARGNRMADQAAREVATRETPETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2395	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPGGGGGTLNIEDEYRLH ETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRP VQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLAGFR IQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPIPKTPRQLREFLGKAGFCR

	LFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAFQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLR MVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHDCLDILAEAHGTRSDLMD QPLPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEI KNKDEILALLKALFLPKRLSIIHCPGHQKGNSAEARGNRMADQAAREVATRETPETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2400	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPEAAAKGGGGGTLNIED EYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGT NDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRD LAGFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPIPKTPRQLREFLGK AGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAFQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGW PPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHDCLDILAEAHGTR SDLMDQPLPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTS EGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGNSAEARGNRMADQAAREVATRETPETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2403	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPGGSGGGGGTLNIEDEY RLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTND YRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLA

	GFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPIPKTPRQLREFLGKAG FCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAFQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPP CLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHDCLDILAEAHGTRSD LMDQPLPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEG KEIKNKDEILALLKALFLPKRLSIIHCPGHQKGNSAEARGNRMADQAAREVATRETPETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2405	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGSSGSSGSSGSSGSSGGTL NIEDEYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVK KPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEA LHRDLAGFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPIPKTPRQLRE FLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAFQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPV AAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHDCLDILAEA HGTRSDLMDQPLPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRG WLTSEGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGNSAEARGNRMADQAAREVATRETPETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2449	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPAPAPAPAPAPGGTLNI EDEYRLHETSKGPDVPLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKP

	GTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQSLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALH RDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFL GTAGFCRLWIPGFAEMAAPLYPLTKPGTLFEWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAA GWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPIVALNPATLLPLPEEGLQHDCLDILAEAHG TRPDLTDQPLPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVVWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWL TSEGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGNRAEARGNRMADQAAREVATRETPETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2503	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSSEAAAKGGTLNIEDEYR LHETSKGPDVPLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDY RPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQSLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLAD FRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGF CRLFIPGFAEMAAPLYPLTKPGTLFEWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPC LRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPIVALNPATLLPLPEEGLQHDCLDILAEAHGTRPDL TDQPLPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVVWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGK EIKNKDEILALLKALFLPKRLSIIHCPGHQKGNRAEARGNRMADQAAREVATRETPETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2504	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGGSGGTLNIEDEYRLHE

	TSKGPDVPLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPV QDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQSLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRI QHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRL FIPGFAEMAAPLYPLTKPGTLFEWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRM VAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPIVALNPATLLPLPEEGLQHDCLDILAEAHGTRPDLTDQ PLPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVVWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIK NKDEILALLKALFLPKRLSIIHCPGHQKGNRAEARGNRMADQAAREVATRETPETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2505	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPEAAAKGGTLNIEDEYR LHETSKGPDVPLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDY RPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQSLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLAD FRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGF CRLFIPGFAEMAAPLYPLTKPGTLFEWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPC LRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPIVALNPATLLPLPEEGLQHDCLDILAEAHGTRPDL TDQPLPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVVWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGK EIKNKDEILALLKALFLPKRLSIIHCPGHQKGNRAEARGNRMADQAAREVATRETPETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2506	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK

	VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKPAPGGGGGTLNIED EYRLHETSKGPDVPLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGT NDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQSLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRD LADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGK AGFCRLFIPGFAEMAAPLYPLTKPGTLFEWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGW PPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPIVALNPATLLPLPEEGLQHDCLDILAEAHGTR PDLTDQPLPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVVWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTS EGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGNRAEARGNRMADQAAREVATRETPETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2507	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKEAAAKEAAAKGGTL NIEDEYRLHETSKGPDVPLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVK KPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQSLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEA LHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLRE FLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFEWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPV AAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPIVALNPATLLPLPEEGLQHDCLDILAEA HGTRPDLTDQPLPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVVWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRG WLTSEGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGNRAEARGNRMADQAAREVATRETPETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2508	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE

	VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSSGGTLNIEDEYRLHETS KGPDVPLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQD LREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQSLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQH PDLILLQYVDDLLLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFI PGFAEMAAPLYPLTKPGTLFEWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVA AIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPIVALNPATLLPLPEEGLQHDCLDILAEAHGTRPDLTDQPL PDADHTWYTDGSSFLQEGQRKAGAAVTTETEVVWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNK DEILALLKALFLPKRLSIIHCPGHQKGNRAEARGNRMADQAAREVATRETPETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2510	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPAPAPAPAPGGTLNIED EYRLHETSKGPDVPLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGT NDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQSLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRD LADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGK AGFCRLFIPGFAEMAAPLYPLTKPGTLFEWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGW PPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPIVALNPATLLPLPEEGLQHDCLDILAEAHGTR PDLTDQPLPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVVWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTS EGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGNRAEARGNRMADQAAREVATRETPETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2511	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM

	PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGGGSGGGGSGGTLNIEDE YRLHETSKGPDVPLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTN DYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQSLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDL ADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKA GFCRLFIPGFAEMAAPLYPLTKPGTLFEWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWP PCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPIVALNPATLLPLPEEGLQHDCLDILAEAHGTRP DLTDQPLPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVVWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSE GKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGNRAEARGNRMADQAAREVATRETPETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2512	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKPAPGGSGGTLNIED EYRLHETSKGPDVPLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGT NDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQSLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRD LADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGK AGFCRLFIPGFAEMAAPLYPLTKPGTLFEWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGW PPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPIVALNPATLLPLPEEGLQHDCLDILAEAHGTR PDLTDQPLPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVVWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTS EGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGNRAEARGNRMADQAAREVATRETPETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2513	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL

	NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSGGSGGSGGSGGSG GTLNIEDEYRLHETSKGPDVPLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLL PVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQSLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLF NEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQ LREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFEWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKL DPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPIVALNPATLLPLPEEGLQHDCLDIL AEAHGTRPDLTDQPLPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVVWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYR RRGWLTSEGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGNRAEARGNRMADQAAREVATRETPETSTLLAGKRTADGSEFEKRTADGSEFESPKKKA KVE
2514	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPEAAAKGSSGGTLNIED EYRLHETSKGPDVPLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGT NDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQSLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRD LADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGK AGFCRLFIPGFAEMAAPLYPLTKPGTLFEWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGW PPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPIVALNPATLLPLPEEGLQHDCLDILAEAHGTR PDLTDQPLPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVVWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTS EGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGNRAEARGNRMADQAAREVATRETPETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2515	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK

	ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSSGGGEAAAKGGTLNIED EYRLHETSKGPDVPLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGT NDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQSLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRD LADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGK AGFCRLFIPGFAEMAAPLYPLTKPGTLFEWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGW PPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPIVALNPATLLPLPEEGLQHDCLDILAEAHGTR PDLTDQPLPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVVWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTS EGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGNRAEARGNRMADQAAREVATRETPETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2518	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGSGSETPGTSESATPESGGT LNIEDEYRLHETSKGPDVPLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPV KKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQSLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNE ALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLR EFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFEWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDP VAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPIVALNPATLLPLPEEGLQHDCLDILAE AHGTRPDLTDQPLPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVVWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRR GWLTSEGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGNRAEARGNRMADQAAREVATRETPETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKV E
2519	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA

	SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKPAPGSSGGTLNIED EYRLHETSKGPDVPLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGT NDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQSLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRD LADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGK AGFCRLFIPGFAEMAAPLYPLTKPGTLFEWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGW PPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPIVALNPATLLPLPEEGLQHDCLDILAEAHGTR PDLTDQPLPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVVWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTS EGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGNRAEARGNRMADQAARE VATRETPETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2521	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGGEAAAKGGSGGTLNIED EYRLHETSKGPDVPLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGT NDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQSLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRD LADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGK AGFCRLFIPGFAEMAAPLYPLTKPGTLFEWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGW PPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPIVALNPATLLPLPEEGLQHDCLDILAEAHGTR PDLTDQPLPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVVWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTS EGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGNRAEARGNRMADQAARE VATRETPETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2525	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ

	SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPAPAPAPGGTLNIEDEY RLHETSKGPDVPLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTND YRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQSLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLA DFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAG FCRLFIPGFAEMAAPLYPLTKPGTLFEWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPP CLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPIVALNPATLLPLPEEGLQHDCLDILAEAHGTRPD LTDQPLPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVVWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEG KEIKNKDEILALLKALFLPKRLSIIHCPGHQKGNRAEARGNRMADQAAREVATRETPETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2526	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGGEAAAKPAPGGTLNIED EYRLHETSKGPDVPLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGT NDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQSLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRD LADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGK AGFCRLFIPGFAEMAAPLYPLTKPGTLFEWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGW PPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPIVALNPATLLPLPEEGLQHDCLDILAEAHGTR PDLTDQPLPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVVWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTS EGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGNRAEARGNRMADQAAREVATRETPETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2527	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL

	LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGSPAPEAAAKGGTLNIED EYRLHETSKGPDVPLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGT NDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQSLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRD LADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGK AGFCRLFIPGFAEMAAPLYPLTKPGTLFEWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGW PPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPIVALNPATLLPLPEEGLQHDCLDILAEAHGTR PDLTDQPLPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVVWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTS EGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGNRAEARGNRMADQAAREVATRETPETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2528	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGGSEAAAKGGGGSGGTL NIEDEYRLHETSKGPDVPLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVK KPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQSLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEA LHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLRE FLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFEWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPV AAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPIVALNPATLLPLPEEGLQHDCLDILAEA HGTRPDLTDQPLPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVVWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRG WLTSEGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGNRAEARGNRMADQAAREVATRETPETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2529	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL

	FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGAEAAAKEAAAKEAAAKEAA AKALEAEAAAKEAAAKEAAAKEAAAKAGGTLNIEDEYRLHETSKGPDVPLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEAR LGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQSLFAFE WRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGY LLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFEWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVD EKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQ FGPIVALNPATLLPLPEEGLQHDCLDILAEAHGTRPDLTDQPLPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVVWAKALPAGTSAQRAELIALTQALK MAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGNRAEARGNRMADQAAREVATRETPETSTLL AGKRTADGSEFEKRTADGSEFESPKKKAKVE
2530	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGSEAAAKPAPGGTLNIED EYRLHETSKGPDVPLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGT NDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQSLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRD LADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGK AGFCRLFIPGFAEMAAPLYPLTKPGTLFEWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGW PPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPIVALNPATLLPLPEEGLQHDCLDILAEAHGTR PDLTDQPLPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVVWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTS EGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGNRAEARGNRMADQAAREVATRETPETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE

2531	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPGSSGGGGGTLNIEDEY RLHETSKGPDVPLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTND YRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQSLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLA DFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAG FCRLFIPGFAEMAAPLYPLTKPGTLFEWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPP CLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPIVALNPATLLPLPEEGLQHDCLDILAEAHGTRPD LTDQPLPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVVWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEG KEIKNKDEILALLKALFLPKRLSIIHCPGHQKGNRAEARGNRMADQAAREVATRETPETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2534	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPAPAPAPAPGGTLNI EDEYRLHETSKGPDVPLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKP GTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQSLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALH RDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFL GKAGFCRLFIPGFAEMAAPLYPLTKPGTLFEWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAA GWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPIVALNPATLLPLPEEGLQHDCLDILAEAHG

	TRPDLTDQPLPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVVWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWL TSEGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGNRAEARGNRMADQAAREVATRETPETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2535	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSSEAAAKPAPGGTLNIED EYRLHETSKGPDVPLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGT NDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQSLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRD LADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGK AGFCRLFIPGFAEMAAPLYPLTKPGTLFEWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGW PPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPIVALNPATLLPLPEEGLQHDCLDILAEAHGTR PDLTDQPLPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVVWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTS EGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGNRAEARGNRMADQAAREVATRETPETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2536	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKEAAAKEAAAKEAAA KEAAAKGGTLNIEDEYRLHETSKGPDVPLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQS PWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQSLFAFEWRDPEMGISGQLTWTRLPQGF KNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQP TPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFEWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPV

	AYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPIVALNPATLLPLPEEGLQ HDCLDILAEAHGTRPDLTDQPLPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVVWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAH IHGEIYRRRGWLTSEGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGNRAEARGNRMADQAAREVATRETPETSTLLAGKRTADGSEFEKRTADGSEF ESPKKKAKVE
2539	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKGGTLNIEDEYRLHE TSKGPDVPLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPV QDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQSLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRI QHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRL FIPGFAEMAAPLYPLTKPGTLFEWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRM VAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPIVALNPATLLPLPEEGLQHDCLDILAEAHGTRPDLTDQ PLPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVVWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIK NKDEILALLKALFLPKRLSIIHCPGHQKGNRAEARGNRMADQAAREVATRETPETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2542	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPGSSEAAAKGGTLNIED EYRLHETSKGPDVPLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGT NDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQSLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRD

	LADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGK AGFCRLFIPGFAEMAAPLYPLTKPGTLFEWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGW PPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPIVALNPATLLPLPEEGLQHDCLDILAEAHGTR PDLTDQPLPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVVWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTS EGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGNRAEARGNRMADQAAREVATRETPETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2544	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGSGGSGGSGGTLNIE DEYRLHETSKGPDVPLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPG TNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQSLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHR DLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLG KAGFCRLFIPGFAEMAAPLYPLTKPGTLFEWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAG WPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPIVALNPATLLPLPEEGLQHDCLDILAEAHGT RPDLTDQPLPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVVWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLT SEGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGNRAEARGNRMADQAAREVATRETPETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2547	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGPAPGGTLNIEDEYRLH ETSKGPDVPLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRP

	VQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQSLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFR IQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCR LFIPGFAEMAAPLYPLTKPGTLFEWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLR MVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPIVALNPATLLPLPEEGLQHDCLDILAEAHGTRPDLTD QPLPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVVWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEI KNKDEILALLKALFLPKRLSIIHCPGHQKGNRAEARGNRMADQAAREVATRETPETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2548	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKGGSGSSGGTLNIED EYRLHETSKGPDVPLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGT NDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQSLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRD LADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGK AGFCRLFIPGFAEMAAPLYPLTKPGTLFEWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGW PPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPIVALNPATLLPLPEEGLQHDCLDILAEAHGTR PDLTDQPLPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVVWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTS EGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGNRAEARGNRMADQAAREVATRETPETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2550	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSSEAAAKGGGGGTLNIED

	EYRLHETSKGPDVPLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGT NDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQSLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRD LADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGK AGFCRLFIPGFAEMAAPLYPLTKPGTLFEWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGW PPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPIVALNPATLLPLPEEGLQHDCLDILAEAHGTR PDLTDQPLPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVVWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTS EGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGNRAEARGNRMADQAARE VATRETPETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2551	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKGGSGGGGGTLNIED EYRLHETSKGPDVPLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGT NDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQSLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRD LADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGK AGFCRLFIPGFAEMAAPLYPLTKPGTLFEWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGW PPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPIVALNPATLLPLPEEGLQHDCLDILAEAHGTR PDLTDQPLPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVVWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTS EGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGNRAEARGNRMADQAARE VATRETPETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2553	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK

	VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSSEAAAKGGSGGTLNIED EYRLHETSKGPDVPLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGT NDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQSLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRD LADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGK AGFCRLFIPGFAEMAAPLYPLTKPGTLFEWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGW PPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPIVALNPATLLPLPEEGLQHDCLDILAEAHGTR PDLTDQPLPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVVWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTS EGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGNRAEARGNRMADQAAREVATRETPETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2556	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKGGGPAPGGTLNIED EYRLHETSKGPDVPLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGT NDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQSLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRD LADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGK AGFCRLFIPGFAEMAAPLYPLTKPGTLFEWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGW PPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPIVALNPATLLPLPEEGLQHDCLDILAEAHGTR PDLTDQPLPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVVWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTS EGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGNRAEARGNRMADQAAREVATRETPETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2559	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE

	VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGSGGGGGTLNIEDEYRLH ETSKGPDVPLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRP VQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQSLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFR IQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCR LFIPGFAEMAAPLYPLTKPGTLFEWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLR MVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPIVALNPATLLPLPEEGLQHDCLDILAEAHGTRPDLTD QPLPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVVWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEI KNKDEILALLKALFLPKRLSIIHCPGHQKGNRAEARGNRMADQAAREVATRETPETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2561	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKGGGGSEAAAKGGTL NIEDEYRLHETSKGPDVPLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVK KPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQSLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEA LHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLRE FLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFEWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPV AAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPIVALNPATLLPLPEEGLQHDCLDILAEA HGTRPDLTDQPLPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVVWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRG WLTSEGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGNRAEARGNRMADQAAREVATRETPETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2562	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM

	PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGGGGGGGTLNIEDEYRLH ETSKGPDVPLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRP VQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQSLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFR IQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCR LFIPGFAEMAAPLYPLTKPGTLFEWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLR MVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPIVALNPATLLPLPEEGLQHDCLDILAEAHGTRPDLTD QPLPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVVWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEI KNKDEILALLKALFLPKRLSIIHCPGHQKGNRAEARGNRMADQAAREVATRETPETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2566	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGGSGGGGSGGGGSGGGG SGGGGSGGGGSGGTLNIEDEYRLHETSKGPDVPLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGIL VPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQSLFAFEWRDPEMGISGQLTWTR LPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKET VMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFEWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGP WRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPIVALNPATLLPLP EEGLQHDCLDILAEAHGTRPDLTDQPLPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVVWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYA FATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGNRAEARGNRMADQAAREVATRETPETSTLLAGKRTADGSEFEKRTA DGSEFESPKKKAKVE
2568	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA

	KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPAPGGTLNIEDEYRLHE TSKGPDVPLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPV QDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQSLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRI QHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRL FIPGFAEMAAPLYPLTKPGTLFEWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRM VAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPIVALNPATLLPLPEEGLQHDCLDILAEAHGTRPDLTDQ PLPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVVWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIK NKDEILALLKALFLPKRLSIIHCPGHQKGNRAEARGNRMADQAAREVATRETPETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2573	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSPAPGGGGGTLNIEDEY RLHETSKGPDVPLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTND YRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQSLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLA DFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAG FCRLFIPGFAEMAAPLYPLTKPGTLFEWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPP CLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPIVALNPATLLPLPEEGLQHDCLDILAEAHGTRPD LTDQPLPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVVWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEG KEIKNKDEILALLKALFLPKRLSIIHCPGHQKGNRAEARGNRMADQAAREVATRETPETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2578	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK

	ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGSEAAAKGGGGGTLNIED EYRLHETSKGPDVPLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGT NDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQSLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRD LADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGK AGFCRLFIPGFAEMAAPLYPLTKPGTLFEWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGW PPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPIVALNPATLLPLPEEGLQHDCLDILAEAHGTR PDLTDQPLPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVVWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTS EGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGNRAEARGNRMADQAARE VATRETPETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2583	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSAGSAAGSGEFGGTLNIE DEYRLHETSKGPDVPLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPG TNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQSLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHR DLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLG KAGFCRLFIPGFAEMAAPLYPLTKPGTLFEWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAG WPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPIVALNPATLLPLPEEGLQHDCLDILAEAHGT RPDLTDQPLPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVVWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLT SEGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGNRAEARGNRMADQAARE VATRETPETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2585	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA

	NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKGSSGGTLNIEDEYR LHETSKGPDVPLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDY RPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQSLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLAD FRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGF CRLFIPGFAEMAAPLYPLTKPGTLFEWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPC LRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPIVALNPATLLPLPEEGLQHDCLDILAEAHGTRPDL TDQPLPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVVWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGK EIKNKDEILALLKALFLPKRLSIIHCPGHQKGNRAEARGNRMADQAAREVATRETPETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2592	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGPAPEAAAKGGTLNIED EYRLHETSKGPDVPLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGT NDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQSLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRD LADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGK AGFCRLFIPGFAEMAAPLYPLTKPGTLFEWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGW PPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPIVALNPATLLPLPEEGLQHDCLDILAEAHGTR PDLTDQPLPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVVWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTS EGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGNRAEARGNRMADQAAREVATRETPETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2599	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA

	SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSSPAPEAAAKGGTLNIED EYRLHETSKGPDVPLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGT NDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQSLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRD LADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGK AGFCRLFIPGFAEMAAPLYPLTKPGTLFEWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGW PPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPIVALNPATLLPLPEEGLQHDCLDILAEAHGTR PDLTDQPLPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVVWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTS EGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGNRAEARGNRMADQAARKVATRETPETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2610	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKEAAAKEAAAKEAAA KGGTLNIEDEYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTP LLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPT LFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTP RQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSK KLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLD ILAEAHGTRPDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEI YRRRGWLTSEGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSPSGGSKRTADGSEFEAGKRTA DGSEFEKRTADGSEFESPKKKAKVE
2611	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL

	LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGAEAAAKEAAAKEAAAKEAA AKALEAEAAAKEAAAKEAAAKEAAAKAGGTLNIEDEYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEAR LGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFE WRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGY LLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVD EKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQ FGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALK MAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLL IENSSPSGGSKRTADGSEFEAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2612	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSSGSSGSSGSSGSSGSSG GTLNIEDEYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLL PVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLF NEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQ LREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKL DPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDIL AEAHGTRPDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYR RRGWLTSEGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSPSGGSKRTADGSEFEAGKRTADG SEFEKRTADGSEFESPKKKAKVE

2614	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKGGGPAPGGTLNIED EYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGT NDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRD LADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGK AGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGW PPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTR PDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTS EGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSPSGGSKRTADGSEFEAGKRTADGSEFEKRT ADGSEFESPKKKAKVE
2615	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGGGSGGGGSGGGGSGGGG SGGTLNIEDEYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTP LLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPT LFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTP RQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSK KLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLD

	ILAEAHGTRPDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEI YRRRGWLTSEGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSPSGGSKRTADGSEFEAGKRTA DGSEFEKRTADGSEFESPKKKAKVE
2618	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGGPAPGGSGGTLNIEDEY RLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTND YRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLA DFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAG FCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPP CLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPD LTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEG KEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSPSGGSKRTADGSEFEAGKRTADGSEFEKRTAD GSEFESPKKKAKVE
2619	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPAPAPAPGGTLNIED EYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGT NDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRD

	LADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGK AGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGW PPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTR PDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTS EGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSPSGGSKRTADGSEFEAGKRTADGSEFEKRT ADGSEFESPKKKAKVE
2620	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKGGTLNIEDEYRLHE TSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPV QDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRI QHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRL FIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRM VAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQ PLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIK NKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSPSGGSKRTADGSEFEAGKRTADGSEFEKRTADGSEF ESPKKKAKVE
2622	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK

	VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGSGGGPAPGGTLNIEDEY RLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTND YRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLA DFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAG FCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPP CLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPD LTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEG KEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSPSGGSKRTADGSEFEAGKRTADGSEFEKRTAD GSEFESPKKKAKVE
2622	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGSGGGPAPGGTLNIEDEY RLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTND YRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLA DFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAG FCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPP CLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPD LTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEG KEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSPSGGSKRTADGSEFEAGKRTADGSEFEKRTAD GSEFESPKKKAKVE
2623	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL

	NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKGGGGSEAAAKGGTL NIEDEYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVK KPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEA LHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLRE FLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPV AAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEA HGTRPDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRG WLTSEGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSPSGGSKRTADGSEFEAGKRTADGSEF EKRTADGSEFESPKKKAKVE
2624	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPGGTLNIEDEYRLHETS KEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQD LREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQH PDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFI PGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVA AIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPL PDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNK DEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSPSGGSKRTADGSEFEAGKRTADGSEFEKRTADGSEFES PKKKAKVE
2624	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA

	NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPGGTLNIEDEYRLHETS KEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQD LREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQH PDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFI PGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVA AIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPL PDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNK DEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSPSGGSKRTADGSEFEAGKRTADGSEFEKRTADGSEFES PKKKAKVE
2627	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKEAAAKEAAAKGGTL NIEDEYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVK KPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEA LHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLRE FLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPV AAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEA HGTRPDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRG WLTSEGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSPSGGSKRTADGSEFEAGKRTADGSEF EKRTADGSEFESPKKKAKVE
2629	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL

	LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGSEAAAKGGGGGTLNIED EYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGT NDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRD LADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGK AGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGW PPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTR PDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTS EGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSPSGGSKRTADGSEFEAGKRTADGSEFEKRT ADGSEFESPKKKAKVE
2631	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGSGGTLNIEDEYRLHETS KEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQD LREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQH PDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFI PGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVA AIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPL PDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNK DEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSPSGGSKRTADGSEFEAGKRTADGSEFEKRTADGSEFES PKKKAKVE

2632	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGGSSGGSGGTLNIEDEY RLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTND YRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLA DFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAG FCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPP CLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPD LTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEG KEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSPSGGSKRTADGSEFEAGKRTADGSEFEKRTAD GSEFESPKKKAKVE
2633	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSSPAPGGGGGTLNIEDEY RLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTND YRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLA DFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAG FCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPP CLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPD

	LTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEG KEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSPSGGSKRTADGSEFEAGKRTADGSEFEKRTAD GSEFESPKKKAKVE
2634	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSSGSSGSSGGTLNIEDEY RLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTND YRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLA DFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAG FCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPP CLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPD LTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEG KEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSPSGGSKRTADGSEFEAGKRTADGSEFEKRTAD GSEFESPKKKAKVE
2636	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGGGSEAAAKGGGGSGGTL NIEDEYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVK KPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEA

	LHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLRE FLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPV AAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEA HGTRPDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRG WLTSEGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSPSGGSKRTADGSEFEAGKRTADGSEF EKRTADGSEFESPKKKAKVE
2637	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKGGSGGGGGTLNIED EYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGT NDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRD LADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGK AGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGW PPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTR PDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTS EGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSPSGGSKRTADGSEFEAGKRTADGSEFEKRT ADGSEFESPKKKAKVE
2638	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK

	VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGGEAAAKGGSGGTLNIED EYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGT NDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRD LADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGK AGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGW PPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTR PDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTS EGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSPSGGSKRTADGSEFEAGKRTADGSEFEKRT ADGSEFESPKKKAKVE
2638	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGGEAAAKGGSGGTLNIED EYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGT NDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRD LADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGK AGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGW PPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTR PDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTS EGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSPSGGSKRTADGSEFEAGKRTADGSEFEKRT ADGSEFESPKKKAKVE
2639	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL

	NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGGGSGGGGSGGTLNIEDE YRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTN DYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDL ADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKA GFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWP PCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRP DLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSE GKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSPSGGSKRTADGSEFEAGKRTADGSEFEKRTA DGSEFESPKKKAKVE
2639	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGGGSGGGGSGGTLNIEDE YRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTN DYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDL ADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKA GFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWP PCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRP DLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSE GKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSPSGGSKRTADGSEFEAGKRTADGSEFEKRTA DGSEFESPKKKAKVE
2641	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA

	NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSSEAAAKPAPGGTLNIED EYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGT NDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRD LADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGK AGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGW PPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTR PDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTS EGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSPSGGSKRTADGSEFEAGKRTADGSEFEKRT ADGSEFESPKKKAKVE
2644	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGGSGGGGSGGGGSGGGG SGGGGSGGGGSGGTLNIEDEYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGIL VPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTR LPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKET VMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGP WRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLP EEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYA FATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSPSGGSKRTADG SEFEAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2647	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL

	LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKEAAAKGGTLNIEDE YRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTN DYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDL ADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKA GFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWP PCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRP DLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSE GKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSPSGGSKRTADGSEFEAGKRTADGSEFEKRTA DGSEFESPKKKAKVE
2647	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKEAAAKGGTLNIEDE YRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTN DYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDL ADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKA GFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWP PCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRP DLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSE GKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSPSGGSKRTADGSEFEAGKRTADGSEFEKRTA DGSEFESPKKKAKVE

2648	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSSPAPEAAAKGGTLNIED EYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGT NDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRD LADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGK AGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGW PPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTR PDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTS EGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSPSGGSKRTADGSEFEAGKRTADGSEFEKRT ADGSEFESPKKKAKVE
2649	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPGGSGGGGGTLNIEDEY RLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTND YRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLA DFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAG FCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPP CLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPD

	LTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEG KEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSPSGGSKRTADGSEFEAGKRTADGSEFEKRTAD GSEFESPKKKAKVE
2649	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPGGSGGGGGTLNIEDEY RLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTND YRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLA DFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAG FCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPP CLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPD LTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEG KEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSPSGGSKRTADGSEFEAGKRTADGSEFEKRTAD GSEFESPKKKAKVE
2651	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPGSSEAAAKGGTLNIED EYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGT NDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRD

	LADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGK AGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGW PPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTR PDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTS EGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSPSGGSKRTADGSEFEAGKRTADGSEFEKRT ADGSEFESPKKKAKVE
2653	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGSGGGGGTLNIEDEYRLH ETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRP VQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFR IQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCR LFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLR MVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTD QPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEI KNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSPSGGSKRTADGSEFEAGKRTADGSEFEKRTADGSE FESPKKKAKVE
2654	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK

	VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKGGSPAPGGTLNIED EYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGT NDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRD LADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGK AGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGW PPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTR PDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTS EGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSPSGGSKRTADGSEFEAGKRTADGSEFEKRT ADGSEFESPKKKAKVE
2655	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSSGGTLNIEDEYRLHETS KEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQD LREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQH PDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFI PGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVA AIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPL PDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNK DEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSPSGGSKRTADGSEFEAGKRTADGSEFEKRTADGSEFES PKKKAKVE
2656	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL

	NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPAPAPAPGGTLNIEDEY RLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTND YRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLA DFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAG FCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPP CLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPD LTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEG KEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSPSGGSKRTADGSEFEAGKRTADGSEFEKRTAD GSEFESPKKKAKVE
2657	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKGGSGGTLNIEDEYR LHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDY RPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLAD FRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGF CRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPC LRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDL TDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGK EIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSPSGGSKRTADGSEFEAGKRTADGSEFEKRTADG SEFESPKKKAKVE
2660	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA

	NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGSGSSEAAAKGGTLNIED EYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGT NDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRD LADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGK AGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGW PPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTR PDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTS EGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSPSGGSKRTADGSEFEAGKRTADGSEFEKRT ADGSEFESPKKKAKVE
2663	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGSGSETPGTSESATPESGGT LNIEDEYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPV KKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNE ALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLR EFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDP VAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAE AHGTRPDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRR GWLTSEGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSPSGGSKRTADGSEFEAGKRTADGSE FEKRTADGSEFESPKKKAKVE
2665	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL

	LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGSSGSSGSSGSSGGTLNIE DEYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPG TNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHR DLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLG KAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAG WPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGT RPDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLT SEGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSPSGGSKRTADGSEFEAGKRTADGSEFEKR TADGSEFESPKKKAKVE
2666	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKGGSGSSGGTLNIED EYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGT NDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRD LADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGK AGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGW PPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTR PDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTS EGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSPSGGSKRTADGSEFEAGKRTADGSEFEKRT ADGSEFESPKKKAKVE

2667	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGSPAPGGGGGTLNIEDEY RLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTND YRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLA DFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAG FCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPP CLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPD LTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEG KEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSPSGGSKRTADGSEFEAGKRTADGSEFEKRTAD GSEFESPKKKAKVE
2669	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSSGSSGSSGSSGSSGGTL NIEDEYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVK KPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEA LHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLRE FLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPV AAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEA

	HGTRPDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRG WLTSEGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSPSGGSKRTADGSEFEAGKRTADGSEF EKRTADGSEFESPKKKAKVE
2675	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSGSSGGGGGTLNIEDEY RLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTND YRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLA DFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAG FCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPP CLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPD LTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEG KEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSPSGGSKRTADGSEFEAGKRTADGSEFEKRTAD GSEFESPKKKAKVE
2676	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSSGGGGGTLNIEDEYRLH ETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRP VQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFR

	IQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCR LFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLR MVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTD QPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEI KNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSPSGGSKRTADGSEFEAGKRTADGSEFEKRTADGSE FESPKKKAKVE
2676	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSSGGGGGTLNIEDEYRLH ETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRP VQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFR IQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCR LFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLR MVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTD QPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEI KNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSPSGGSKRTADGSEFEAGKRTADGSEFEKRTADGSE FESPKKKAKVE
2677	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK

	VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGGEAAAKGSSGGTLNIED EYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGT NDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRD LADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGK AGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGW PPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTR PDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTS EGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSPSGGSKRTADGSEFEAGKRTADGSEFEKRT ADGSEFESPKKKAKVE
2678	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKEAAAKEAAAKEAAA KEAAAKGGTLNIEDEYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQS PWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGF KNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQP TPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPV AYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQ HNCLDILAEAHGTRPDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAH IHGEIYRRRGWLTSEGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSPSGGSKRTADGSEFEA GKRTADGSEFEKRTADGSEFESPKKKAKVE
2681	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL

	NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKPAPGGGGGTLNIED EYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGT NDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRD LADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGK AGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGW PPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTR PDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTS EGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSPSGGSKRTADGSEFEAGKRTADGSEFEKRT ADGSEFESPKKKAKVE
2684	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSPAPGSSGGTLNIEDEY RLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTND YRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLA DFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAG FCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPP CLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPD LTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEG KEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSPSGGSKRTADGSEFEAGKRTADGSEFEKRTAD GSEFESPKKKAKVE
2688	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA

	NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGGGSSEAAAKGGTLNIED EYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGT NDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRD LADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGK AGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGW PPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTR PDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTS EGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSPSGGSKRTADGSEFEAGKRTADGSEFEKRT ADGSEFESPKKKAKVE
2692	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSGGGEAAAKGGTLNIED EYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGT NDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRD LADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGK AGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGW PPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTR PDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTS EGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSPSGGSKRTADGSEFEAGKRTADGSEFEKRT ADGSEFESPKKKAKVE
2696	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL

	LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSAGSAAGSGEFGGTLNIE DEYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPG TNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHR DLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLG KAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAG WPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGT RPDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLT SEGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSPSGGSKRTADGSEFEAGKRTADGSEFEKR TADGSEFESPKKKAKVE
2700	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSEAAAKGGTLNIEDEYR LHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDY RPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLAD FRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGF CRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPC LRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDL TDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGK EIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSPSGGSKRTADGSEFEAGKRTADGSEFEKRTADG SEFESPKKKAKVE

2701	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSPAPEAAAKGGTLNIED EYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGT NDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRD LADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGK AGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGW PPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTR PDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTS EGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSPSGGSKRTADGSEFEAGKRTADGSEFEKRT ADGSEFESPKKKAKVE
2711	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGAEAAAKEAAAKEAAAKEAA AKALEAEAAAKEAAAKEAAAKEAAAKAGGTLNIEDEHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEAR LGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFE WRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGY LLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGTAGFCRLWIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVD EKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQ

	FGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALK MAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLL AGKRTADGSEFEKRTADGSEFESPKKKAKVE
2712	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKGGGGSEAAAKGGTL NIEDEHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVK KPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEA LHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLRE FLGTAGFCRLWIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPV AAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEA HGTRPDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRG WLTSEGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2712	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKGGGGSEAAAKGGTL NIEDEHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVK KPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEA LHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLRE

	FLGTAGFCRLWIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPV AAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEA HGTRPDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRG WLTSEGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2713	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGSEAAAKGGGGGTLNIED EHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGT NDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRD
2713	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGSEAAAKGGGGGTLNIED EHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGT NDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRD

	LADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGT AGFCRLWIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGW PPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTR PDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTS EGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2714	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKPAPGGSGGTLNIED EHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGT NDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRD LADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGT AGFCRLWIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGW PPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTR PDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTS EGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2715	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSSGGGGGSGGTLNIEDEH RLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTND

	YRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLA DFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGTAG FCRLWIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPP CLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPD LTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEG KEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2716	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKEAAAKEAAAKEAAA KEAAAKGGTLNIEDEHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQS PWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGF KNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQP TPKTPRQLREFLGTAGFCRLWIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPV AYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQ HNCLDILAEAHGTRPDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAH IHGEIYRRRGWLTSEGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEF ESPKKKAKVE
2716	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK

	VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKEAAAKEAAAKEAAA KEAAAKGGTLNIEDEHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQS PWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGF KNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQP TPKTPRQLREFLGTAGFCRLWIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPV AYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQ HNCLDILAEAHGTRPDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAH IHGEIYRRRGWLTSEGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEF ESPKKKAKVE
2718	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSSEAAAKGGTLNIEDEHR LHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDY RPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLAD FRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGTAGF CRLWIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPC LRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDL TDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGK EIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2719	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM

	PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGGEAAAKPAPGGTLNIED EHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGT NDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRD LADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGT AGFCRLWIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGW PPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTR PDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTS EGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2721	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGGEAAAKGGSGGTLNIED EHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGT NDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRD LADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGT AGFCRLWIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGW PPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTR PDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTS EGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2722	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL

	NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGGGGSEAAAKGGTLNIED EHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGT NDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRD LADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGT AGFCRLWIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGW PPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTR PDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTS EGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2723	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKGSSPAPGGTLNIED EHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGT NDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRD LADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGT AGFCRLWIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGW PPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTR PDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTS EGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2723	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA

	KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKGSSPAPGGTLNIED EHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGT NDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRD LADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGT AGFCRLWIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGW PPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTR PDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTS EGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2724	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKPAPGGTLNIEDEHR LHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDY RPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLAD FRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGTAGF CRLWIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPC LRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDL TDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGK EIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2726	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK

	ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKGGSGGTLNIEDEHR LHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDY RPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLAD FRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGTAGF CRLWIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPC LRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDL TDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGK EIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2731	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPAPAPAPGGTLNIEDEH RLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTND YRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLA DFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGTAG FCRLWIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPP CLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPD LTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEG KEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2734	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA

	NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGSGGSSGGSSGSETPGTSES ATPESSGGSSGGSSGGTLNIEDEHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQ GILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLT WTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEAR KETVMGQPTPKTPRQLREFLGTAGFCRLWIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQK LGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLL PLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDS RYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEK RTADGSEFESPKKKAKVE
2737	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKGSSGGTLNIEDEHR LHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDY RPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLAD FRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGTAGF CRLWIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPC LRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDL TDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGK EIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2741	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ

	SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGGGSGGGGSGGGGSGGGG SGGGGSGGGGSGGTLNIEDEHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGIL VPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTR LPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKET VMGQPTPKTPRQLREFLGTAGFCRLWIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGP WRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLP EEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYA FATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTA DGSEFESPKKKAKVE
2741	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGGGSGGGGSGGGGSGGGG SGGGGSGGGGSGGTLNIEDEHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGIL VPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTR LPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKET VMGQPTPKTPRQLREFLGTAGFCRLWIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGP WRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLP EEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYA FATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTA DGSEFESPKKKAKVE
2744	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV

	QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGSEAAAKPAPGGTLNIED EHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGT NDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRD LADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGT AGFCRLWIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGW PPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTR PDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTS EGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2745	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKGGGGGSGGTLNIED EHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGT NDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRD LADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGT AGFCRLWIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGW PPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTR PDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTS EGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE

2748	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPGSSEAAAKGGTLNIED EHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGT NDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRD LADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGT AGFCRLWIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGW PPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTR PDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTS EGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2753	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPGGSEAAAKGGTLNIED EHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGT NDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRD LADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGT AGFCRLWIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGW PPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTR

	PDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTS EGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2760	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSSGGSEAAAKGGTLNIED EHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGT NDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRD LADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGT AGFCRLWIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGW PPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTR PDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTS EGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2764	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGGSSEAAAKGGTLNIED EHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGT NDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRD LADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGT AGFCRLWIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGW

	PPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTR PDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTS EGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2771	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGGSGGGGSGGGGSGGGG SGGTLNIEDEHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTP LLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPT LFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTP RQLREFLGTAGFCRLWIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSK KLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLD ILAEAHGTRPDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEI YRRRGWLTSEGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKK KAKVE
2772	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKEAAAKEAAAKGGTL NIEDEHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVK KPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEA

	LHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLRE FLGTAGFCRLWIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPV AAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEA HGTRPDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRG WLTSEGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2776	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGSPAPEAAAKGGTLNIED EHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGT NDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRD LADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGT AGFCRLWIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGW PPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTR PDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTS EGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2780	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGGGSGGTLNIEDEHRLH ETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRP

	VQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFR IQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCR LFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLR MVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTD QPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEI KNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2780	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGGGGSGGTLNIEDEHRLH ETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRP VQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFR IQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCR LFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLR MVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTD QPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEI KNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2781	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKPAPGSSGGTLNIED

	EHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGT NDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRD LADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGK AGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGW PPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTR PDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTS EGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2782	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKGGSPAPGGTLNIED EHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGT NDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRD LADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGK AGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGW PPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTR PDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTS EGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2782	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK

	VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKGGSPAPGGTLNIED EHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGT NDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRD LADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGK AGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGW PPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTR PDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTS EGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2783	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKGGSGGTLNIEDEHR LHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDY RPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLAD FRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGF CRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPC LRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDL TDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGK EIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2784	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE

	VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGAEAAAKEAAAKEAAAKEAA AKALEAEAAAKEAAAKEAAAKEAAAKAGGTLNIEDEHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEAR LGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFE WRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGY LLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVD EKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQ FGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALK MAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLL AGKRTADGSEFEKRTADGSEFESPKKKAKVE
2786	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPGGSEAAAKGGTLNIED EHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGT NDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRD LADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGK AGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGW PPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTR PDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTS EGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2787	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL

	NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGSEAAAKGGGGGTLNIED EHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGT NDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRD LADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGK AGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGW PPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTR PDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTS EGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2787	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGSEAAAKGGGGGTLNIED EHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGT NDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRD LADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGK AGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGW PPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTR PDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTS EGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2788	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA

	KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKGGGGSEAAAKGGTL NIEDEHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVK KPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEA LHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLRE FLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPV AAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEA HGTRPDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRG WLTSEGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2789	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKGGGGSSGGTLNIED EHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGT NDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRD LADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGK AGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGW PPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTR PDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTS EGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2790	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK

	ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGGGGGGGGTLNIEDEHRL HETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYR PVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADF RIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFC RLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCL RMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLT DQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKE IKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2791	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKEAAAKEAAAKGGTL NIEDEHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVK KPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEA LHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLRE FLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPV AAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEA HGTRPDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRG WLTSEGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2792	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA

	NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKGSSPAPGGTLNIED EHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGT NDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRD LADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGK AGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGW PPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTR PDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTS EGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2793	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPGGGGSSGGTLNIEDEH RLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTND YRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLA DFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAG FCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPP CLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPD LTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEG KEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2794	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA

	SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKGGSGGGGGTLNIED EHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGT NDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRD LADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGK AGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGW PPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTR PDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTS EGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2795	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGSGGSGGSGGSGGTLNIE DEHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPG TNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHR DLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLG KAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAG WPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGT RPDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLT SEGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2795	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ

	SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSGGSGGSGGSGGTLNIE DEHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPG TNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHR DLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLG KAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAG WPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGT RPDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLT SEGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2797	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPAPAPAPAPGGTLNI EDEHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKP GTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALH RDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFL GKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAA GWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHG TRPDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWL TSEGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2797	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL

	LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPAPAPAPAPGGTLNI EDEHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKP GTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALH RDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFL GKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAA GWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHG TRPDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWL TSEGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2798	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPGSSEAAAKGGTLNIED EHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGT NDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRD LADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGK AGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGW PPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTR PDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTS EGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2798	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL

	FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPGSSEAAAKGGTLNIED EHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGT NDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRD LADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGK AGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGW PPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTR PDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTS EGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2800	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGGPAPGGSGGTLNIEDEH RLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTND YRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLA DFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAG FCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPP CLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPD LTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEG KEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2800	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV

	QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGGPAPGGSGGTLNIEDEH RLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTND YRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLA DFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAG FCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPP CLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPD LTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEG KEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2801	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGSPAPGGGGGTLNIEDEH RLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTND YRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLA DFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAG FCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPP CLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPD LTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEG KEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE

2801	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGSPAPGGGGGTLNIEDEH RLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTND YRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLA DFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAG FCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPP CLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPD LTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEG KEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2802	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSSGSSGSSGSSGSSGGTL NIEDEHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVK KPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEA LHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLRE FLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPV AAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEA

	HGTRPDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRG WLTSEGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2803	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKEAAAKEAAAKEAAA KEAAAKGGTLNIEDEHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQS PWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGF KNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQP TPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPV AYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQ HNCLDILAEAHGTRPDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAH IHGEIYRRRGWLTSEGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEF ESPKKKAKVE
2804	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGSGGGPAPGGTLNIEDEH RLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTND YRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLA DFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAG

	FCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPP CLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPD LTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEG KEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2804	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGSGGGPAPGGTLNIEDEH RLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTND YRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLA DFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAG FCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPP CLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPD LTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEG KEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2805	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGSPAPEAAAKGGTLNIED EHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGT NDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRD

	LADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGK AGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGW PPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTR PDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTS EGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2808	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGSPAPGGTLNIEDEHRLH ETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRP VQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFR IQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCR LFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLR MVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTD QPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEI KNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2808	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGSPAPGGTLNIEDEHRLH ETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRP

	VQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFR IQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCR LFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLR MVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTD QPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEI KNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2809	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSGGSGGSGGTLNIEDEH RLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTND YRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLA DFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAG FCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPP CLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPD LTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEG KEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2810	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSSGGGEAAAKGGTLNIED

	EHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGT NDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRD LADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGK AGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGW PPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTR PDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTS EGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2810	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSSGGGEAAAKGGTLNIED EHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGT NDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRD LADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGK AGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGW PPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTR PDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTS EGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2812	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK

	VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPGGTLNIEDEHRLHETS KEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQD LREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQH PDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFI PGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVA AIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPL PDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNK DEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2813	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKEAAAKEAAAKEAAA KEAAAKEAAAKGGTLNIEDEHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGIL VPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTR LPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKET VMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGP WRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLP EEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYA FATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTA DGSEFESPKKKAKVE
2815	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM

	PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKGGGGGSGGTLNIED EHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGT NDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRD LADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGK AGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGW PPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTR PDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTS EGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2815	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKGGGGGSGGTLNIED EHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGT NDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRD LADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGK AGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGW PPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTR PDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTS EGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2817	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL

	NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKGGSGSSGGTLNIED EHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGT NDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRD LADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGK AGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGW PPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTR PDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTS EGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2817	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKGGSGSSGGTLNIED EHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGT NDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRD LADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGK AGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGW PPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTR PDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTS EGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2818	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA

	KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGSGSSGGGGGTLNIEDEH RLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTND YRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLA DFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAG FCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPP CLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPD LTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEG KEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2818	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGSGSSGGGGGTLNIEDEH RLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTND YRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLA DFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAG FCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPP CLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPD LTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEG KEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2819	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK

	ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGGGSGGGGSGGGGSGGTL NIEDEHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVK KPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEA LHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLRE FLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPV AAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEA HGTRPDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRG WLTSEGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2820	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGGSSGGTLNIEDEHRLH ETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRP VQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFR IQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCR LFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLR MVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTD QPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEI KNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2822	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA

	NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPGGGEAAAKGGTLNIED EHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGT NDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRD LADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGK AGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGW PPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTR PDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTS EGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2823	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKGGTLNIEDEHRLHE TSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPV QDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRI QHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRL FIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRM VAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQ PLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIK NKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2825	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA

	SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGGGSGGTLNIEDEHRLHE TSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPV QDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRI QHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRL FIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRM VAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQ PLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIK NKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2826	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGSEAAAKGSSGGTLNIED EHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGT NDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRD LADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGK AGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGW PPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTR PDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTS EGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2827	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ

	SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGGSGGGGSGGGGSGGGG SGGGGSGGGGSGGTLNIEDEHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGIL VPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTR LPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKET VMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGP WRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLP EEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYA FATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTA DGSEFESPKKKAKVE
2828	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSSEAAAKGGTLNIEDEHR LHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDY RPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLAD FRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGF CRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPC LRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDL TDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGK EIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2829	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL

	FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPEAAAKGGSGGTLNIED EHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGT NDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRD LADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGK AGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGW PPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTR PDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTS EGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2830	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGGEAAAKPAPGGTLNIED EHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGT NDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRD LADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGK AGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGW PPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTR PDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTS EGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2830	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV

	QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGGEAAAKPAPGGTLNIED EHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGT NDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRD LADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGK AGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGW PPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTR PDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTS EGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2831	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGGGSSEAAAKGGTLNIED EHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGT NDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRD LADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGK AGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGW PPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTR PDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTS EGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE

2833	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPGGSGGGGGTLNIEDEH RLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTND YRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLA DFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAG FCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPP CLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPD LTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEG KEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2834	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGGGGGTLNIEDEHRLHE TSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPV QDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRI QHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRL FIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRM VAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQ

	PLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIK NKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2835	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSSPAPGGGGGTLNIEDEH RLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTND YRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLA DFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAG FCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPP CLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPD LTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEG KEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2836	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGGSEAAAKGGGGSGGTL NIEDEHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVK KPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEA LHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLRE FLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPV

	AAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEA HGTRPDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRG WLTSEGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2838	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKPAPGGGGGTLNIED EHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGT NDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRD LADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGK AGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGW PPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTR PDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTS EGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2839	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSSPAPEAAAKGGTLNIED EHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGT NDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRD LADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGK

	AGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGW PPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTR PDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTS EGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2840	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGGGGSPAPGGTLNIEDEH RLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTND YRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLA DFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAG FCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPP CLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPD LTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEG KEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2840	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGGGGSPAPGGTLNIEDEH RLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTND YRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLA

	DFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAG FCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPP CLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPD LTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEG KEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2844	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKEAAAKEAAAKEAAA KGGTLNIEDEHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTP LLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPT LFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTP RQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSK KLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLD ILAEAHGTRPDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEI YRRRGWLTSEGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKK KAKVE
2845	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKEAAAKGGTLNIEDE

	HRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTN DYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDL ADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKA GFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWP PCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRP DLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSE GKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2846	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGGGGSGSSGGTLNIEDEH RLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTND YRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLA DFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAG FCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPP CLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPD LTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEG KEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2848	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK

	VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGGGSSPAPGGTLNIEDEH RLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTND YRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLA DFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAG FCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPP CLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPD LTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEG KEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2849	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGSEAAAKGGTLNIEDEHR LHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDY RPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLAD FRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGF CRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPC LRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDL TDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGK EIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2850	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE

	VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKPAPGGTLNIEDEHR LHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDY RPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLAD FRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGF CRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPC LRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDL TDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGK EIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2850	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKPAPGGTLNIEDEHR LHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDY RPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLAD FRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGF CRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPC LRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDL TDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGK EIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2851	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM

	PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPAPAPAPAPGGTLNIED EHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGT NDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRD LADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGK AGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGW PPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTR PDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTS EGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2852	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGSPAPGSSGGTLNIEDEH RLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTND YRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLA DFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAG FCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPP CLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPD LTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEG KEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2855	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL

	NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSSGGSGGTLNIEDEHRLH ETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRP VQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFR IQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCR LFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLR MVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTD QPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEI KNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2857	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGSEAAAKPAPGGTLNIED EHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGT NDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRD LADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGK AGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGW PPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTR PDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTS EGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2860	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA

	KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSSGGSEAAAKGGTLNIED EHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGT NDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRD LADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGK AGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGW PPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTR PDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTS EGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2862	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKGGSGGGGGTLNIED EYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGT NDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRD LADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGK AGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGW PPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTR PDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTS EGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSPSGGSKRTADGSEFEAGKRTADGSEFEKRT ADGSEFESPKKKAKVE
2863	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA

	NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKGGGGGSGGTLNIED EYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGT NDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRD LADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGK AGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGW PPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTR PDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTS EGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSPSGGSKRTADGSEFEAGKRTADGSEFEKRT ADGSEFESPKKKAKVE
2864	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSSGGTLNIEDEYRLHETS KEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQD LREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQH PDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFI PGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVA AIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPL PDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNK DEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSPSGGSKRTADGSEFEAGKRTADGSEFEKRTADGSEFES PKKKAKVE
2865	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL

	LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPGGTLNIEDEYRLHETS KEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQD LREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQH PDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFI PGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVA AIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPL PDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNK DEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSPSGGSKRTADGSEFEAGKRTADGSEFEKRTADGSEFES PKKKAKVE
2865	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPGGTLNIEDEYRLHETS KEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQD LREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQH PDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFI PGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVA AIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPL PDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNK DEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSPSGGSKRTADGSEFEAGKRTADGSEFEKRTADGSEFES PKKKAKVE

2866	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSGGGEAAAKGGTLNIED EYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGT NDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRD LADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGK AGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGW PPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTR PDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTS EGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSPSGGSKRTADGSEFEAGKRTADGSEFEKRT ADGSEFESPKKKAKVE
2867	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSSGSSGSSGSSGGTLNIE DEYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPG TNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHR DLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLG KAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAG WPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGT

	RPDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLT SEGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSPSGGSKRTADGSEFEAGKRTADGSEFEKR TADGSEFESPKKKAKVE
2868	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPAPAPAPAPGGTLNI EDEYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKP GTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALH RDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFL GKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAA GWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHG TRPDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWL TSEGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSPSGGSKRTADGSEFEAGKRTADGSEFEK RTADGSEFESPKKKAKVE
2869	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPGGGGSSGGTLNIEDEY RLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTND YRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLA

	DFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAG FCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPP CLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPD LTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEG KEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSPSGGSKRTADGSEFEAGKRTADGSEFEKRTAD GSEFESPKKKAKVE
2870	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGGEAAAKGSSGGTLNIED EYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGT NDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRD LADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGK AGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGW PPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTR PDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTS EGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSPSGGSKRTADGSEFEAGKRTADGSEFEKRT ADGSEFESPKKKAKVE
2871	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK

	VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSSGGGGGTLNIEDEYRLH ETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRP VQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFR IQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCR LFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLR MVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTD QPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEI KNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSPSGGSKRTADGSEFEAGKRTADGSEFEKRTADGSE FESPKKKAKVE
2871	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSSGGGGGTLNIEDEYRLH ETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRP VQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFR IQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCR LFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLR MVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTD QPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEI KNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSPSGGSKRTADGSEFEAGKRTADGSEFEKRTADGSE FESPKKKAKVE
2872	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL

	NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPGGGEAAAKGGTLNIED EYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGT NDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRD LADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGK AGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGW PPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTR PDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTS EGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSPSGGSKRTADGSEFEAGKRTADGSEFEKRT ADGSEFESPKKKAKVE
2873	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPGSSEAAAKGGTLNIED EYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGT NDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRD LADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGK AGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGW PPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTR PDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTS EGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSPSGGSKRTADGSEFEAGKRTADGSEFEKRT ADGSEFESPKKKAKVE
2874	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA

	NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGGEAAAKGGSGGTLNIED EYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGT NDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRD LADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGK AGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGW PPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTR PDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTS EGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSPSGGSKRTADGSEFEAGKRTADGSEFEKRT ADGSEFESPKKKAKVE
2874	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGGEAAAKGGSGGTLNIED EYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGT NDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRD LADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGK AGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGW PPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTR PDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTS EGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSPSGGSKRTADGSEFEAGKRTADGSEFEKRT ADGSEFESPKKKAKVE
2877	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL

	LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKEAAAKEAAAKGGTL NIEDEYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVK KPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEA LHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLRE FLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPV AAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEA HGTRPDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRG WLTSEGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSPSGGSKRTADGSEFEAGKRTADGSEF EKRTADGSEFESPKKKAKVE
2878	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPGGSGGGGGTLNIEDEY RLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTND YRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLA DFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAG FCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPP CLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPD LTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEG KEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSPSGGSKRTADGSEFEAGKRTADGSEFEKRTAD GSEFESPKKKAKVE

2878	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPGGSGGGGGTLNIEDEY RLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTND YRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLA DFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAG FCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPP CLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPD LTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEG KEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSPSGGSKRTADGSEFEAGKRTADGSEFEKRTAD GSEFESPKKKAKVE
2879	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGGEAAAKPAPGGTLNIED EYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGT NDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRD LADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGK AGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGW PPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTR

	PDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTS EGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSPSGGSKRTADGSEFEAGKRTADGSEFEKRT ADGSEFESPKKKAKVE
2880	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKEAAAKEAAAKEAAA KEAAAKGGTLNIEDEYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQS PWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGF KNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQP TPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPV AYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQ HNCLDILAEAHGTRPDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAH IHGEIYRRRGWLTSEGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSPSGGSKRTADGSEFEA GKRTADGSEFEKRTADGSEFESPKKKAKVE
2881	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKGGTLNIEDEYRLHE TSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPV QDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRI

	QHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRL FIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRM VAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQ PLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIK NKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSPSGGSKRTADGSEFEAGKRTADGSEFEKRTADGSEF ESPKKKAKVE
2883	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPEAAAKGGTLNIEDEYR LHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDY RPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLAD FRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGF CRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPC LRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDL TDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGK EIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSPSGGSKRTADGSEFEAGKRTADGSEFEKRTADG SEFESPKKKAKVE
2885	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK

	VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGGGSSEAAAKGGTLNIED EYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGT NDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRD LADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGK AGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGW PPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTR PDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTS EGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSPSGGSKRTADGSEFEAGKRTADGSEFEKRT ADGSEFESPKKKAKVE
2886	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGSGGGGGTLNIEDEYRLH ETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRP VQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFR IQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCR LFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLR MVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTD QPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEI KNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSPSGGSKRTADGSEFEAGKRTADGSEFEKRTADGSE FESPKKKAKVE
2887	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL

	NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKEAAAKGGTLNIEDE YRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTN DYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDL ADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKA GFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWP PCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRP DLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSE GKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSPSGGSKRTADGSEFEAGKRTADGSEFEKRTA DGSEFESPKKKAKVE
2887	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKEAAAKGGTLNIEDE YRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTN DYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDL ADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKA GFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWP PCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRP DLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSE GKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSPSGGSKRTADGSEFEAGKRTADGSEFEKRTA DGSEFESPKKKAKVE
2888	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA

	NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKEAAAKEAAAKEAAA KGGTLNIEDEYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTP LLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPT LFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTP RQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSK KLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLD ILAEAHGTRPDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEI YRRRGWLTSEGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSPSGGSKRTADGSEFEAGKRTA DGSEFEKRTADGSEFESPKKKAKVE
2890	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSSPAPGGGGGTLNIEDEY RLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTND YRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLA DFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAG FCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPP CLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPD LTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEG KEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSPSGGSKRTADGSEFEAGKRTADGSEFEKRTAD GSEFESPKKKAKVE
2891	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL

	LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSSEAAAKPAPGGTLNIED EYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGT NDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRD LADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGK AGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGW PPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTR PDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTS EGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSPSGGSKRTADGSEFEAGKRTADGSEFEKRT ADGSEFESPKKKAKVE
2893	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGSPAPEAAAKGGTLNIED EYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGT NDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRD LADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGK AGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGW PPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTR PDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTS EGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSPSGGSKRTADGSEFEAGKRTADGSEFEKRT ADGSEFESPKKKAKVE

2894	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGSPAPGSSGGTLNIEDEY RLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTND YRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLA DFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAG FCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPP CLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPD LTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEG KEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSPSGGSKRTADGSEFEAGKRTADGSEFEKRTAD GSEFESPKKKAKVE
2895	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGSGGGPAPGGTLNIEDEY RLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTND YRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLA DFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAG FCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPP CLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPD

	LTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEG KEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSPSGGSKRTADGSEFEAGKRTADGSEFEKRTAD GSEFESPKKKAKVE
2895	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGSGGGPAPGGTLNIEDEY RLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTND YRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLA DFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAG FCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPP CLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPD LTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEG KEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSPSGGSKRTADGSEFEAGKRTADGSEFEKRTAD GSEFESPKKKAKVE
2901	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGSEAAAKGGGGGTLNIED EYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGT NDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRD

	LADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGK AGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGW PPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTR PDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTS EGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSPSGGSKRTADGSEFEAGKRTADGSEFEKRT ADGSEFESPKKKAKVE
2902	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSAGSAAGSGEFGGTLNIE DEYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPG TNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHR DLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLG KAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAG WPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGT RPDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLT SEGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSPSGGSKRTADGSEFEAGKRTADGSEFEKR TADGSEFESPKKKAKVE
2903	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK

	VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSSGSSGSSGGTLNIEDEY RLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTND YRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLA DFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAG FCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPP CLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPD LTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEG KEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSPSGGSKRTADGSEFEAGKRTADGSEFEKRTAD GSEFESPKKKAKVE
2904	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGGPAPGGSGGTLNIEDEY RLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTND YRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLA DFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAG FCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPP CLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPD LTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEG KEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSPSGGSKRTADGSEFEAGKRTADGSEFEKRTAD GSEFESPKKKAKVE
2905	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL

	NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSSGSSGGTLNIEDEYRLH ETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRP VQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFR IQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCR LFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLR MVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTD QPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEI KNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSPSGGSKRTADGSEFEAGKRTADGSEFEKRTADGSE FESPKKKAKVE
2907	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGSGSETPGTSESATPESGGT LNIEDEYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPV KKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNE ALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLR EFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDP VAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAE AHGTRPDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRR GWLTSEGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSPSGGSKRTADGSEFEAGKRTADGSE FEKRTADGSEFESPKKKAKVE
2909	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA

	NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGGGSGGGGSGGTLNIEDE YRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTN DYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDL ADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKA GFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWP PCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRP DLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSE GKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSPSGGSKRTADGSEFEAGKRTADGSEFEKRTA DGSEFESPKKKAKVE
2909	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGGSGGGGSGGTLNIEDE YRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTN DYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDL ADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKA GFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWP PCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRP DLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSE GKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSPSGGSKRTADGSEFEAGKRTADGSEFEKRTA DGSEFESPKKKAKVE
2913	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL

	LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGSGSSEAAAKGGTLNIED EYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGT NDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRD LADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGK AGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGW PPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTR PDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTS EGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSPSGGSKRTADGSEFEAGKRTADGSEFEKRT ADGSEFESPKKKAKVE
2914	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGSGSSGGTLNIEDEYRLH ETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRP VQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFR IQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCR LFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLR MVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTD QPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEI KNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSPSGGSKRTADGSEFEAGKRTADGSEFEKRTADGSE FESPKKKAKVE

2916	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSSEAAAKGGTLNIEDEYR LHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDY RPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLAD FRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGF CRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPC LRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDL TDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGK EIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSPSGGSKRTADGSEFEAGKRTADGSEFEKRTADG SEFESPKKKAKVE
2920	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSSPAPEAAAKGGTLNIED EYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGT NDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRD LADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGK AGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGW PPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTR

	PDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTS EGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSPSGGSKRTADGSEFEAGKRTADGSEFEKRT ADGSEFESPKKKAKVE
2922	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKGGSGSSGGTLNIED EYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGT NDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRD LADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGK AGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGW PPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTR PDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTS EGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSPSGGSKRTADGSEFEAGKRTADGSEFEKRT ADGSEFESPKKKAKVE
2924	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPEAAAKGGSGGTLNIED EYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGT NDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRD

	LADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGK AGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGW PPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTR PDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTS EGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSPSGGSKRTADGSEFEAGKRTADGSEFEKRT ADGSEFESPKKKAKVE
2927	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGGGGGTLNIEDEYRLHET SKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQ DLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQ HPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLF IPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMV AAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQP LPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKN KDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSPSGGSKRTADGSEFEAGKRTADGSEFEKRTADGSEFE SPKKKAKVE
2928	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK

	VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGGGGSEAAAKGGTLNIED EYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGT NDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRD LADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGK AGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGW PPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTR PDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTS EGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSPSGGSKRTADGSEFEAGKRTADGSEFEKRT ADGSEFESPKKKAKVE
2929	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGSEAAAKGGTLNIEDEYR LHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDY RPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLAD FRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGF CRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPC LRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDL TDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGK EIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSPSGGSKRTADGSEFEAGKRTADGSEFEKRTADG SEFESPKKKAKVE
2930	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL

	NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPAPAPAPGGTLNIEDEY RLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTND YRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLA DFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAG FCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPP CLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPD LTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEG KEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSPSGGSKRTADGSEFEAGKRTADGSEFEKRTAD GSEFESPKKKAKVE
2932	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKGGGGSEAAAKGGTL NIEDEYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVK KPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEA LHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLRE FLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPV AAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEA HGTRPDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRG WLTSEGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSPSGGSKRTADGSEFEAGKRTADGSEF EKRTADGSEFESPKKKAKVE
2933	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA

	NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKGGSGGTLNIEDEYR LHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDY RPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLAD FRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGF CRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPC LRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDL TDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGK EIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSPSGGSKRTADGSEFEAGKRTADGSEFEKRTADG SEFESPKKKAKVE
2937	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGGGSEAAAKGGGGSGGTL NIEDEYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVK KPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEA LHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLRE FLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPV AAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEA HGTRPDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRG WLTSEGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSPSGGSKRTADGSEFEAGKRTADGSEF EKRTADGSEFESPKKKAKVE
2941	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL

	LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSSGSSGSSGSSGSSGGTL NIEDEYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVK KPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEA LHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLRE FLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPV AAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEA HGTRPDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRG WLTSEGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSPSGGSKRTADGSEFEAGKRTADGSEF EKRTADGSEFESPKKKAKVE
2943	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSSGSSGSSGSSGSSGSSG GTLNIEDEYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLL PVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLF NEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQ LREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKL DPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDIL AEAHGTRPDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYR RRGWLTSEGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSPSGGSKRTADGSEFEAGKRTADG SEFEKRTADGSEFESPKKKAKVE

2948	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGSGSSGGGGGTLNIEDEY RLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTND YRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLA DFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAG FCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPP CLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPD LTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEG KEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSPSGGSKRTADGSEFEAGKRTADGSEFEKRTAD GSEFESPKKKAKVE
2950	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGGSSGGSGGTLNIEDEY RLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTND YRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLA DFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAG FCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPP CLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPD

	LTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEG KEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSPSGGSKRTADGSEFEAGKRTADGSEFEKRTAD GSEFESPKKKAKVE
2953	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGGEAAAKGGTLNIEDEYR LHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDY RPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLAD FRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGF CRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPC LRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDL TDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGK EIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSPSGGSKRTADGSEFEAGKRTADGSEFEKRTADG SEFESPKKKAKVE
2957	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGAEAAAKEAAAKEAAAKEAA AKALEAEAAAKEAAAKEAAAKEAAAKAGGTLNIEDEHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEAR LGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFE

	WRDPEMGISGQLTWTRLPQGFKNSPTLFDEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGY LLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGTAGFCRLWIPGFAEMAAPLYPLTKTGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVD EKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQ FGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALK MAEGKKLNVYTDSRYAFATAHIHGEIYRRRGLLTSEGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLL AGKRTADGSEFEKRTADGSEFESPKKKAKVE
2957	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGAEAAAKEAAAKEAAAKEAA AKALEAEAAAKEAAAKEAAAKEAAAKAGGTLNIEDEHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEAR LGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFE WRDPEMGISGQLTWTRLPQGFKNSPTLFDEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGY LLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGTAGFCRLWIPGFAEMAAPLYPLTKTGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVD EKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQ FGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALK MAEGKKLNVYTDSRYAFATAHIHGEIYRRRGLLTSEGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLL AGKRTADGSEFEKRTADGSEFESPKKKAKVE
2965	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK

	VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSSGSSGSSGSSGSSGSSG GTLNIEDEHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLL PVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLF NEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQ LREFLGTAGFCRLWIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKL DPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDIL AEAHGTRPDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYR RRGWLTSEGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKA KVE
2966	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGSEAAAKGGGGGTLNIED EHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGT NDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRD LADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGT AGFCRLWIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGW PPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTR PDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTS EGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2966	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM

	PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGSEAAAKGGGGGTLNIED EHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGT NDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRD LADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGT AGFCRLWIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGW PPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTR PDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTS EGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2967	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSSGGGGGTLNIEDEHRLH ETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRP VQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFR IQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGTAGFCR LWIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLR MVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTD QPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEI KNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2968	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL

	NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGGSGGGGSGGGGSGGGG SGGTLNIEDEHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTP LLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPT LFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTP RQLREFLGTAGFCRLWIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSK KLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLD ILAEAHGTRPDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEI YRRRGWLTSEGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKK KAKVE
2969	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPGGSEAAAKGGTLNIED EHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGT NDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRD LADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGT AGFCRLWIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGW PPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTR PDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTS EGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2971	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK

	ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKPAPGGTLNIEDEHR LHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDY RPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLAD FRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGTAGF CRLWIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPC LRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDL TDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGK EIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2972	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGAEAAAKEAAAKEAAAKEAA AKALEAEAAAKEAAAKEAAAKEAAAKAGGTLNIEDEHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEAR LGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFE WRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGY LLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGTAGFCRLWIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVD EKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQ FGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALK MAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLL AGKRTADGSEFEKRTADGSEFESPKKKAKVE
2976	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA

	SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKGSSPAPGGTLNIED EHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGT NDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRD LADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGT AGFCRLWIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGW PPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTR PDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTS EGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2976	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKGSSPAPGGTLNIED EHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGT NDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRD LADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGT AGFCRLWIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGW PPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTR PDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTS EGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2979	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ

	SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGSGSSGGGGGTLNIEDEH RLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTND YRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLA DFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGTAG FCRLWIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPP CLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPD LTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEG KEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2982	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKGGSGGTLNIEDEHR LHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDY RPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLAD FRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGTAGF CRLWIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPC LRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDL TDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGK EIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2983	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL

	LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGGSGGGGSGGGGSGGGG SGGGGSGGGGSGGTLNIEDEHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGIL VPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTR LPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKET VMGQPTPKTPRQLREFLGTAGFCRLWIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGP WRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLP EEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYA FATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTA DGSEFESPKKKAKVE
2983	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGGSGGGGSGGGGSGGGG SGGGGSGGGGSGGTLNIEDEHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGIL VPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTR LPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKET VMGQPTPKTPRQLREFLGTAGFCRLWIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGP WRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLP EEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYA FATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTA DGSEFESPKKKAKVE

2987	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGSPAPEAAAKGGTLNIED EHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGT NDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRD LADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGT AGFCRLWIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGW PPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTR PDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTS EGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2990	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGGSSEAAAKGGTLNIED EHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGT NDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRD LADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGT AGFCRLWIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGW PPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTR

	PDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTS EGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2991	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKEAAAKEAAAKEAAA KEAAAKGGTLNIEDEHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQS PWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGF KNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQP TPKTPRQLREFLGTAGFCRLWIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPV AYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQ HNCLDILAEAHGTRPDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAH IHGEIYRRRGWLTSEGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEF ESPKKKAKVE
2991	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKEAAAKEAAAKEAAA KEAAAKGGTLNIEDEHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQS PWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGF KNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQP

	TPKTPRQLREFLGTAGFCRLWIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPV AYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQ HNCLDILAEAHGTRPDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAH IHGEIYRRRGWLTSEGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEF ESPKKKAKVE
2995	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSAGSAAGSGEFGGTLNIE DEHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPG TNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHR DLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLG TAGFCRLWIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAG WPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGT RPDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLT SEGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
2999	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGGEAAAKPAPGGTLNIED EHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGT

	NDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRD LADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGT AGFCRLWIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGW PPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTR PDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTS EGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
3007	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPGSSEAAAKGGTLNIED EHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGT NDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRD LADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGT AGFCRLWIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGW PPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTR PDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTS EGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
3014	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKPAPGGSGGTLNIED

	EHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGT NDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRD LADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGT AGFCRLWIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGW PPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTR PDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTS EGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
3015	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSSEAAAKGGTLNIEDEHR LHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDY RPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLAD FRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGTAGF CRLWIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPC LRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDL TDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGK EIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
3018	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK

	VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGGEAAAKGGSGGTLNIED EHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGT NDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRD LADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGT AGFCRLWIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGW PPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTR PDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTS EGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
3026	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSSGGGGGSGGTLNIEDEH RLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTND YRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLA DFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGTAG FCRLWIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPP CLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPD LTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEG KEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
3035	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE

	VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGSGGSGGSGGSGGSG GTLNIEDEHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLL PVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLF NEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQ LREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKL DPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDIL AEAHGTRPDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYR RRGWLTSEGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKA KVE
3036	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKEAAAKEAAAKEAAA KGGTLNIEDEHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTP LLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPT LFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTP RQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSK KLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLD ILAEAHGTRPDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEI YRRRGWLTSEGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKK KAKVE
3037	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA

	KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPGGTLNIEDEHRLHETS KEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQD LREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQH PDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFI PGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVA AIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQPL PDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNK DEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
3039	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSGGSGGSGGSGGTLNIE DEHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPG TNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHR DLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLG KAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAG WPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGT RPDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLT SEGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
3039	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK

	ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGSGGSGGSGGSGGTLNIE DEHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPG TNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHR DLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLG KAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAG WPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGT RPDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLT SEGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
3040	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGGSSEAAAKGGTLNIED EHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGT NDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRD LADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGK AGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGW PPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTR PDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTS EGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
3041	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA

	NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKEAAAKGGTLNIEDE HRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTN DYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDL ADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKA GFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWP PCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRP DLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSE GKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
3042	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSGSSGGGGGTLNIEDEH RLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTND YRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLA DFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAG FCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPP CLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPD LTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEG KEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
3042	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA

	SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGSGSSGGGGGTLNIEDEH RLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTND YRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLA DFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAG FCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPP CLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPD LTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEG KEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
3043	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKEAAAKEAAAKEAAA KEAAAKGGTLNIEDEHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQS PWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGF KNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQP TPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPV AYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQ HNCLDILAEAHGTRPDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAH IHGEIYRRRGWLTSEGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEF ESPKKKAKVE
3044	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL

	LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGGGGGGGTLNIEDEHRLH ETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRP VQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFR IQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCR LFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLR MVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTD QPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEI KNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
3044	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGGGGGGGTLNIEDEHRLH ETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRP VQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFR IQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCR LFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLR MVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTD QPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEI KNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
3045	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL

	FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGGEAAAKGGSGGTLNIED EHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGT NDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRD LADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGK AGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGW PPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTR PDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTS EGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
3045	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGGEAAAKGGSGGTLNIED EHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGT NDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRD LADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGK AGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGW PPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTR PDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTS EGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
3046	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV

	QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPEAAAKGGSGGTLNIED EHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGT NDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRD LADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGK AGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGW PPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTR PDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTS EGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
3047	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGSSGGGGSGGTLNIEDEH RLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTND YRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLA DFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAG FCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPP CLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPD LTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEG KEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE

3048	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSPAPGSSGGTLNIEDEH RLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTND YRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLA DFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAG FCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPP CLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPD LTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEG KEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
3052	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPGGGEAAAKGGTLNIED EHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGT NDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRD LADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGK AGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGW PPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTR

	PDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTS EGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
3053	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKGGSGSSGGTLNIED EHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGT NDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRD LADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGK AGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGW PPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTR PDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTS EGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
3053	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKGGSGSSGGTLNIED EHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGT NDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRD LADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGK AGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGW

	PPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTR PDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTS EGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
3054	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPAPAPAPGGTLNIED EHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGT NDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRD LADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGK AGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGW PPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTR PDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTS EGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
3055	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSSPAPGGTLNIEDEHRLH ETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRP VQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFR IQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCR

	LFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLR MVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTD QPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEI KNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
3056	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSSGGGPAPGGTLNIEDEH RLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTND YRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLA DFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAG FCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPP CLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPD LTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEG KEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
3057	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSSGGGEAAAKGGTLNIED EHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGT NDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRD

	LADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGK AGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGW PPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTR PDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTS EGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
3057	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSSGGGEAAAKGGTLNIED EHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGT NDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRD LADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGK AGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGW PPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTR PDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTS EGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
3059	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSGGGPAPGGTLNIEDEH RLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTND

	YRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLA DFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAG FCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPP CLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPD LTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEG KEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
3059	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSGGGPAPGGTLNIEDEH RLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTND YRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLA DFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAG FCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPP CLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPD LTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEG KEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
3060	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPGGSGGTLNIEDEHRLH

	ETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRP VQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFR IQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCR LFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLR MVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTD QPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEI KNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
3061	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPEAAAKGGTLNIEDEHR LHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDY RPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLAD FRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGF CRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPC LRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDL TDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGK EIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
3062	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK

	VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSSEAAAKGGTLNIEDEHR LHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDY RPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLAD FRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGF CRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPC LRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDL TDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGK EIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
3063	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGGSGGGGSGGGGSGGGG SGGTLNIEDEHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTP LLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPT LFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTP RQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSK KLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLD ILAEAHGTRPDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEI YRRRGWLTSEGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKK KAKVE
3063	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM

	PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGGGSGGGGSGGGGSGGGG SGGTLNIEDEHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTP LLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPT LFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTP RQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSK KLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLD ILAEAHGTRPDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEI YRRRGWLTSEGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKK KAKVE
3064	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPGGSGSSGGTLNIEDEH RLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTND YRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLA DFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAG FCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPP CLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPD LTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEG KEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
3065	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA

	KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGGGSGGTLNIEDEHRLHE TSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPV QDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRI QHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRL FIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRM VAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQ PLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIK NKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
3067	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGSEAAAKGGGGGTLNIED EHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGT NDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRD LADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGK AGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGW PPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTR PDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTS EGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
3067	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK

	ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGSEAAAKGGGGGTLNIED EHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGT NDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRD LADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGK AGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGW PPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTR PDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTS EGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
3068	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPEAAAKGGGGGTLNIED EHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGT NDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRD LADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGK AGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGW PPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTR PDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTS EGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
3070	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA

	NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSGGSGGSGGTLNIEDEH RLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTND YRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLA DFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAG FCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPP CLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPD LTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEG KEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
3075	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSSGGSPAPGGTLNIEDEH RLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTND YRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLA DFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAG FCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPP CLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPD LTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEG KEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
3076	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA

	SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGGGGSGGTLNIEDEHRLH ETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRP VQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFR IQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCR LFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLR MVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTD QPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEI KNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
3076	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGGGGSGGTLNIEDEHRLH ETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRP VQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFR IQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCR LFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLR MVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTD QPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEI KNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
3079	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ

	SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKGGGGSEAAAKGGTL NIEDEHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVK KPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEA LHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLRE FLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPV AAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEA HGTRPDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRG WLTSEGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
3080	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKPAPGGSGGTLNIED EHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGT NDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRD LADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGK AGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGW PPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTR PDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTS EGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
3081	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL

	LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGGGSGGGGSGGGGSGGGG SGGGGSGGGGSGGTLNIEDEHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGIL VPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTR LPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKET VMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGP WRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLP EEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYA FATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTA DGSEFESPKKKAKVE
3083	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPGGSEAAAKGGTLNIED EHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGT NDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRD LADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGK AGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGW PPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTR PDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTS EGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
3084	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV

	QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPAPAPAPAPAPGGTLNI EDEHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKP GTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALH RDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFL GKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAA GWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHG TRPDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWL TSEGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
3084	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPAPAPAPAPAPGGTLNI EDEHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKP GTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALH RDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFL GKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAA GWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHG TRPDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWL TSEGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE

3085	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGGEAAAKPAPGGTLNIED EHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGT NDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRD LADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGK AGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGW PPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTR PDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTS EGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
3085	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGGEAAAKPAPGGTLNIED EHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGT NDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRD LADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGK AGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGW PPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTR

	PDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTS EGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
3086	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPAPAPGGTLNIEDEH RLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTND YRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLA DFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAG FCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPP CLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPD LTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEG KEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
3087	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGSPAPGGTLNIEDEHRLH ETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRP VQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFR IQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCR LFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLR

	MVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTD QPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEI KNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
3087	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGSPAPGGTLNIEDEHRLH ETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRP VQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFR IQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCR LFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLR MVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTD QPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEI KNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
3088	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGSEAAAKPAPGGTLNIED EHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGT NDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRD LADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGK

	AGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGW PPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTR PDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTS EGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
3089	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGSSGGSGGTLNIEDEHRLH ETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRP VQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFR IQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCR LFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLR MVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTD QPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEI KNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
3091	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPGSSEAAAKGGTLNIED EHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGT NDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRD

	LADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGK AGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGW PPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTR PDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTS EGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
3091	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPGSSEAAAKGGTLNIED EHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGT NDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRD LADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGK AGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGW PPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTR PDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTS EGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
3092	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGGGSGGGGSGGGGSGGTL NIEDEHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVK

	KPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEA LHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLRE FLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPV AAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEA HGTRPDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRG WLTSEGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
3093	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSSPAPGGGGGTLNIEDEH RLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTND YRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLA DFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAG FCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPP CLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPD LTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEG KEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
3094	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGGGGGTLNIEDEHRLHET

	SKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQ DLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQ HPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLF IPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMV AAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQP LPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKN KDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
3096	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGGGGGGGGTLNIEDEHRL HETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYR PVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADF RIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFC RLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCL RMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLT DQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKE IKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
3097	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK

	VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGSEAAAKGGTLNIEDEHR LHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDY RPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLAD FRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGF CRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPC LRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDL TDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGK EIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
3098	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPGGGGSSGGTLNIEDEH RLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTND YRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLA DFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAG FCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPP CLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPD LTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEG KEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
3099	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE

	VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGGGSEAAAKGGGGSGGTL NIEDEHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVK KPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEA LHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLRE FLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPV AAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEA HGTRPDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRG WLTSEGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
3101	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGGGGSGSSGGTLNIEDEH RLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTND YRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLA DFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAG FCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPP CLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPD LTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEG KEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
3103	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM

	PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKGGGGGSGGTLNIED EHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGT NDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRD LADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGK AGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGW PPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTR PDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTS EGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
3103	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKGGGGGSGGTLNIED EHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGT NDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRD LADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGK AGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGW PPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTR PDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTS EGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
3107	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL

	NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGGGSSGGTLNIEDEHRLH ETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRP VQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFR IQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCR LFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLR MVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTD QPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEI KNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
3108	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKGGSPAPGGTLNIED EHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGT NDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRD LADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGK AGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGW PPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTR PDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTS EGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
3108	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA

	KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKGGSPAPGGTLNIED EHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGT NDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRD LADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGK AGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGW PPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTR PDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTS EGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
3109	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSSGGSEAAAKGGTLNIED EHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGT NDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRD LADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGK AGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGW PPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTR PDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTS EGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
3110	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK

	ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGGGSGGGGSGGTLNIEDE HRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTN DYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDL ADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKA GFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWP PCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRP DLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSE GKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
3111	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGGPAPGGSGGTLNIEDEH RLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTND YRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLA DFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAG FCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPP CLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPD LTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEG KEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
3111	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA

	NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGGPAPGGSGGTLNIEDEH RLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTND YRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLA DFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAG FCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPP CLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPD LTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEG KEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
3112	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKGSSPAPGGTLNIED EHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGT NDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRD LADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGK AGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGW PPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTR PDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTS EGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
3113	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA

	SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGSGSSGGTLNIEDEHRLH ETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRP VQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFR IQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCR LFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLR MVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTD QPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEI KNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
3114	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGGGGGTLNIEDEHRLHE TSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPV QDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRI QHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRL FIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRM VAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQ PLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIK NKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
3116	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ

	SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKGGGGSSGGTLNIED EHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGT NDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRD LADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGK AGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGW PPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTR PDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTS EGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
3117	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGGGSSPAPGGTLNIEDEH RLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTND YRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLA DFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAG FCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPP CLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPD LTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEG KEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
3118	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL

	LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGSPAPEAAAKGGTLNIED EHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGT NDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRD LADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGK AGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGW PPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTR PDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTS EGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
3120	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKEAAAKEAAAKEAAA KEAAAKEAAAKGGTLNIEDEHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGIL VPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTR LPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKET VMGQPTPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGP WRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLP EEGLQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYA FATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTA DGSEFESPKKKAKVE
3121	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV

	QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGSGGGGSSGGTLNIEDEH RLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTND YRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLA DFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAG FCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPP CLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPD LTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEG KEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
3121	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGSGGGGSSGGTLNIEDEH RLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTND YRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLA DFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAG FCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPP CLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPD LTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEG KEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE

3123	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKGGTLNIEDEHRLHE TSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPV QDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRI QHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRL FIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRM VAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTDQ PLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIK NKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
3124	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPGGSGGGGGTLNIEDEH RLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTND YRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLA DFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAG FCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPP CLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPD

	LTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEG KEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
3125	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKGGSGGGGGTLNIED EHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGT NDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRD LADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGK AGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGW PPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTR PDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTS EGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
3126	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSSGSSGSSGSSGSSGGTL NIEDEHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVK KPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEA LHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLRE FLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPV

	AAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEA HGTRPDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRG WLTSEGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
3127	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSSPAPEAAAKGGTLNIED EHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGT NDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRD LADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGK AGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGW PPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTR PDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTS EGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
3130	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSPAPGGGGGTLNIEDEH RLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTND YRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLA DFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAG

	FCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPP CLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPD LTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEG KEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
3130	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSPAPGGGGGTLNIEDEH RLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTND YRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLA DFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAG FCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPP CLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPD LTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEG KEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
3131	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSSEAAAKGGSGGTLNIED EHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGT NDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRD

	LADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGK AGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGW PPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTR PDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTS EGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
3136	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGGPAPEAAAKGGTLNIED EHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGT NDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRD LADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGK AGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGW PPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTR PDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTS EGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
4501	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGSGGSGGSGGTAPLEEEY RLFLEAPIQNVTLLEQWKREIPKVWAEINPPGLASTQAPIHVQLLSTALPVRVRQYPITLEAKRSLRETIRKFRAAGILRPVHSPWNTPLLPVRKSGTSE

	YRMVQDLREVNKRVETIHPTVPNPYTLLSLLPPDRIWYSVLDLKDAFFCIPLAPESQLIFAFEWADAEEGESGQLTWTRLPQGFKNSPTLFNEALNRDLQ GFRLDHPSVSLLQYVDDLLIAADTQAACLSATRDLLMTLAELGYRVSGKKAQLCQEEVTYLGFKIHKGSRSLSNSRTQAILQIPVPKTKRQVREFLGKIG YCRLFIPGFAELAQPLYAATRPGNDPLVWGEKEEEAFQSLKLALTQPPALALPSLDKPFQLFVEETSGAAKGVLTQALGPWKRPVAYLSKRLDPVAAGWP RCLRAIAAAALLTREASKLTFGQDIEITSSHNLESLLRSPPDKWLTNARITQYQVLLLDPPRVRFKQTAALNPATLLPETDDTLPIHHCLDTLDSLTSTR PDLTDQPLAQAEATLFTDGSSYIRDGKRYAGAAVVTLDSVIWAEPLPIGTSAQKAELIALTKALEWSKDKSVNIYTDSRYAFATLHVHGMIYRERGWLTA GGKAIKNAPEILALLTAVWLPKRVAVMHCKGHQKDDAPTSTGNRRADEVAREVAIRPLSTQATISAGKRTADGSEFEKRTADGSEFESPKKKAKVE
4502	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGSGGSGGSGGSGGSGGVL NLEEEYRLHEKPVPSSIDPSWLQLFPTVWAERAGMGLANQVPPVVVELRSGASPVAVRQYPMSKEAREGIRPHIQRFLDLGVLVPCQSPWNTPLLPVKKP GTNDYRPVQDLREINKRVQDIHPTVPNPYNLLSSLPPSHTWYSVLDLKDAFFCLKLHPNSQPLFAFEWRDPEKGNTGQLTWTRLPQGFKNSPTLFNEALH RDLAPFRALNPQVVLLQYVDDLLVAAPTYRDCKEGTQKLLQELSKLGYRVSAKKAQLCQKEVTYLGYLLKEGKRWLTPARKATVMKIPPPTTPRQVREFL GTAGFCRLWIPGFASLAAPLYPLTKPSIPFIWTEEHQKAFDRIKEALLSAPALALPDLTKPFTLYVDERAGVARGVLTQTLGPWRRPVAYLSKKLDPVAS GWPTCLKAVAAVALLLKDADKLTLGQNVTVIASHSLESIVRQPPDRWMTNARMTHYQSLLLNERVSFAPPAVLNPATLLPVESEATPVHRCSEILAEETG TRRDLKDQPLPGVPAWYTDGSSFIAEGKRRAGAAIVDGKRTVWASSLPEGTSAQKAELVALTQALRLAEGKDINIYTDSRYAFATAHIHGAIYKQRGWLT SAGKDIKNKEEILALLEAIHLPKRVAIIHCPGHQKGNDPVATGNRRADEAAKQAALSTRVLAETTKPAGKRTADGSEFEKRTADGSEFESPKKKAKVE
4503	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGSGGSGGSGGSGGSGGSG

	GLGIEDEYRLHETSTEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIQQYPMSHEARLGIKPHIQRLLDQGILVPCQSPWNTPLLP VKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGMGISGQLTWTRLPQGFKNSPTLFN EALHRDLADFRIQHPDLILLQYVDDILLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLREGQRWLTEARKETVMGQPVPKTPRQL REFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFSWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLD PVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEEGAPHDCLEILA ETHGTRPDLTDQPIPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVIWAGALPAGTSAQRAELIALTQALKMAEGKRLNVYTDSRYAFATAHIHGEIYRR RGWLTSEGREIKNKSEILALLKALFLPKRLSIIHCLGHQKGDSAEARGNRLADQAAREAAIKTPPDTSTLLIAGKRTADGSEFEKRTADGSEFESPKKKA KVE
4504	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGGSGGGGSGGGGSGGGG SGGGGSGGTLNIEDEHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQS PWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGF KNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQP TPKTPRQLREFLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPV AYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQ HNCLDILAEAHGTRPDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAH IHGEIYRRRGWLTSEGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEF ESPKKKAKVE
4505	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM

	PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSSGSSGSSGGTLNIEDEH RLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTND YRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLA DFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGTAG FCRLWIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPP CLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPD LTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEG KEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
4506	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKEAAAKEAAAKGGTL NIEDEYRLHETSKEPDVPLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVK KPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEA LHRDLADFRIQHPDLILLQYVDDLLLAATSEQDCQRGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLRE FLGKAGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPV AAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEKEAPHDCLEILAET HGTRPDLTDQPIPDADYTWYTDGSSFLQEGQRRAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHVHGEIYRRRG WLTSEGREIKNKNEILALLKALFLPKRLSIIHCPGHQKGNSAEARGNRMADQAAREAAMKAVLETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
4507	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL

	NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKEAAAKEAAAKEAAA KEAAAKGGTLNIEDEYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQS PWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGF KNSPTLFNEALHRDLAGFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQP IPKTPRQLREFLGTAGFCRLWIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAFQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPV AYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQ HDCLDILAEAHGTRSDLMDQPLPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAH IHGEIYRRRGWLTSEGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGNSAEARGNRMADQAARKVATRETPETSTLLAGKRTADGSEFEKRTADGSEF ESPKKKAKVE
4508	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPAPAPGGTLNIEDEYRL HETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYR PVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADF RIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFC RLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCL RMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLT DQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKE IKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSPSGGSKRTADGSEFEAGKRTADGSEFEKRTADGS EFESPKKKAKVE
4509	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA

	NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPAPAPAPAPGGVLNL EEEYRLHEKPVPSSIDPSWLQLFPTVWAERAGMGLANQVPPVVVELRSGASPVAVRQYPMSKEAREGIRPHIQRFLDLGVLVPCQSPWNTPLLPVKKPGT NDYRPVQDLREINKRVQDIHPTVPNPYNLLSSLPPSHTWYSVLDLKDAFFCLKLHPNSQPLFAFEWRDPEKGNTGQLTWTRLPQGFKNSPTLFNEALHRD LAPFRALNPQVVLLQYVDDLLVAAPTYRDCKEGTQKLLQELSKLGYRVSAKKAQLCQKEVTYLGYLLKEGKRWLTPARKATVMKIPPPTTPRQVREFLGT AGFCRLWIPGFASLAAPLYPLTKPSIPFIWTEEHQKAFDRIKEALLSAPALALPDLTKPFTLYVDERAGVARGVLTQTLGPWRRPVAYLSKKLDPVASGW PTCLKAVAAVALLLKDADKLTLGQNVTVIASHSLESIVRQPPDRWMTNARMTHYQSLLLNERVSFAPPAVLNPATLLPVESEATPVHRCSEILAEETGTR RDLKDQPLPGVPAWYTDGSSFIAEGKRRAGAAIVDGKRTVWASSLPEGTSAQKAELVALTQALRLAEGKDINIYTDSRYAFATAHIHGAIYKQRGWLTSA GKDIKNKEEILALLEAIHLPKRVAIIHCPGHQKGNDPVATGNRRADEAAKQAALSTRVLAETTKPAGKRTADGSEFEKRTADGSEFESPKKKAKVE
4510	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPAPAPAPAPGGTLNI EDEYRLHETSKEPDVPLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKP GTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALH RDLADFRIQHPDLILLQYVDDLLLAATSEQDCQRGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFL GTAGFCRLWIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAA GWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEKEAPHDCLEILAETHG TRPDLTDQPIPDADYTWYTDGSSFLQEGQRRAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHVHGEIYRRRGWL TSEGREIKNKNEILALLKALFLPKRLSIIHCPGHQKGNSAEARGNRMADQAAREAAMKAVLETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
4511	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA

	SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGGGGSGGLGIEDEYRLHE TSTEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIQQYPMSHEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPV QDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRI QHPDLILLQYVDDILLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLREGQRWLTEARKETVMGQPVPKTPRQLREFLGKAGFCRL FIPGFAEMAAPLYPLTKPGTLFSWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRM VAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEEGAPHDCLEILAETHGTRPDLTDQ PIPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVIWAGALPAGTSAQRAELIALTQALKMAEGKRLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGREIK NKSEILALLKALFLPKRLSIIHCLGHQKGDSAEARGNRLADQAAREAAIKTPPDTSTLLIAGKRTADGSEFEKRTADGSEFESPKKKAKVE
4512	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKGSSGGLGIEDEYRL HETSTEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIQQYPMSHEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYR PVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADF RIQHPDLILLQYVDDILLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLREGQRWLTEARKETVMGQPVPKTPRQLREFLGKAGFC RLFIPGFAEMAAPLYPLTKPGTLFSWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCL RMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEEGAPHDCLEILAETHGTRPDLT DQPIPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVIWAGALPAGTSAQRAELIALTQALKMAEGKRLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGRE IKNKSEILALLKALFLPKRLSIIHCLGHQKGDSAEARGNRLADQAAREAAIKTPPDTSTLLIAGKRTADGSEFEKRTADGSEFESPKKKAKVE
4513	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ

	SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPGSSGGTLNIEDEHRLH ETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRP VQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFR IQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCR LFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLR MVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTD QPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEI KNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
4514	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPGSSGGTLNIEDEHRLH ETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRP VQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFR IQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCR LFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLR MVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPDLTD QPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEI KNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
4515	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL

	LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKPAPGGVLNLEEEYR LHEKPVPSSIDPSWLQLFPTVWAERAGMGLANQVPPVVVELRSGASPVAVRQYPMSKEAREGIRPHIQRFLDLGVLVPCQSPWNTPLLPVKKPGTNDYRP VQDLREINKRVQDIHPTVPNPYNLLSSLPPSHTWYSVLDLKDAFFCLKLHPNSQPLFAFEWRDPEKGNTGQLTWTRLPQGFKNSPTLFNEALHRDLAPFR ALNPQVVLLQYVDDLLVAAPTYRDCKEGTQKLLQELSKLGYRVSAKKAQLCQKEVTYLGYLLKEGKRWLTPARKATVMKIPPPTTPRQVREFLGKAGFCR LFIPGFASLAAPLYPLTKPSIPFIWTEEHQKAFDRIKEALLSAPALALPDLTKPFTLYVDERAGVARGVLTQTLGPWRRPVAYLSKKLDPVASGWPTCLK AVAAVALLLKDADKLTLGQNVTVIASHSLESIVRQPPDRWMTNARMTHYQSLLLNERVSFAPPAVLNPATLLPVESEATPVHRCSEILAEETGTRRDLKD QPLPGVPAWYTDGSSFIAEGKRRAGAAIVDGKRTVWASSLPEGTSAQKAELVALTQALRLAEGKDINIYTDSRYAFATAHIHGAIYKQRGWLTSAGKDIK NKEEILALLEAIHLPKRVAIIHCPGHQKGNDPVATGNRRADEAAKQAALSTRVLAETTKPAGKRTADGSEFEKRTADGSEFESPKKKAKVE
4516	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPEAAAKGGLGIEDEYRL HETSTEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIQQYPMSHEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYR PVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADF RIQHPDLILLQYVDDILLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLREGQRWLTEARKETVMGQPVPKTPRQLREFLGKAGFC RLFIPGFAEMAAPLYPLTKPGTLFSWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCL RMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEEGAPHDCLEILAETHGTRPDLT DQPIPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVIWAGALPAGTSAQRAELIALTQALKMAEGKRLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGRE IKNKSEILALLKALFLPKRLSIIHCLGHQKGDSAEARGNRLADQAAREAAIKTPPDTSTLLIAGKRTADGSEFEKRTADGSEFESPKKKAKVE
4517	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL

	FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSSGGGGGSGGLGIEDEYR LHETSTEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIQQYPMSHEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDY RPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGMGISGQLTWTRLPQGFKNSPTLFNEALHRDLAD FRIQHPDLILLQYVDDILLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLREGQRWLTEARKETVMGQPVPKTPRQLREFLGKAGF CRLFIPGFAEMAAPLYPLTKPGTLFSWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPC LRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEEGAPHDCLEILAETHGTRPDL TDQPIPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVIWAGALPAGTSAQRAELIALTQALKMAEGKRLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGR EIKNKSEILALLKALFLPKRLSIIHCLGHQKGDSAEARGNRLADQAAREAAIKTPPDTSTLLIAGKRTADGSEFEKRTADGSEFESPKKKAKVE
4518	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSSGGGGGSGGTLNIEDEY RLHETSKEPDVPLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTND YRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLA DFRIQHPDLILLQYVDDLLLAATSEQDCQRGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAG FCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPP CLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEKEAPHDCLEILAETHGTRPD LTDQPIPDADYTWYTDGSSFLQEGQRRAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHVHGEIYRRRGWLTSEG REIKNKNEILALLKALFLPKRLSIIHCPGHQKGNSAEARGNRMADQAAREAAMKAVLETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
4519	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV

	QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGGGGSEAAAKGGTLNIED EYRLHETSKEPDVPLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGT NDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRD LADFRIQHPDLILLQYVDDLLLAATSEQDCQRGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGK AGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGW PPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEKEAPHDCLEILAETHGTR PDLTDQPIPDADYTWYTDGSSFLQEGQRRAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHVHGEIYRRRGWLTS EGREIKNKNEILALLKALFLPKRLSIIHCPGHQKGNSAEARGNRMADQAAREAAMKAVLETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
4520	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGGGGSPAPGGTLNLEDEY RLYETSAEPEVSPGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEAKLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTND YRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHRWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGMGISGQLTWTRLPQGFKNSPTLFNEALHRDLA DFRIQHPDLILLQYVDDILLAATSELDCQQGTRALLLTLGNLGYRASAKKAQLCQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAG FCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPP CLRMVAAIAVLRKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEEGAPHDCLEILAETHGTRPD LTDQPIPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKRLNVYTDSRYAFATAHIHGEIYRRRGWLTSEG REIKNKSEILALLKALFLPKRLSIIHCLGHQKGDSAEARGNRLADQAAREAAIKTPPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE

4521	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPGGGGGSGGTLNIEDEH RLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTND YRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLA DFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAG FCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPP CLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPD LTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEG KEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
4522	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGSEAAAKGSSGGTLNIED EYRLHETSKEPDVPLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGT NDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRD LADFRIQHPDLILLQYVDDLLLAATSEQDCQRGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGK AGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGW PPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEKEAPHDCLEILAETHGTR

	PDLTDQPIPDADYTWYTDGSSFLQEGQRRAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHVHGEIYRRRGWLTS EGREIKNKNEILALLKALFLPKRLSIIHCPGHQKGNSAEARGNRMADQAAREAAMKAVLETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
4523	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKGGSGSSGGTLNIED EYRLHETSKEPDVPLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGT NDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRD LADFRIQHPDLILLQYVDDLLLAATSEQDCQRGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGT AGFCRLWIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGW PPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEKEAPHDCLEILAETHGTR PDLTDQPIPDADYTWYTDGSSFLQEGQRRAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHVHGEIYRRRGWLTS EGREIKNKNEILALLKALFLPKRLSIIHCPGHQKGNSAEARGNRMADQAAREAAMKAVLETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
4524	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKGSSGGSGGTLNIED EYRLHETSKEPDVPLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGT NDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRD LADFRIQHPDLILLQYVDDLLLAATSEQDCQRGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGT AGFCRLWIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGW

	PPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEKEAPHDCLEILAETHGTR PDLTDQPIPDADYTWYTDGSSFLQEGQRRAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHVHGEIYRRRGWLTS EGREIKNKNEILALLKALFLPKRLSIIHCPGHQKGNSAEARGNRMADQAAREAAMKAVLETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
4525	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSPAPGSSGGTLNIEDEY RLHETSKEPDVPLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTND YRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLA DFRIQHPDLILLQYVDDLLLAATSEQDCQRGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAG FCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPP CLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEKEAPHDCLEILAETHGTRPD LTDQPIPDADYTWYTDGSSFLQEGQRRAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHVHGEIYRRRGWLTSEG REIKNKNEILALLKALFLPKRLSIIHCPGHQKGNSAEARGNRMADQAAREAAMKAVLETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
4526	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSSPAPGGSGGLLGRDLLT KLKAQIQFSTEGPQVTWEDRPAMCLVLNLEEEYRLHEKPVPPSIDPSWLQLFPMVWAEKAGMGLANQVPPVVVELKSDASPVAVRQYPMSKEAREGIRPH IQRFLDLGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVQDIHPTVPNPYNLLSSLPPSHTWYSVLDLKDAFFCLKLHPNSQPLFAFEWRDPEK GNTGQLTWTRLPQGFKNSPTLFNEALHRDLASFRALNPQVVMLQYVDDLLVAAPTYRDCKEGTRRLLQELSKLGYRVSAKKAQLCREEVTYLGYLLKGGK

	RWLTPARKATVMKIPTPTTPRQVREFLGTAGFCRLWIPGFASLAAPLYPLTRPKVPFTWTEAHQEAFGRIKEALLSAPALALPDLTKPFALYVDEKEGVA RGVLTQTLGPWRRPVAYLSKKLDPVASGWPTCLKAIAAVALLLKDADKLTLGQNVLVIAPHNLESIVRQPPDRWMTNARMTHYQSLLLNERVSFAPPAIL NPATLLPVESDDTPIHICSEILAEETGTRPDLRDQPLPGVPAWYTDGSSFIMDGRRQAGAAIVDNKRTVWASNLPEGTSAQKAELIALTQALRLAEGKSI NIYTDSRYAFATAHVHGAIYKQRGWLTSAGKDIKNKEEILALLEAIHLPKRVAIIHCPGHQRGTDPVATGNRKADEAAKQAAQSTRILTETTKNAGKRTA DGSEFEKRTADGSEFESPKKKAKVE
4527	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKPAPGGSGGTLNIED EYRLHETSKEPDVPLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGT NDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRD LADFRIQHPDLILLQYVDDLLLAATSEQDCQRGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGK AGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGW PPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEKEAPHDCLEILAETHGTR PDLTDQPIPDADYTWYTDGSSFLQEGQRRAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHVHGEIYRRRGWLTS EGREIKNKNEILALLKALFLPKRLSIIHCPGHQKGNSAEARGNRMADQAAREAAMKAVLETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
4528	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPEAAAKGGSGGTLNLED EYRLYETSAEPEVSPGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEAKLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGT

	NDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHRWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGMGISGQLTWTRLPQGFKNSPTLFNEALHRD LADFRIQHPDLILLQYVDDILLAATSELDCQQGTRALLLTLGNLGYRASAKKAQLCQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGK AGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGW PPCLRMVAAIAVLRKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEEGAPHDCLEILAETHGTR PDLTDQPIPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKRLNVYTDSRYAFATAHIHGEIYRRRGWLTS EGREIKNKSEILALLKALFLPKRLSIIHCLGHQKGDSAEARGNRLADQAAREAAIKTPPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
4529	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPEAAAKGGSGGLDDEYR LYSPLVKPDQNIQFWLEQFPQAWAETAGMGLAKQVPPQVIQLKASATPVSVRQYPLSKEAQEGIRPHVQRLIQQGILVPVQSPWNTPLLPVRKPGTNDYR PVQDLREVNKRVQDIHPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGTGRTGQLTWTRLPQGFKNSPTIFNEALHRDLANF RIQHPQVTLLQYVDDLLLAGATKQDCLEGTKALLLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWLTEARKKTVVQIPAPTTAKQVREFLGKAGFC RLFIPGFATLAAPLYPLTKPKGEFSWAPEHQKAFDAIKKALLSAPALALPDVTKPFTLYVDERKGVARGVLTQTLGPWRRPVAYLSKKLDPVASGWPVCL KAIAAVAILVKDADKLTLGQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNPATLLPEETDEPVTHDCHQLLIEETGVRKDLT DIPLTGEVLTWFTDGSSYVVEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSINIYTDSRYAFATAHVHGAIYKQRGWLTSAGRE IKNKEEILSLLEALHLPKRLAIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLPAGKRTADGSEFEKRTADGSEFESPKKKAKVE
4530	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGGEAAAKGSSGGTLNIED

	EHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGT NDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRD LADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGT AGFCRLWIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGW PPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTR PDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTS EGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
4531	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKGGGGSSGGVLNLEE EYRLHEKPVPSSIDPSWLQLFPTVWAERAGMGLANQVPPVVVELRSGASPVAVRQYPMSKEAREGIRPHIQRFLDLGVLVPCQSPWNTPLLPVKKPGTND YRPVQDLREINKRVQDIHPTVPNPYNLLSSLPPSHTWYSVLDLKDAFFCLKLHPNSQPLFAFEWRDPEKGNTGQLTWTRLPQGFKNSPTLFNEALHRDLA PFRALNPQVVLLQYVDDLLVAAPTYRDCKEGTQKLLQELSKLGYRVSAKKAQLCQKEVTYLGYLLKEGKRWLTPARKATVMKIPPPTTPRQVREFLGKAG FCRLFIPGFASLAAPLYPLTKPSIPFIWTEEHQKAFDRIKEALLSAPALALPDLTKPFTLYVDERAGVARGVLTQTLGPWRRPVAYLSKKLDPVASGWPT CLKAVAAVALLLKDADKLTLGQNVTVIASHSLESIVRQPPDRWMTNARMTHYQSLLLNERVSFAPPAVLNPATLLPVESEATPVHRCSEILAEETGTRRD LKDQPLPGVPAWYTDGSSFIAEGKRRAGAAIVDGKRTVWASSLPEGTSAQKAELVALTQALRLAEGKDINIYTDSRYAFATAHIHGAIYKQRGWLTSAGK DIKNKEEILALLEAIHLPKRVAIIHCPGHQKGNDPVATGNRRADEAAKQAALSTRVLAETTKPAGKRTADGSEFEKRTADGSEFESPKKKAKVE
4532	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK

	VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSSGGGPAPGGTLQLDDEY RLYSPLVKPDQNIQFWLEQFPQAWAETAGMGLAKQVPPQVIQLKASATPVSVRQYPLSKEAQEGIRPHVQRLIQQGILVPVQSPWNTPLLPVRKPGTNDY RPVQDLREVNKRVQDIHPTVPNPYNLLCALPPQRSWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGTGRTGQLTWTRLPQGFKNSPTIFNEALHRDLAN FRIQHPQVTLLQYVDDLLLAGATKQDCLEGTKALLLELSDLGYRASAKKAQICRREVTYLGYSLRDGQRWLTEARKKTVVQIPAPTTAKQVREFLGTAGF CRLWIPGFATLAAPLYPLTKPKGEFSWAPEHQKAFDAIKKALLSAPALALPDVTKPFTLYVDERKGVARGVLTQTLGPWRRPVAYLSKKLDPVASGWPVC LKAIAAVAILVKDADKLTLGQNITVIAPHALENIVRQPPDRWMTNARMTHYQSLLLTERVTFAPPAALNPATLLPEETDEPVTHDCHQLLIEETGVRKDL TDIPLTGEVLTWFTDGSSYVVEGKRMAGAAVVDGTRTIWASSLPEGTSAQKAELMALTQALRLAEGKSINIYTDSRYAFATAHVHGAIYKQRGWLTSAGR EIKNKEEILSLLEALHLPKRLAIIHCPGHQKAKDPISRGNQMADRVAKQAAQGVNLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
4533	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPGSSGGGGGTLNLEDEY RLYETSAEPEVSPGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEAKLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTND YRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHRWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPGMGISGQLTWTRLPQGFKNSPTLFNEALHRDLA DFRIQHPDLILLQYVDDILLAATSELDCQQGTRALLLTLGNLGYRASAKKAQLCQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAG FCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPP CLRMVAAIAVLRKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEEGAPHDCLEILAETHGTRPD LTDQPIPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKRLNVYTDSRYAFATAHIHGEIYRRRGWLTSEG REIKNKSEILALLKALFLPKRLSIIHCLGHQKGDSAEARGNRLADQAAREAAIKTPPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
4534	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE

	VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGGGPAPEAAAKGGTLNIED EHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGT NDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRD LADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGT AGFCRLWIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGW PPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTR PDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTS EGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
4535	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKGGGPAPGGTLNIED EHRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGT NDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRD LADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGT AGFCRLWIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGW PPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTR PDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTS EGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPDTSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
4536	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM

	PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGEAAAKPAPGGGGGTLNIED EYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGT NDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRD LAGFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPIPKTPRQLREFLGK AGFCRLFIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAFQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGW PPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHDCLDILAEAHGTR SDLMDQPLPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTS EGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGNSAEARGNRMADQAARE VATRETPETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
4537	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGPAPEAAAKGGGGGLLGRDL LTKLKAQIQFSTEGPQVTWEDRPAMCLVLNLEEEYRLHEKPVPPSIDPSWLQLFPMVWAEKAGMGLANQVPPVVVELKSDASPVAVRQYPMSKEAREGIR PHIQRFLDLGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVQDIHPTVPNPYNLLSSLPPSHTWYSVLDLKDAFFCLKLHPNSQPLFAFEWRDP EKGNTGQLTWTRLPQGFKNSPTLFNEALHRDLASFRALNPQVVMLQYVDDLLVAAPTYRDCKEGTRRLLQELSKLGYRVSAKKAQLCREEVTYLGYLLKG GKRWLTPARKATVMKIPTPTTPRQVREFLGTAGFCRLWIPGFASLAAPLYPLTRPKVPFTWTEAHQEAFGRIKEALLSAPALALPDLTKPFALYVDEKEG VARGVLTQTLGPWRRPVAYLSKKLDPVASGWPTCLKAIAAVALLLKDADKLTLGQNVLVIAPHNLESIVRQPPDRWMTNARMTHYQSLLLNERVSFAPPA ILNPATLLPVESDDTPIHICSEILAEETGTRPDLRDQPLPGVPAWYTDGSSFIMDGRRQAGAAIVDNKRTVWASNLPEGTSAQKAELIALTQALRLAEGK SINIYTDSRYAFATAHVHGAIYKQRGWLTSAGKDIKNKEEILALLEAIHLPKRVAIIHCPGHQRGTDPVATGNRKADEAAKQAAQSTRILTETTKNAGKR TADGSEFEKRTADGSEFESPKKKAKVE
4538	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA

	KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSSEAAAKPAPGGTLNIED EYRLHETSKEPDVPLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGT NDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRD LADFRIQHPDLILLQYVDDLLLAATSEQDCQRGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGT AGFCRLWIPGFAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGW PPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQAMLLDTDRVQFGPVVALNPATLLPLPEKEAPHDCLEILAETHGTR PDLTDQPIPDADYTWYTDGSSFLQEGQRRAGAAVTTETEVIWARALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHVHGEIYRRRGWLTS EGREIKNKNEILALLKALFLPKRLSIIHCPGHQKGNSAEARGNRMADQAAREAAMKAVLETSTLLAGKRTADGSEFEKRTADGSEFESPKKKAKVE
4539	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGGSSPAPEAAAKGGTAPLEE EYRLFLEAPIQNVTLLEQWKREIPKVWAEINPPGLASTQAPIHVQLLSTALPVRVRQYPITLEAKRSLRETIRKFRAAGILRPVHSPWNTPLLPVRKSGT SEYRMVQDLREVNKRVETIHPTVPNPYTLLSLLPPDRIWYSVLDLKDAFFCIPLAPESQLIFAFEWADAEEGESGQLTWTRLPQGFKNSPTLFNEALNRD LQGFRLDHPSVSLLQYVDDLLIAADTQAACLSATRDLLMTLAELGYRVSGKKAQLCQEEVTYLGFKIHKGSRSLSNSRTQAILQIPVPKTKRQVREFLGK IGYCRLFIPGFAELAQPLYAATRPGNDPLVWGEKEEEAFQSLKLALTQPPALALPSLDKPFQLFVEETSGAAKGVLTQALGPWKRPVAYLSKRLDPVAAG WPRCLRAIAAAALLTREASKLTFGQDIEITSSHNLESLLRSPPDKWLTNARITQYQVLLLDPPRVRFKQTAALNPATLLPETDDTLPIHHCLDTLDSLTS TRPDLTDQPLAQAEATLFTDGSSYIRDGKRYAGAAVVTLDSVIWAEPLPIGTSAQKAELIALTKALEWSKDKSVNIYTDSRYAFATLHVHGMIYRERGWL TAGGKAIKNAPEILALLTAVWLPKRVAVMHCKGHQKDDAPTSTGNRRADEVAREVAIRPLSTQATISAGKRTADGSEFEKRTADGSEFESPKKKAKVE
4540	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK

	ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGAEAAAKEAAAKEAAAKEAA AKALEAEAAAKEAAAKEAAAKEAAAKAGGTLNIEDEYRLHETSKGPDVPLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEAR LGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQSLFAFE WRDPEMGISGQLTWTRLPQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGDLGYRASAKKAQICQKQVKYLGY LLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGTAGFCRLWIPGFAEMAAPLYPLTKPGTLFEWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVD EKQGYAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQ FGPIVALNPATLLPLPEEGLQHDCLDILAEAHGTRPDLTDQPLPDADHTWYTDGSSFLQEGQRKAGAAVTTETEVVWAKALPAGTSAQRAELIALTQALK MAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGNRAEARGNRMADQAARFVATRETPETSTLL AGKRTADGSEFEKRTADGSEFESPKKKAKVE
4541	MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNE MAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLV QTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADL FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEEL LVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQ SFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNA SLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFA NRNFMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIK ELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNA KLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYL NAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKE VKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDK VLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDGGAEAAAKEAAAKEAAAKEAA AKALEAEAAAKEAAAKEAAAKEAAAKAGGIPWLMKKPLQLTTLVPLQEYEERLLKQTMLTGSYKEKLQSLFLKYDALWQHWENQVGHRRIKPHHIATGTV NPRPQKQYPINPKAKASIQTVINDLLKQGVLIQQNSIMNTPVYPVPKPDGKWRMVLDYREVNKTIPLIAAQNQHSAGILSSIFRGKYKTTLDLSNGFWAH SITPESYWLTAFTWLGQQYCWTRLPQGFLNSPALFNADVVDLLKEVPNVQVYVDDIYISHDDPREHLEQLEKVFSLLLNAGYVVSLKKSEIAQHEVEFLG FNITKEGRGLTETFKQKLLNITPPRDLKQLQSILGKLNFARNFIPNFSELVKPLYNIIATAPGKYITWTTDNSQQLQNIISMLNSAENLEERNPEVRLIM KVNTSPSAGYIRFYNEFAKRPIMYLNYVYTKAEVKFTNTEKLLTTIHKGLIKALDLGMGQEILVYSPIVSMTKIQKTPLPERKALPIRWITWMSYLEDPR IQFHYDKTLPELQQVPTVTDDIIAKIKHPSEFSMVFYTDGSAIKHPNVNKSHNAGMGIAQVQFKPEFTVINTWSIPLGDHTAQLAEVAAVEFACKKALKI DGPVLIVTDSFYVAESVNKELPYWQSNGFFNNKKKPLKHVSKWKSIADCIQLKPDIIIIHEKGHQPTASTFHTEGNNLADKLATQGSYVVNAGKRTADGS EFEKRTADGSEFESPKKKAKVE

Localization sequences for gene modifying systems

In certain embodiments, a gene editor system RNA further comprises an intracellular localization sequence, e.g., a nuclear localization sequence (NLS). In some embodiments, a gene modifying polypeptide comprises an NLS as comprised in SEQ ID NO: 4000 and/or SEQ ID NO: 4001, or an NLS having an amino acid sequence having at least 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, or 99% identity thereto.

The nuclear localization sequence may be an RNA sequence that promotes the import of the RNA into the nucleus. In certain embodiments the nuclear localization signal is located on the template RNA. In certain embodiments, the gene modifying polypeptide is encoded on a first RNA, and the template RNA is a second, separate, RNA, and the nuclear localization signal is located on the template RNA and not on an RNA encoding the gene modifying polypeptide. While not wishing to be bound by theory, in some embodiments, the RNA encoding the gene modifying polypeptide is targeted primarily to the cytoplasm to promote its translation, while the template RNA is targeted primarily to the nucleus to promote insertion into the genome. In some embodiments the nuclear localization signal is at the 3′ end, 5′ end, or in an internal region of the template RNA. In some embodiments the nuclear localization signal is 3′ of the heterologous sequence (e.g., is directly 3′ of the heterologous sequence) or is 5′ of the heterologous sequence (e.g., is directly 5′ of the heterologous sequence). In some embodiments the nuclear localization signal is placed outside of the 5′ UTR or outside of the 3′ UTR of the template RNA. In some embodiments the nuclear localization signal is placed between the 5′ UTR and the 3′ UTR, wherein optionally the nuclear localization signal is not transcribed with the transgene (e.g., the nuclear localization signal is an anti-sense orientation or is downstream of a transcriptional termination signal or polyadenylation signal). In some embodiments the nuclear localization sequence is situated inside of an intron. In some embodiments a plurality of the same or different nuclear localization signals are in the RNA, e.g., in the template RNA. In some embodiments the nuclear localization signal is less than 5, 10, 25, 50, 75, 100, 150, 200, 250, 300, 350, 400, 450, 500, 600, 700, 800, 900 or 1000 bp in length. Various RNA nuclear localization sequences can be used. For example, Lubelsky and Ulitsky, *Nature* 555 (107-111), 2018 describe RNA sequences which drive RNA localization into the nucleus. In some embodiments, the nuclear localization signal is a SINE-derived nuclear RNA localization (SIRLOIN) signal. In some

embodiments the nuclear localization signal binds a nuclear-enriched protein. In some embodiments the nuclear localization signal binds the HNRNPK protein. In some embodiments the nuclear localization signal is rich in pyrimidines, e.g., is a C/T rich, C/U rich, C rich, T rich, or U rich region. In some embodiments the nuclear localization signal is derived from a long non-coding RNA. In some embodiments the nuclear localization signal is derived from MALAT1 long non-coding RNA or is the 600 nucleotide M region of MALAT1 (described in Miyagawa et al., *RNA* 18, (738-751), 2012). In some embodiments the nuclear localization signal is derived from BORG long non-coding RNA or is a AGCCC motif (described in Zhang et al., *Molecular and Cellular Biology* 34, 2318-2329 (2014). In some embodiments the nuclear localization sequence is described in Shukla et al., *The EMBO Journal* e98452 (2018). In some embodiments the nuclear localization signal is derived from a retrovirus.

In some embodiments, a polypeptide described herein comprises one or more (e.g., 2, 3, 4, 5) nuclear targeting sequences, for example a nuclear localization sequence (NLS). In some embodiments, the NLS is a bipartite NLS. In some embodiments, an NLS facilitates the import of a protein comprising an NLS into the cell nucleus. In some embodiments, the NLS is fused to the N-terminus of a gene modifying polypeptide as described herein. In some embodiments, the NLS is fused to the C-terminus of the gene modifying polypeptide. In some embodiments, the NLS is fused to the N-terminus or the C-terminus of a Cas domain. In some embodiments, a linker sequence is disposed between the NLS and the neighboring domain of the gene modifying polypeptide.

In some embodiments, an NLS comprises the amino acid sequence MDSLLMNRRKFLYQFKNVRWAKGRRETYLC (SEQ ID NO: 5009), PKKRKVEGADKRTADGSEFESPKKKRKV(SEQ ID NO: 5010), RKSGKIAAIWKRPRKPKKKRKV (SEQ ID NO: 5011) KRTADGSEFESPKKKRKV(SEQ ID NO: 5012), KKTELQTTNAENKTKKL (SEQ ID NO: 5013), or KRGINDRNFWRGENGRKTR (SEQ ID NO: 5014), KRPAATKKAGQAKKKK (SEQ ID NO: 5015), PAAKRVKLD (SEQ ID NO: 4644), KRTADGSEFEKRTADGSEFESPKKKAKVE (SEQ ID NO: 4649), KRTADGSEFE (SEQ ID NO: 4650), KRTADGSEFESPKKKAKVE (SEQ ID NO: 11098), AGKRTADGSEFEKRTADGSEFESPKKKAKVE (SEQ ID NO: 4651), or a functional fragment or variant thereof. Exemplary NLS sequences are also described in

PCT/EP2000/011690, the contents of which are incorporated herein by reference for their disclosure of exemplary nuclear localization sequences. In some embodiments, an NLS comprises an amino acid sequence as disclosed in Table 11. An NLS of this table may be utilized with one or more copies in a polypeptide in one or more locations in a polypeptide, e.g., 1, 2, 3 or more copies of an NLS in an N-terminal domain, between peptide domains, in a C-terminal domain, or in a combination of locations, in order to improve subcellular localization to the nucleus. Multiple unique sequences may be used within a single polypeptide. Sequences may be naturally monopartite or bipartite, e.g., having one or two stretches of basic amino acids, or may be used as chimeric bipartite sequences. Sequence references correspond to UniProt accession numbers, except where indicated as SeqNLS for sequences mined using a subcellular localization prediction algorithm (Lin et al BMC Bioinformat 13:157 (2012), incorporated herein by reference in its entirety).

Table 11 Exemplary nuclear localization signals for use in gene modifying systems

Sequence	Sequence References	SEQ ID No.
AHFKISGEKRPSTDPGKKAK NPKKKKKKDP	Q76IQ7	5223
AHRAKKMSKTHA	P21827	5224
ASPEYVNLPINGNG	SeqNLS	5225
CTKRPRW	O88622, Q86W56, Q9QYM2, O02776	5226
DKAKRVSRNKSEKKRR	O15516, Q5RAK8, Q91YB2, Q91YB0, Q8QGQ6, O08785, Q9WVS9, Q6YGZ4	5227
EELRLKEELLKGIYA	Q9QY16, Q9UHL0, Q2TBP1, Q9QY15	5228
EEQLRRRKNSRLNNTG	G5EFF5	5229
EVLKVIRTGKRKKKAWKR MVTKVC	SeqNLS	5230
HHHHHHHHHHHHQPH	Q63934, G3V7L5, Q12837	5231
HKKKHPDASVNFSEFSK	P10103, Q4R844, P12682, B0CM99, A9RA84, Q6YKA4, P09429, P63159, Q08IE6, P63158, Q9YH06, B1MTB0	5232
HKRTKK	Q2R2D5	5233

IINGRKLKLKKSRRRSSQTSNNSFTSRRS	SeqNLS	5234
KAEQERRK	Q8LH59	5235
KEKRKRREELFIEQKKRK	SeqNLS	5236
KKGKDEWFSRGKKP	P30999	5237
KKGPSVQKRKKT	Q6ZN17	5238
KKKTVINDLLHYKKEK	SeqNLS, P32354	5239
KKNGGKGKNKPSAKIKK	SeqNLS	5240
KKPKWDDFKKKKK	Q15397, Q8BKS9, Q562C7	5241
KKRKKD	SeqNLS, Q91Z62, Q1A730, Q969P5, Q2KHT6, Q9CPU7	5242
KKRRKRRRK	SeqNLS	5243
KKRRRRARK	Q9UMS6, D4A702, Q91YE8	5244
KKSKRGR	Q9UBS0	5245
KKSRKRGS	B4FG96	5246
KKSTALSRELGKIMRRR	SeqNLS, P32354	5247
KKSYQDPEIIAHSRPRK	Q9U7C9	5248
KKTGKNRKLKSKRVKTR	Q9Z301, O54943, Q8K3T2	5249
KKVSIAGQSGKLWRWKR	Q6YUL8	5250
KKYENVVIKRSPRKRGRPRK	SeqNLS	5251
KNKKRK	SeqNLS	5252
KPKKKR	SeqNLS	5253
KRAMKDDSHGNSTSPKRRK	Q0E671	5254
KRANSNLVAAYEKAKKK	P23508	5255
KRASEDTTSGSPPKKSSAGPKR	Q9BZZ5, Q5R644	5256
KRFKRRWMVRKMKTKK	SeqNLS	5257
KRGLNSSFETSPKKVK	Q8IV63	5258
KRGNSSIGPNDLSKRKQRKK	SeqNLS	5259

KRIHSVSLSQSQIDPSKKVKRAK	SeqNLS	5260
KRKGKLKNKGSKRKK	O15381	5261
KRRRRRREKRKR	Q96GM8	5262
KRSNDRTYSPEEEKQRRA	Q91ZF2	5263
KRTVATNGDASGAHRAKKMSK	SeqNLS	5264
KRVYNKGEDEQEHLPKGKKR	SeqNLS	5265
KSGKAPRRRAVSMDNSNK	Q9WVH4, O43524	5266
KVNFLDMSLDDIIIYKELE	Q9P127	5267
KVQHRIAKKTTRRRR	Q9DXE6	5268
LSPSLSPL	Q9Y261, P32182, P35583	5269
MDSLLMNRRKFLYQFKNVRWAKGRRETYLC	Q9GZX7	5270
MPQNEYIELHRKRYGYRLDYHEKKRKKESREAHERSKKAKKMIGLKAKLYHK	SeqNLS	5271
MVQLRPRASR	SeqNLS	5272
NNKLLAKRRKGGASPKDDPMDDIK	Q965G5	5273
NYKRPMDGTYGPPAKRHEGE	O14497, A2BH40	5274
PDTKRAKLDSSETTMVKKK	SeqNLS	5275
PEKRTKI	SeqNLS	5276
PGGRGKKK	Q719N1, Q9UBP0, A2VDN5	5277
PGKMDKGEHRQERRDRPY	Q01844, Q61545	5278
PKKGDKYDKTD	Q45FA5	5279
PKKKSRK	O35914, Q01954	5280
PKKNKPE	Q22663	5281
PKKRAKV	P04295, P89438	5282
PKPKKLKVE	P55263, P55262, P55264, Q64640	5283
PKRGRGR	Q9FYS5, Q43386	5284

PKRRLVDDA	P0C797	5285
PKRRRTY	SeqNLS	5286
PLFKRR	A8X6H4, Q9TXJ0	5287
PLRKAKR	Q86WB0, Q5R8V9	5288
PPAKRKCIF	Q6AZ28, O75928, Q8C5D8	5289
PPARRRRL	Q8NAG6	5290
PPKKKRKV	Q3L6L5, P03070, P14999, P03071	5291
PPNKRMKVKH	Q8BN78	5292
PPRIYPQLPSAPT	P0C799	5293
PQRSPFPKSSVKR	SeqNLS	5294
PRPRKVPR	P0C799	5295
PRRRVQRKR	SeqNLS, Q5R448, Q5TAQ9	5296
PRRVRLK	Q58DJ0, P56477, Q13568	5297
PSRKRPR	Q62315, Q5F363, Q92833	5298
PSSKKRKV	SeqNLS	5299
PTKKRVK	P07664	5300
QRPGPYDRP	SeqNLS	5301
RGKGGKGLGKGGAKRHRK	SeqNLS	5302
RKAGKGGGGHKTTKKRSAKDEKVP	B4FG96	5303
RKIKLKRAK	A1L3G9	5304
RKIKRKRAK	B9X187	5305
RKKEAPGPREELRSRGR	O35126, P54258, Q5IS70, P54259	5306
RKKRKGK	SeqNLS, Q29243, Q62165, Q28685, O18738, Q9TSZ6, Q14118	5307
RKKRRQRRR	P04326, P69697, P69698, P05907, P20879, P04613, P19553, P0C1J9, P20893, P12506, P04612, Q73370, P0C1K0, P05906, P35965, P04609, P04610, P04614, P04608, P05905	5308
RKKSIPLSIKNLKRKHKRKKNKITR	Q9C0C9	5309

RKLVKPKNTKMKTKLRTNPY	Q14190	5310
RKRLILSDKGQLDWKK	SeqNLS, Q91Z62, Q1A730, Q2KHT6, Q9CPU7	5311
RKRLKSK	Q13309	5312
RKRRVRDNM	Q8QPH4, Q809M7, A8C8X1, Q2VNC5, Q38SQ0, O89749, Q6DNQ9, Q809L9, Q0A429, Q20NV3, P16509, P16505, Q6DNQ5, P16506, Q6XT06, P26118, Q2ICQ2, Q2RCG8, Q0A2D0, Q0A2H9, Q9IQ46, Q809M3, Q6J847, Q6J856, B4URE4, A4GCM7, Q0A440, P26120, P16511,	5313
RKRSPKDKKEKDLDGAGKRRKT	Q7RTP6	5314
RKRTPRVDGQTGENDMNKRRRK	O94851	5315
RLPVRRRRRR	P04499, P12541, P03269, P48313, P03270	5316
RLRFRKPKSK	P69469	5317
RQQRKR	Q14980	5318
RRDLNSSFETSPKKVK	Q8K3G5	5319
RRDRAKLR	Q9SLB8	5320
RRGDGRRR	Q80WE1, Q5R9B4, Q06787, P35922	5321
RRGRKRKAEKQ	Q812D1, Q5XXA9, Q99JF8, Q8MJG1, Q66T72, O75475	5322
RRKKRR	Q0VD86, Q58DS6, Q5R6G2, Q9ERI5, Q6AYK2, Q6NYC1	5323
RRKRSKSEDMDSVESKRRR	Q7TT18	5324
RRKRSR	Q99PU7, D3ZHS6, Q92560, A2VDM8	5325
RRPKGKTLQKRKPK	Q6ZN17	5326
RRRGFERFGPDNMGRKRK	Q63014, Q9DBR0	5327
RRRGKNKVAAQNCRK	SeqNLS	5328
RRRKRR	Q5FVH8, Q6MZT1, Q08DH5, Q8BQP9	5329
RRRQKQKGGASRRR	SeqNLS	5330

RRRREGPRARRRR	P08313, P10231	5331
RRTIRLKLVYDKCDRSCKIQKKNRNKCQYCRFHKCLSVGMSHNAIRFGRMPRSEKAKLKAE	SeqNLS	5332
RRVPQRKEVSRCRKCRK	Q5RJN4, Q32L09, Q8CAK3, Q9NUL5	5333
RVGGRRQAVECIEDLLNEPGQPLDLSCKRPRP	P03255	5334
RVVKLRIAP	P52639, Q8JMN0	5335
RVVRRR	P70278	5336
SKRKTKISRKTR	Q5RAY1, O00443	5337
SYVKTVPNRTRTYIKL	P21935	5338
TGKNEAKKRKIA	P52739, Q8K3J5, Q5RAU9	5339
TLSPASSPSSVSCPVIPASTDESPGSALNI	SeqNLS	5340
VSKKQRTGKKIH	P52739, Q8K3J5, Q5RAU9	5341
SPKKKRKVE		5342
KRTAD GSEFE SPKKKRKVE		5343
PAAKRVKLD		5344
PKKKRKV		5345
MDSLLMNRRKFLYQFKNVRWAKGRRETYLC		5346
SPKKKRKVEAS		5347
MAPKKKRKVGIHRGVP		5348
KRTADGSEFEKRTADGSEFESPKKKAKVE		5349
KRTADGSEFE		5350
KRTADGSEFESPKKKAKVE		5351
AGKRTADGSEFEKRTADGSEFESPKKKAKVE		4001

In some embodiments, the NLS is a bipartite NLS. A bipartite NLS typically comprises two basic amino acid clusters separated by a spacer sequence (which may be, e.g., about 10

amino acids in length). A monopartite NLS typically lacks a spacer. An example of a bipartite NLS is the nucleoplasmin NLS, having the sequence KR[PAATKKAGQA]KKKK (SEQ ID NO: 5015), wherein the spacer is bracketed. Another exemplary bipartite NLS has the sequence PKKKRKVEGADKRTADGSEFESPKKKRKV (SEQ ID NO: 5016). Exemplary NLSs are described in International Application WO2020051561, which is herein incorporated by reference in its entirety, including for its disclosures regarding nuclear localization sequences.

In certain embodiments, a gene editor system polypeptide (e.g., a gene modifying polypeptide as described herein) further comprises an intracellular localization sequence, e.g., a nuclear localization sequence and/or a nucleolar localization sequence. The nuclear localization sequence and/or nucleolar localization sequence may be amino acid sequences that promote the import of the protein into the nucleus and/or nucleolus, where it can promote integration of heterologous sequence into the genome. In certain embodiments, a gene editor system polypeptide (e.g., (e.g., a gene modifying polypeptide as described herein) further comprises a nucleolar localization sequence. In certain embodiments, the gene modifying polypeptide is encoded on a first RNA, and the template RNA is a second, separate, RNA, and the nucleolar localization signal is encoded on the RNA encoding the gene modifying polypeptide and not on the template RNA. In some embodiments, the nucleolar localization signal is located at the N-terminus, C-terminus, or in an internal region of the polypeptide. In some embodiments, a plurality of the same or different nucleolar localization signals are used. In some embodiments, the nuclear localization signal is less than 5, 10, 25, 50, 75, or 100 amino acids in length. Various polypeptide nucleolar localization signals can be used. For example, Yang et al., *Journal of Biomedical Science* 22, 33 (2015), describe a nuclear localization signal that also functions as a nucleolar localization signal. In some embodiments, the nucleolar localization signal may also be a nuclear localization signal. In some embodiments, the nucleolar localization signal may overlap with a nuclear localization signal. In some embodiments, the nucleolar localization signal may comprise a stretch of basic residues. In some embodiments, the nucleolar localization signal may be rich in arginine and lysine residues. In some embodiments, the nucleolar localization signal may be derived from a protein that is enriched in the nucleolus. In some embodiments, the nucleolar localization signal may be derived from a protein enriched at ribosomal RNA loci. In some embodiments, the nucleolar localization signal may be derived from a protein that binds rRNA. In some embodiments, the nucleolar localization signal may be derived from MSP58. In

some embodiments, the nucleolar localization signal may be a monopartite motif. In some embodiments, the nucleolar localization signal may be a bipartite motif. In some embodiments, the nucleolar localization signal may consist of a multiple monopartite or bipartite motifs. In some embodiments, the nucleolar localization signal may consist of a mix of monopartite and bipartite motifs. In some embodiments, the nucleolar localization signal may be a dual bipartite motif. In some embodiments, the nucleolar localization motif may be a KRASSQALGTIPKRRSSSRFIKRKK (SEQ ID NO: 5017). In some embodiments, the nucleolar localization signal may be derived from nuclear factor-κB-inducing kinase. In some embodiments, the nucleolar localization signal may be an RKKRKKK motif (SEQ ID NO: 5018) (described in Birbach et al., Journal of Cell Science, 117 (3615-3624), 2004).

Evolved Variants of Gene Modifying Polypeptides and Systems

In some embodiments, the invention provides evolved variants of gene modifying polypeptides as described herein. Evolved variants can, in some embodiments, be produced by mutagenizing a reference gene modifying polypeptide, or one of the fragments or domains comprised therein. In some embodiments, one or more of the domains (e.g., the reverse transcriptase domain) is evolved. One or more of such evolved variant domains can, in some embodiments, be evolved alone or together with other domains. An evolved variant domain or domains may, in some embodiments, be combined with unevolved cognate component(s) or evolved variants of the cognate component(s), e.g., which may have been evolved in either a parallel or serial manner.

In some embodiments, the process of mutagenizing a reference gene modifying polypeptide, or fragment or domain thereof, comprises mutagenizing the reference gene modifying polypeptide or fragment or domain thereof. In embodiments, the mutagenesis comprises a continuous evolution method (e.g., PACE) or non-continuous evolution method (e.g., PANCE), e.g., as described herein. In some embodiments, the evolved gene modifying polypeptide, or a fragment or domain thereof, comprises one or more amino acid variations introduced into its amino acid sequence relative to the amino acid sequence of the reference gene modifying polypeptide, or fragment or domain thereof. In embodiments, amino acid sequence variations may include one or more mutated residues (e.g., conservative substitutions, non-conservative substitutions, or a combination thereof) within the amino acid sequence of a

reference gene modifying polypeptide, e.g., as a result of a change in the nucleotide sequence encoding the gene modifying polypeptide that results in, e.g., a change in the codon at any particular position in the coding sequence, the deletion of one or more amino acids (e.g., a truncated protein), the insertion of one or more amino acids, or any combination of the foregoing. The evolved variant gene modifying polypeptide may include variants in one or more components or domains of the gene modifying polypeptide (e.g., variants introduced into a reverse transcriptase domain).

In some aspects, the disclosure provides gene modifying polypeptides, systems, kits, and methods using or comprising an evolved variant of a gene modifying polypeptide, e.g., employs an evolved variant of a gene modifying polypeptide or a gene modifying polypeptide produced or producible by PACE or PANCE. In embodiments, the unevolved reference gene modifying polypeptide is a gene modifying polypeptide as disclosed herein.

The term "phage-assisted continuous evolution (PACE),"as used herein, generally refers to continuous evolution that employs phage as viral vectors. Examples of PACE technology have been described, for example, in International PCT Application No. PCT/US 2009/056194, filed September 8, 2009, published as WO 2010/028347 on March 11, 2010; International PCT Application, PCT/US2011/066747, filed December 22, 2011, published as WO 2012/088381 on June 28, 2012; U.S. Patent No. 9,023,594, issued May 5, 2015; U.S. Patent No. 9,771,574, issued September 26, 2017; U.S. Patent No. 9,394,537, issued July 19, 2016; International PCT Application, PCT/US2015/012022, filed January 20, 2015, published as WO 2015/134121 on September 11, 2015; U.S. Patent No. 10,179,911, issued January 15, 2019; and International PCT Application, PCT/US2016/027795, filed April 15, 2016, published as WO 2016/168631 on October 20, 2016, the entire contents of each of which are incorporated herein by reference.

The term "phage-assisted non-continuous evolution (PANCE)," as used herein, generally refers to non-continuous evolution that employs phage as viral vectors. Examples of PANCE technology have been described, for example, in Suzuki T. et al, Crystal structures reveal an elusive functional domain of pyrrolysyl-tRNA synthetase, Nat Chem Biol. 13(12): 1261-1266 (2017), incorporated herein by reference in its entirety. Briefly, PANCE is a technique for rapid *in vivo* directed evolution using serial flask transfers of evolving selection phage (SP), which contain a gene of interest to be evolved, across fresh host cells (e.g., E. coli cells). Genes inside the host cell may be held constant while genes contained in the SP continuously evolve.

Following phage growth, an aliquot of infected cells may be used to transfect a subsequent flask containing host E. coli. This process can be repeated and/or continued until the desired phenotype is evolved, e.g., for as many transfers as desired.

Methods of applying PACE and PANCE to gene modifying polypeptides may be readily appreciated by the skilled artisan by reference to, *inter alia*, the foregoing references. Additional exemplary methods for directing continuous evolution of genome-modifying proteins or systems, e.g., in a population of host cells, e.g., using phage particles, can be applied to generate evolved variants of gene modifying polypeptides, or fragments or subdomains thereof. Non-limiting examples of such methods are described in International PCT Application, PCT/US2009/056194, filed September 8, 2009, published as WO 2010/028347 on March 11, 2010; International PCT Application, PCT/US2011/066747, filed December 22, 2011, published as WO 2012/088381 on June 28, 2012; U.S. Patent No. 9,023,594, issued May 5, 2015; U.S. Patent No. 9,771,574, issued September 26, 2017; U.S. Patent No. 9,394,537, issued July 19, 2016; International PCT Application, PCT/US2015/012022, filed January 20, 2015, published as WO 2015/134121 on September 11, 2015; U.S. Patent No. 10,179,911, issued January 15, 2019; International Application No. PCT/US2019/37216, filed June 14, 2019, International Patent Publication WO 2019/023680, published January 31, 2019, International PCT Application, PCT/US2016/027795, filed April 15, 2016, published as WO 2016/168631 on October 20, 2016, and International Patent Publication No. PCT/US2019/47996, filed August 23, 2019, each of which is incorporated herein by reference in its entirety.

In some non-limiting illustrative embodiments, a method of evolution of a evolved variant gene modifying polypeptide, of a fragment or domain thereof, comprises: (a) contacting a population of host cells with a population of viral vectors comprising the gene of interest (the starting gene modifying polypeptide or fragment or domain thereof), wherein: (1) the host cell is amenable to infection by the viral vector; (2) the host cell expresses viral genes required for the generation of viral particles; (3) the expression of at least one viral gene required for the production of an infectious viral particle is dependent on a function of the gene of interest; and/or (4) the viral vector allows for expression of the protein in the host cell, and can be replicated and packaged into a viral particle by the host cell. In some embodiments, the method comprises (b) contacting the host cells with a mutagen, using host cells with mutations that elevate mutation rate (e.g., either by carrying a mutation plasmid or some genome modification—e.g., proofing-

impaired DNA polymerase, SOS genes, such as UmuC, UmuD', and/or RecA, which mutations, if plasmid-bound, may be under control of an inducible promoter), or a combination thereof. In some embodiments, the method comprises (c) incubating the population of host cells under conditions allowing for viral replication and the production of viral particles, wherein host cells are removed from the host cell population, and fresh, uninfected host cells are introduced into the population of host cells, thus replenishing the population of host cells and creating a flow of host cells. In some embodiments, the cells are incubated under conditions allowing for the gene of interest to acquire a mutation. In some embodiments, the method further comprises (d) isolating a mutated version of the viral vector, encoding an evolved gene product (e.g., an evolved variant gene modifying polypeptide, or fragment or domain thereof), from the population of host cells.

The skilled artisan will appreciate a variety of features employable within the above-described framework. For example, in some embodiments, the viral vector or the phage is a filamentous phage, for example, an M13 phage, e.g., an M13 selection phage. In certain embodiments, the gene required for the production of infectious viral particles is the M13 gene III (gIII). In embodiments, the phage may lack a functional gIII, but otherwise comprise gI, gII, gIV, gV, gVI, gVII, gVIII, gIX, and a gX. In some embodiments, the generation of infectious VSV particles involves the envelope protein VSV-G. Various embodiments can use different retroviral vectors, for example, Murine Leukemia Virus vectors, or Lentiviral vectors. In embodiments, the retroviral vectors can efficiently be packaged with VSV-G envelope protein, e.g., as a substitute for the native envelope protein of the virus.

In some embodiments, host cells are incubated according to a suitable number of viral life cycles, e.g., at least 10, at least 20, at least 30, at least 40, at least 50, at least 100, at least 200, at least 300, at least 400, at least, 500, at least 600, at least 700, at least 800, at least 900, at least 1000, at least 1250, at least 1500, at least 1750, at least 2000, at least 2500, at least 3000, at least 4000, at least 5000, at least 7500, at least 10000, or more consecutive viral life cycles, which in on illustrative and non-limiting examples of M13 phage is 10-20 minutes per virus life cycle. Similarly, conditions can be modulated to adjust the time a host cell remains in a population of host cells, e.g., about 10, about 11, about 12, about 13, about 14, about 15, about 16, about 17, about 18, about 19, about 20, about 21, about 22, about 23, about 24, about 25, about 30, about 35, about 40, about 45, about 50, about 55, about 60, about 70, about 80, about 90, about 100, about 120, about 150, or about 180 minutes. Host cell populations can be

controlled in part by density of the host cells, or, in some embodiments, the host cell density in an inflow, e.g., 10^3 cells/ml, about 10^4 cells/ml, about 10^5 cells/ml, about 5- 10^5 cells/ml, about 10^6 cells/ml, about 5- 10^6 cells/ml, about 10^7 cells/ml, about 5- 10^7 cells/ml, about 10^8 cells/ml, about 5- 10^8 cells/ml, about 10^9 cells/ml, about $5\cdot 10^9$ cells/ml, about 10^{10} cells/ml, or about $5\cdot 10^{10}$ cells/ml.

Inteins

In some embodiments, as described in more detail below, an intein-N (intN) domain may be fused to the N-terminal portion of a first domain of a gene modifying polypeptide described herein, and an intein-C (intC) domain may be fused to the C-terminal portion of a second domain of a gene modifying polypeptide described herein for the joining of the N-terminal portion to the C-terminal portion, thereby joining the first and second domains. In some embodiments, the first and second domains are each independently chosen from a DNA binding domain, an RNA binding domain, an RT domain, and an endonuclease domain.

Inteins can occur as self-splicing protein intron (e.g., peptide), e.g., which ligates flanking N-terminal and C-terminal exteins (e.g., fragments to be joined). An intein may, in some instances, comprise a fragment of a protein that is able to excise itself and join the remaining fragments (the exteins) with a peptide bond in a process known as protein splicing. Inteins are also referred to as “protein introns.” The process of an intein excising itself and joining the remaining portions of the protein is herein termed “protein splicing” or “intein-mediated protein splicing.”

In some embodiments, an intein of a precursor protein (an intein containing protein prior to intein-mediated protein splicing) comes from two genes. Such intein is referred to herein as a split intein (e.g., split intein-N and split intein-C). Accordingly, an intein-based approach may be used to join a first polypeptide sequence and a second polypeptide sequence together. For example, in cyanobacteria, DnaE, the catalytic subunit a of DNA polymerase III, is encoded by two separate genes, dnaE-n and dnaE-c. An intein-N domain, such as that encoded by the dnaE-n gene, when situated as part of a first polypeptide sequence, may join the first polypeptide sequence with a second polypeptide sequence, wherein the second polypeptide sequence comprises an intein-C domain, such as that encoded by the dnaE-c gene. Accordingly, in some embodiments, a protein can be made by providing nucleic acid encoding the first and second polypeptide sequences (e.g., wherein a first nucleic acid molecule encodes the first polypeptide

sequence and a second nucleic acid molecule encodes the second polypeptide sequence), and the nucleic acid is introduced into the cell under conditions that allow for production of the first and second polypeptide sequences, and for joining of the first to the second polypeptide sequence via an intein-based mechanism.

Use of inteins for joining heterologous protein fragments is described, for example, in Wood et al., J. Biol. Chem.289(21); 14512-9 (2014) (incorporated herein by reference in its entirety). For example, when fused to separate protein fragments, the inteins IntN and IntC may recognize each other, splice themselves out, and/or simultaneously ligate the flanking N- and C-terminal exteins of the protein fragments to which they were fused, thereby reconstituting a full-length protein from the two protein fragments.

In some embodiments, a synthetic intein based on the dnaE intein, the Cfa-N (e.g., split intein-N) and Cfa-C (e.g., split intein-C) intein pair, is used. Examples of such inteins have been described, e.g., in Stevens et al., J Am Chem Soc. 2016 Feb. 24; 138(7):2162-5 (incorporated herein by reference in its entirety). Non-limiting examples of intein pairs that may be used in accordance with the present disclosure include: Cfa DnaE intein, Ssp GyrB intein, Ssp DnaX intein, Ter DnaE3 intein, Ter ThyX intein, Rma DnaB intein and Cne Prp8 intein (e.g., as described in U.S. Pat. No. 8,394,604, incorporated herein by reference.

In some embodiments involving a split Cas9, an intein-N domain and an intein-C domain may be fused to the N-terminal portion of the split Cas9 and the C-terminal portion of a split Cas9, respectively, for the joining of the N-terminal portion of the split Cas9 and the C-terminal portion of the split Cas9. For example, in some embodiments, an intein-N is fused to the C-terminus of the N-terminal portion of the split Cas9, i.e., to form a structure of N— [N-terminal portion of the split Cas9]-[intein-N]~ C. In some embodiments, an intein-C is fused to the N-terminus of the C-terminal portion of the split Cas9, i.e., to form a structure of N-[intein-C]~ [C-terminal portion of the split Cas9]-C. The mechanism of intein-mediated protein splicing for joining the proteins the inteins are fused to (e.g., split Cas9) is described in Shah et al., Chem Sci. 2014; 5(l):446-46l, incorporated herein by reference. Methods for designing and using inteins are known in the art and described, for example by WO2020051561, W02014004336, WO2017132580, US20150344549, and US20180127780, each of which is incorporated herein by reference in their entirety.

In some embodiments, a split refers to a division into two or more fragments. In some embodiments, a split Cas9 protein or split Cas9 comprises a Cas9 protein that is provided as an N-terminal fragment and a C-terminal fragment encoded by two separate nucleotide sequences. The polypeptides corresponding to the N-terminal portion and the C-terminal portion of the Cas9 protein may be spliced to form a reconstituted Cas9 protein. In embodiments, the Cas9 protein is divided into two fragments within a disordered region of the protein, e.g., as described in Nishimasu et al., Cell, Volume 156, Issue 5, pp. 935-949, 2014, or as described in Jiang et al. (2016) Science 351: 867-871 and PDB file: 5F9R (each of which is incorporated herein by reference in its entirety). A disordered region may be determined by one or more protein structure determination techniques known in the art, including, without limitation, X-ray crystallography, NMR spectroscopy, electron microscopy (e.g., cryoEM), and/or *in silico* protein modeling. In some embodiments, the protein is divided into two fragments at any C, T, A, or S, e.g., within a region of SpCas9 between amino acids A292- G364, F445-K483, or E565-T637, or at corresponding positions in any other Cas9, Cas9 variant (e.g., nCas9, dCas9), or other napDNAbp. In some embodiments, protein is divided into two fragments at SpCas9 T310, T313, A456, S469, or C574. In some embodiments, the process of dividing the protein into two fragments is referred to as splitting the protein.

In some embodiments, a protein fragment ranges from about 2-1000 amino acids (e.g., between 2-10, 10-50, 50-100, 100-200, 200-300, 300-400, 400-500, 500-600, 600-700, 700-800, 800-900, or 900-1000 amino acids) in length. In some embodiments, a protein fragment ranges from about 5-500 amino acids (e.g., between 5-10, 10-50, 50-100, 100-200, 200-300, 300-400, or 400-500 amino acids) in length. In some embodiments, a protein fragment ranges from about 20-200 amino acids (e.g., between 20-30, 30-40, 40-50, 50-100, or 100-200 amino acids) in length.

In some embodiments, a portion or fragment of a gene modifying polypeptide is fused to an intein. The nuclease can be fused to the N-terminus or the C-terminus of the intein. In some embodiments, a portion or fragment of a fusion protein is fused to an intein and fused to an AAV capsid protein. The intein, nuclease and capsid protein can be fused together in any arrangement (e.g., nuclease-intein-capsid, intein-nuclease-capsid, capsid-intein-nuclease, etc.). In some embodiments, the N-terminus of an intein is fused to the C-terminus of a fusion protein and the C-terminus of the intein is fused to the N-terminus of an AAV capsid protein.

In some embodiments, an endonuclease domain (e.g., a nickase Cas9 domain) is fused to intein-N and a polypeptide comprising an RT domain is fused to an intein-C.

Exemplary nucleotide and amino acid sequences of intein-N domains and compatible intein-C domains are provided below:

DnaE Intein-N DNA:
TGCCTGTCATACGAAACCGAGATACTGACAGTAGAATATGGCCTTCTGCCAATCGGG
AAGATTGTGGAGAAACGGATAGAATGCACAGTTTACTCTGTCGATAACAATGGTAA
CATTTATACTCAGCCAGTTGCCCAGTGGCACGACCGGGGAGAGCAGGAAGTATTCG
AATACTGTCTGGAGGATGGAAGTCTCATTAGGGCCACTAAGGACCACAAATTTATG
ACAGTCGATGGCCAGATGCTGCCTATAGACGAAATCTTTGAGCGAGAGTTGGACCTC
ATGCGAGTTGACAACCTTCCTAAT (SEQ ID NO: 5029)

DnaE Intein-N Protein:
CLSYETEILTVEYGLLPIGKIVEKRIECTVYSVDNNGNIYTQPVAQWHDRGEQEVFEYCL
EDGSLIRATKDHKFMTVDGQMLPIDEIFERELDLMRVDNLPN (SEQ ID NO: 5030)

DnaE Intein-C DNA:
ATGATCAAGATAGCTACAAGGAAGTATCTTGGCAAACAAAACGTTTATGATATTGG
AGTCGAAAGAGATCACAACTTTGCTCTGAAGAACGGATTCATAGCTTCTAAT (SEQ
ID NO: 5031)

DnaE Intein-C Protein:
MIKIATRKYLGKQNVYDIGVERDHNFALKNGFIASN (SEQ ID NO: 5032)

Cfa-N DNA:
TGCCTGTCTTATGATACCGAGATACTTACCGTTGAATATGGCTTCTTGCCTATTGGAA
AGATTGTCGAAGAGAGAATTGAATGCACAGTATATACTGTAGACAAGAATGGTTTC
GTTTACACACAGCCCATTGCTCAATGGCACAATCGCGGCGAACAAGAAGTATTTGA
GTACTGTCTCGAGGATGGAAGCATCATACGAGCAACTAAAGATCATAAATTCATGA
CCACTGACGGGCAGATGTTGCCAATAGATGAGATATTCGAGCGGGGCTTGGATCTC
AAACAAGTGGATGGATTG CCA (SEQ ID NO: 5033)

Cfa-N Protein:
CLSYDTEILTVEYGFLPIGKIVEERIECTVYTVDKNGFVYTQPIAQWHNRGEQEVFEYCL
EDGSIIRATKDHKFMTTDGQMLPIDEIFERGLDLKQVDGLP (SEQ ID NO: 5034)

Cfa-C DNA:
ATGAAGAGGACTGCCGATGGATCAGAGTTTGAATCTCCCAAGAAGAAGAGGAAAGT
AAAGATAATATCTCGAAAAAGTCTTGGTACCCAAAATGTCTATGATATTGGAGTGGA
GAAAGATCACAACTTCCTTCTCAAGAACGGTCTCGTAGCCAGCAAC (SEQ ID NO:
5035)

Cfa-C Protein:
MKRTADGSEFESPKKKRKVKIISRKSLGTQNVYDIGVEKDHNFLLKNGLVASN (SEQ ID NO: 5036)

Additional domains

The gene modifying polypeptide can bind a target DNA sequence and template nucleic acid (e.g., template RNA), nick the target site, and write (e.g., reverse transcribe) the template into DNA, resulting in a modification of the target site. In some embodiments, additional domains may be added to the polypeptide to enhance the efficiency of the process. In some embodiments, the gene modifying polypeptide may contain an additional DNA ligation domain to join reverse transcribed DNA to the DNA of the target site. In some embodiments, the polypeptide may comprise a heterologous RNA-binding domain. In some embodiments, the polypeptide may comprise a domain having 5′ to 3′ exonuclease activity (e.g., wherein the 5′ to 3′ exonuclease activity increases repair of the alteration of the target site, e.g., in favor of alteration over the original genomic sequence). In some embodiments, the polypeptide may comprise a domain having 3′ to 5′ exonuclease activity, e.g., proof-reading activity. In some embodiments, the writing domain, e.g., RT domain, has 3′ to 5′ exonuclease activity, e.g., proof-reading activity.

Template nucleic acids

The gene modifying systems described herein can modify a host target DNA site using a template nucleic acid sequence. In some embodiments, the gene modifying systems described herein transcribe an RNA sequence template into host target DNA sites by target-primed reverse transcription (TPRT). By modifying DNA sequence(s) via reverse transcription of the RNA sequence template directly into the host genome, the gene modifying system can insert an object sequence into a target genome without the need for exogenous DNA sequences to be introduced into the host cell (unlike, for example, CRISPR systems), as well as eliminate an exogenous DNA insertion step. The gene modifying system can also delete a sequence from the target genome or introduce a substitution using an object sequence. Therefore, the gene modifying system provides a platform for the use of customized RNA sequence templates containing object sequences, e.g., sequences comprising heterologous gene coding and/or function information.

In some embodiments, the template nucleic acid comprises one or more sequence (e.g., 2 sequences) that binds the gene modifying polypeptide.

In some embodiments a system or method described herein comprises a single template nucleic acid (e.g., template RNA). In some embodiments a system or method described herein comprises a plurality of template nucleic acids (e.g., template RNAs). For example, a system described herein comprises a first RNA comprising (e.g., from 5´ to 3´) a sequence that binds the gene modifying polypeptide (e.g., the DNA-binding domain and/or the endonuclease domain, e.g., a gRNA) and a sequence that binds a target site (e.g., a second strand of a site in a target genome), and a second RNA (e.g., a template RNA) comprising (e.g., from 5´ to 3´) optionally a sequence that binds the gene modifying polypeptide (e.g., that specifically binds the RT domain), a heterologous object sequence, and a PBS sequence. In some embodiments, when the system comprises a plurality of nucleic acids, each nucleic acid comprises a conjugating domain. In some embodiments, a conjugating domain enables association of nucleic acid molecules, e.g., by hybridization of complementary sequences. For example, in some embodiments a first RNA comprises a first conjugating domain and a second RNA comprises a second conjugating domain, and the first and second conjugating domains are capable of hybridizing to one another, e.g., under stringent conditions. In some embodiments, the stringent conditions for hybridization include hybridization in 4x sodium chloride/sodium citrate (SSC), at about 65 C, followed by a wash in 1xSSC, at about 65 C.

In some embodiments, the template nucleic acid comprises RNA. In some embodiments, the template nucleic acid comprises DNA (e.g., single stranded or double stranded DNA).

In some embodiments, the template nucleic acid comprises one or more (e.g., 2) homology domains that have homology to the target sequence. In some embodiments, the homology domains are about 10-20, 20-50, or 50-100 nucleotides in length.

In some embodiments, a template RNA can comprise a gRNA sequence, e.g., to direct the gene modifying polypeptide to a target site of interest. In some embodiments, a template RNA comprises (e.g., from 5′ to 3′) (i) optionally a gRNA spacer that binds a target site (e.g., a second strand of a site in a target genome), (ii) optionally a gRNA scaffold that binds a polypeptide described herein (e.g., a gene modifying polypeptide or a Cas polypeptide), (iii) a heterologous object sequence comprising a mutation region (optionally the heterologous object

sequence comprises, from 5’ to 3’, a first homology region, a mutation region, and a second homology region), and (iv) a primer binding site (PBS) sequence comprising a 3′ target homology domain.

The template nucleic acid (e.g., template RNA) component of a genome editing system described herein typically is able to bind the gene modifying polypeptide of the system. In some embodiments the template nucleic acid (e.g., template RNA) has a 3′ region that is capable of binding a gene modifying polypeptide. The binding region, e.g., 3′ region, may be a structured RNA region, e.g., having at least 1, 2 or 3 hairpin loops, capable of binding the gene modifying polypeptide of the system. The binding region may associate the template nucleic acid (e.g., template RNA) with any of the polypeptide modules. In some embodiments, the binding region of the template nucleic acid (e.g., template RNA) may associate with an RNA-binding domain in the polypeptide. In some embodiments, the binding region of the template nucleic acid (e.g., template RNA) may associate with the reverse transcription domain of the gene modifying polypeptide (e.g., specifically bind to the RT domain). In some embodiments, the template nucleic acid (e.g., template RNA) may associate with the DNA binding domain of the polypeptide, e.g., a gRNA associating with a Cas9-derived DNA binding domain. In some embodiments, the binding region may also provide DNA target recognition, e.g., a gRNA hybridizing to the target DNA sequence and binding the polypeptide, e.g., a Cas9 domain. In some embodiments, the template nucleic acid (e.g., template RNA) may associate with multiple components of the polypeptide, e.g., DNA binding domain and reverse transcription domain.

In some embodiments the template RNA has a poly-A tail at the 3´ end. In some embodiments the template RNA does not have a poly-A tail at the 3´ end.

In some embodiments, the template nucleic acid is a template RNA. In some embodiments, the template RNA comprises one or more modified nucleotides. For example, in some embodiments, the template RNA comprises one or more deoxyribonucleotides. In some embodiments, regions of the template RNA are replaced by DNA nucleotides, e.g., to enhance stability of the molecule. For example, the 3´ end of the template may comprise DNA nucleotides, while the rest of the template comprises RNA nucleotides that can be reverse transcribed. For instance, in some embodiments, the heterologous object sequence is primarily or wholly made up of RNA nucleotides (e.g., at least 90%, 95%, 98%, or 99% RNA nucleotides). In some embodiments, the PBS sequence is primarily or wholly made up of DNA

nucleotides (e.g., at least 90%, 95%, 98%, or 99% DNA nucleotides). In other embodiments, the heterologous object sequence for writing into the genome may comprise DNA nucleotides. In some embodiments, the DNA nucleotides in the template are copied into the genome by a domain capable of DNA-dependent DNA polymerase activity. In some embodiments, the DNA-dependent DNA polymerase activity is provided by a DNA polymerase domain in the polypeptide. In some embodiments, the DNA-dependent DNA polymerase activity is provided by a reverse transcriptase domain that is also capable of DNA-dependent DNA polymerization, e.g., second strand synthesis. In some embodiments, the template molecule is composed of only DNA nucleotides.

In some embodiments, a system described herein comprises two nucleic acids which together comprise the sequences of a template RNA described herein. In some embodiments, the two nucleic acids are associated with each other non-covalently, e.g., directly associated with each other (e.g., via base pairing), or indirectly associated as part of a complex comprising one or more additional molecule.

A template RNA described herein may comprise, from 5’ to 3’: (1) a gRNA spacer; (2) a gRNA scaffold; (3) heterologous object sequence (4) a primer binding site (PBS) sequence. Each of these components is now described in more detail.

gRNA spacer and gRNA scaffold

A template RNA described herein may comprise a gRNA spacer that directs the gene modifying system to a target nucleic acid, and a gRNA scaffold that promotes association of the template RNA with the Cas domain of the gene modifying polypeptide. The systems described herein can also comprise a gRNA that is not part of a template nucleic acid. For example, a gRNA that comprises a gRNA spacer and gRNA scaffold, but not a heterologous object sequence or a PBS sequence, can be used, e.g., to induce second strand nicking, e.g., as described in the section herein entitled “Second Strand Nicking”.

In some embodiments, the gRNA is a short synthetic RNA composed of a scaffold sequence that participates in CRISPR-associated protein binding and a user-defined ~20 nucleotide targeting sequence for a genomic target. The structure of a complete gRNA was described by Nishimasu et al. Cell 156, P935-949 (2014). The gRNA (also referred to as sgRNA for single-guide RNA) consists of crRNA- and tracrRNA-derived sequences connected by an

artificial tetraloop. The crRNA sequence can be divided into guide (20 nt) and repeat (12 nt) regions, whereas the tracrRNA sequence can be divided into anti-repeat (14 nt) and three tracrRNA stem loops (Nishimasu et al. Cell 156, P935-949 (2014)). In practice, guide RNA sequences are generally designed to have a length of between 17 – 24 nucleotides (e.g., 19, 20, or 21 nucleotides) and be complementary to a targeted nucleic acid sequence. Custom gRNA generators and algorithms are available commercially for use in the design of effective guide RNAs. In some embodiments, the gRNA comprises two RNA components from the native CRISPR system, e.g. crRNA and tracrRNA. As is well known in the art, the gRNA may also comprise a chimeric, single guide RNA (sgRNA) containing sequence from both a tracrRNA (for binding the nuclease) and at least one crRNA (to guide the nuclease to the sequence targeted for editing/binding). Chemically modified sgRNAs have also been demonstrated to be effective for use with CRISPR-associated proteins; see, for example, Hendel et al. (2015) Nature Biotechnol., 985 – 991. In some embodiments, a gRNA spacer comprises a nucleic acid sequence that is complementary to a DNA sequence associated with a target gene.

In some embodiments, the region of the template nucleic acid, e.g., template RNA, comprising the gRNA adopts an underwound ribbon-like structure of gRNA bound to target DNA (e.g., as described in Mulepati et al. Science 19 Sep 2014:Vol. 345, Issue 6203, pp. 1479-1484). Without wishing to be bound by theory, this non-canonical structure is thought to be facilitated by rotation of every sixth nucleotide out of the RNA-DNA hybrid. Thus, in some embodiments, the region of the template nucleic acid, e.g., template RNA, comprising the gRNA may tolerate increased mismatching with the target site at some interval, e.g., every sixth base. In some embodiments, the region of the template nucleic acid, e.g., template RNA, comprising the gRNA comprising homology to the target site may possess wobble positions at a regular interval, e.g., every sixth base, that do not need to base pair with the target site.

In some embodiments, the template nucleic acid (e.g., template RNA) has at least 15, 16, 17, 18, 19, 20, 21, 22, 23, or 24 bases of at least 80%, 85%, 90%, 95%, 99%, or 100% homology to the target site, e.g., at the 5’ end, e.g., comprising a gRNA spacer sequence of length appropriate to the Cas9 domain of the gene modifying polypeptide (Table 8).

In some embodiments, a Cas9 derivative with enhanced activity may be used in the gene modification polypeptide. In some embodiments, a Cas9 derivative may comprise mutations that improve activity of the HNH endonuclease domain, e.g., SpyCas9 R221K, N394K, or mutations

that improve R-loop formation, e.g., SpyCas9 L1245V, or comprise a combination of such mutations, e.g., SpyCas9 R221K/N394K, SpyCas9 N394K/L1245V, SpyCas9 R221K/L1245V, or SpyCas9 R221K/N394K/L1245V (see, e.g., Spencer and Zhang Sci Rep 7:16836 (2017), the Cas9 derivatives and comprising mutations of which are incorporated herein by reference). In some embodiments, a Cas9 derivative may comprise one or more types of mutations described herein, e.g., PAM-modifying mutations, protein stabilizing mutations, activity enhancing mutations, and/or mutations partially or fully inactivating one or two endonuclease domains relative to the parental enzyme (e.g., one or more mutations to abolish endonuclease activity towards one or both strands of a target DNA, e.g., a nickase or catalytically dead enzyme). In some embodiments, a Cas9 enzyme used in a system described herein may comprise mutations that confer nickase activity toward the enzyme (e.g., SpyCas9 N863A or H840A) in addition to mutations improving catalytic efficiency (e.g., SpyCas9 R221K, N394K, and/or L1245V). In some embodiments, a Cas9 enzyme used in a system described herein is a SpyCas9 enzyme or derivative that further comprises an N863A mutation to confer nickase activity in addition to R221K and N394K mutations to improve catalytic efficiency.

Table 12 provides parameters to define components for designing gRNA and/or Template RNAs to apply Cas variants listed in Table 8 for gene modifying. The cut site indicates the validated or predicted protospacer adjacent motif (PAM) requirements, validated or predicted location of cut site (relative to the most upstream base of the PAM site). The gRNA for a given enzyme can be assembled by concatenating the crRNA, Tetraloop, and tracrRNA sequences, and further adding a 5′ spacer of a length within Spacer (min) and Spacer (max) that matches a protospacer at a target site. Further, the predicted location of the ssDNA nick at the target is important for designing a PBS sequence of a Template RNA that can anneal to the sequence immediately 5′ of the nick in order to initiate target primed reverse transcription. In some embodiments, a gRNA scaffold described herein comprises a nucleic acid sequence comprising, in the 5’ to 3’ direction, a crRNA of Table 12, a tetraloop from the same row of Table 12, and a tracrRNA from the same row of Table 12, or a sequence having at least 70%, 80%, 85%, 90%, 95%, or 99% identity thereto. In some embodiments, the gRNA or template RNA comprising the scaffold further comprises a gRNA spacer having a length within the Spacer (min) and Spacer (max) indicated in the same row of Table 12. In some embodiments, the gRNA or template RNA having a sequence according to Table 12 is comprised by a system that further

comprises a gene modifying polypeptide, wherein the gene modifying polypeptide comprises a Cas domain described in the same row of Table 12.

Table 12 Parameters to define components for designing gRNA and/or Template RNAs to apply Cas variants listed in Table 8 in gene modifying systems.

Variant	PAM(s)	Cut	Tier	Spacer (min)	Spacer (max)	crRNA	SEQ ID NO:	Tetraloop	tracrRNA	SEQ ID NO:
Nme2Cas9	NNNNCC	-3	1	22	24	GTTGTAGC TCCCTTTCT CATTTCG	10,051	GAAA	CGAAATGAGAACCGTTGCTACAATAAGGC CGTCTGAAAAGATGTGCCGCAACGCTCTG CCCCTTAAAGCTTCTGCTTTAAGGGGCATC GTTTA	10,151
PpnCas9	NNNNRTT		1	21	24	GTTGTAGC TCCCTTTTT CATTTCGC	10,052	GAAA	GCGAAATGAAAAACGTTGTTACAATAAGA GATGAATTTCTCGCAAAGCTCTGCCTCTTG AAATTTCGGTTTCAAGAGGCATC	10,152
SauCas9	NNGRR;N NGRRT	-3	1	21	23	GTTTTAGT ACTCTG	10,053	GAAA	CAGAATCTACTAAAACAAGGCAAAATGCC GTGTTTATCTCGTCAACTTGTTGGCGAGA	10,153
SauCas9-KKH	NNNRR;N NNRRT	-3	1	21	21	GTTTTAGT ACTCTG	10,054	GAAA	CAGAATCTACTAAAACAAGGCAAAATGCC GTGTTTATCTCGTCAACTTGTTGGCGAGA	10,154
SauriCas9	NNGG	-3	1	21	21	GTTTTAGT ACTCTG	10,055	GAAA	CAGAATCTACTAAAACAAGGCAAAATGCC GTGTTTATCTCGTCAACTTGTTGGCGAGA	10,155
SauriCas9-KKH	NNRG	-3	1	21	21	GTTTTAGT ACTCTG	10,056	GAAA	CAGAATCTACTAAAACAAGGCAAAATGCC GTGTTTATCTCGTCAACTTGTTGGCGAGA	10,156
ScaCas9-Sc++	NNG	-3	1	20	20	GTTTTAGA GCTA	10,057	GAAA	TAGCAAGTTAAAATAAGGCTAGTCCGTTA TCAACTTGAAAAAGTGGCACCGAGTCGGT GC	10,157
SpyCas9	NGG	-3	1	20	20	GTTTTAGA GCTA	10,058	GAAA	TAGCAAGTTAAAATAAGGCTAGTCCGTTA TCAACTTGAAAAAGTGGCACCGAGTCGGT GC	10,158
SpyCas9_i_v1	NGG	-3	1	20	20	GTTTTAGA GCTA	10,058	GAAA	TAGCAAGTTAAAATAAGGCTAGTCCGTTA TCAACTTGGACTTCGGTCCAAGTGGCACC GAGTCGGTGC	10,193
SpyCas9_i_v2	NGG	-3	1	20	20	GTTTTAGA GCTA	10,058	GAAA	TAGCAAGTTAAAATAAGGCTAGTCCGTTA TCAACTTGGAGCTTGCTCCAAGTGGCACC GAGTCGGTGC	10,194

SpyCas9_i_v3	NGG	-3	1	20	20	GTTTTAGAGCTA	10,058	GAAA	GTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCGACTTGAAAAAGTCGCACCGAGTCGGTGC	10,195
SpyCas9-NG	NG (NGG=NGA=NGT>NGC)	-3	1	20	20	GTTTTAGAGCTA	10,059	GAAA	TAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGC	10,159
SpyCas9-SpRY	NRN>NYN	-3	1	20	20	GTTTTAGAGCTA	10,060	GAAA	TAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGC	10,160
St1Cas9	NNAGAAW>NNAGGAW=NNGGAAW	-3	1	20	20	GTCTTTGTACTCTG	10,061	GTAC	CAGAAGCTACAAAGATAAGGCTTCATGCCGAAATCAACACCCTGTCATTTTATGGCAGGGTGTTTT	10,161
BlatCas9	NNNNCNAA>NNNNCNDD>NNNNC	-3	1	19	23	GCTATAGTTCCTTACT	10,062	GAAA	GGTAAGTTGCTATAGTAAGGGCAACAGACCCGAGGCGTTGGGGATCGCCTAGCCCGTGTTTACGGGCTCTCCCCATATTCAAAATAATGACAGACGAGCACCTTGGAGCATTTATCTCCGAGGTGCT	10,162
cCas9-v16	NNVACT;NNVATGM;NNVATT;NNVGCT;NNVGTG;NNVGTT	-3	2	21	21	GTCTTAGTACTCTG	10,063	GAAA	CAGAATCTACTAAGACAAGGCAAAATGCCGTGTTTATCTCGTCAACTTGTTGGCGAGA	10,163
cCas9-v17	NNVRRN	-3	2	21	21	GTCTTAGTACTCTG	10,064	GAAA	CAGAATCTACTAAGACAAGGCAAAATGCCGTGTTTATCTCGTCAACTTGTTGGCGAGA	10,164
cCas9-v21	NNVACT;NNVATGM;NNVATT;NNVGCT;NNVGTG;NNVGTT	-3	2	21	21	GTCTTAGTACTCTG	10,065	GAAA	CAGAATCTACTAAGACAAGGCAAAATGCCGTGTTTATCTCGTCAACTTGTTGGCGAGA	10,165
cCas9-v42	NNVRRN	-3	2	21	21	GTCTTAGTACTCTG	10,066	GAAA	CAGAATCTACTAAGACAAGGCAAAATGCCGTGTTTATCTCGTCAACTTGTTGGCGAGA	10,166

CdiCas9	NNRHHHY;NNRAAAY		2	22	22	ACTGGGGTTCAG	10,067	GAAA	CTGAACCTCAGTAAGCATTGGCTCGTTTCCAATGTTGATTGCTCCGCCGGTGCTCCTTATTTTTAAGGGCGCCGGC	10,167
CjeCas9	NNNNRYAC	-3	2	21	23	GTTTTAGTCCCT	10,068	GAAA	AGGGACTAAAATAAAGAGTTTGCGGGACTCTGCGGGGTTACAATCCCCTAAAACCGC	10,168
GeoCas9	NNNNCRAA		2	21	23	GTCATAGTTCCCCTGA	10,069	GAAA	TCAGGGTTACTATGATAAGGGCTTTCTGCCTAAGGCAGACTGACCCGCGGCGTTGGGGATCGCCTGTCGCCCGCTTTTGGCGGGCATTCCCCATCCTT	10,169
iSpyMacCas9	NAAN	-3	2	19	21	GTTTTAGAGCTA	10,070	GAAA	TAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGC	10,170
NmeCas9	NNNNGAYT;NNNNGYTT;NNNNGAYA;NNNNGTCT	-3	2	20	24	GTTGTAGCTCCCTTTCTCATTTCG	10,071	GAAA	CGAAATGAGAACCGTTGCTACAATAAGGCCGTCTGAAAAGATGTGCCGCAACGCTCTGCCCCTTAAAGCTTCTGCTTTAAGGGGCATCGTTTA	10,171
ScaCas9	NNG	-3	2	20	20	GTTTTAGAGCTA	10,072	GAAA	TAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGC	10,172
ScaCas9-HiFi-Sc++	NNG	-3	2	20	20	GTTTTAGAGCTA	10,073	GAAA	TAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGC	10,173
SpyCas9-3var-NRRH	NRRH	-3	2	20	20	GTTTAAGAGCTATGCTG	10,074	GAAA	CAGCATAGCAAGTTTAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGC	10,174
SpyCas9-3var-NRTH	NRTH	-3	2	20	20	GTTTAAGAGCTATGCTG	10,075	GAAA	CAGCATAGCAAGTTTAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGC	10,175
SpyCas9-3var-NRCH	NRCH	-3	2	20	20	GTTTAAGAGCTATGCTG	10,076	GAAA	CAGCATAGCAAGTTTAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGC	10,176

SpyCas9-HF1	NGG	-3	2	20	20	GTTTTAGAGCTA	10,077	GAAA	TAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGC	10,177
SpyCas9-QQR1	NAAG	-3	2	20	20	GTTTTAGAGCTA	10,078	GAAA	TAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGC	10,178
SpyCas9-SpG	NGN	-3	2	20	20	GTTTTAGAGCTA	10,079	GAAA	TAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGC	10,179
SpyCas9-VQR	NGAN	-3	2	20	20	GTTTTAGAGCTA	10,080	GAAA	TAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGC	10,180
SpyCas9-VRER	NGCG	-3	2	20	20	GTTTTAGAGCTA	10,081	GAAA	TAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGC	10,181
SpyCas9-xCas	NG;GAA;GAT	-3	2	20	20	GTTTAAGAGCTATGCTG	10,082	GAAA	CAGCATAGCAAGTTTAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGC	10,182
SpyCas9-xCas-NG	NG	-3	2	20	20	GTTTAAGAGCTATGCTG	10,083	GAAA	CAGCATAGCAAGTTTAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGC	10,183
St1Cas9-CNRZ1066	NNACAA	-3	2	20	20	GTCTTTGTACTCTG	10,084	GTAC	CAGAAGCTACAAAGATAAGGCTTCATGCCGAAATCAACACCCTGTCATTTTATGGCAGGGTGTTTT	10,184
St1Cas9-LMG1831	NNGCAA	-3	2	20	20	GTCTTTGTACTCTG	10,085	GTAC	CAGAAGCTACAAAGATAAGGCTTCATGCCGAAATCAACACCCTGTCATTTTATGGCAGGGTGTTTT	10,185
St1Cas9-MTH17CL396	NNAAAA	-3	2	20	20	GTCTTTGTACTCTG	10,086	GTAC	CAGAAGCTACAAAGATAAGGCTTCATGCCGAAATCAACACCCTGTCATTTTATGGCAGGGTGTTTT	10,186
St1Cas9-TH1477	NNGAAA	-3	2	20	20	GTCTTTGTACTCTG	10,087	GTAC	CAGAAGCTACAAAGATAAGGCTTCATGCCGAAATCAACACCCTGTCATTTTATGGCAGGGTGTTTT	10,187

sRGN3.1	NNGG		1	21	23	GTTTTAGTACTCTG	10,088	GAAA	CAGAATCTACTGAAACAAGACAATATGTCGTGTTTATCCCATCAATTTATTGGTGGGATTTT	10,188
sRGN3.3	NNGG		1	21	23	GTTTTAGTACTCTG	10,089	GAAA	CAGAATCTACTGAAACAAGACAATATGTCGTGTTTATCCCATCAATTTATTGGTGGGATTTT	10,189

Herein, when an RNA sequence (e.g., a template RNA sequence) is said to comprise a particular sequence (e.g., a sequence of Table 12 or a portion thereof) that comprises thymine (T), it is of course understood that the RNA sequence may (and frequently does) comprise uracil (U) in place of T. For instance, the RNA sequence may comprise U at every position shown as T in the sequence in Table 12. More specifically, the present disclosure provides an RNA sequence according to every gRNA scaffold sequence of Table 12, wherein the RNA sequence has a U in place of each T in the sequence in Table 12. Additionally, it is understood that terminal Us and Ts may optionally be added or removed from tracrRNA sequences and may be modified or unmodified when provided as RNA. Without wishing to be bound by example, versions of gRNA scaffold sequences alternative to those exemplified in Table 12 may also function with the different Cas9 enzymes or derivatives thereof exemplified in Table 8, e.g., alternate gRNA scaffold sequences with nucleotide additions, substitutions, or deletions, e.g., sequences with stem-loop structures added or removed. It is contemplated herein that the gRNA scaffold sequences represent a component of gene modifying systems that can be similarly optimized for a given system, Cas-RT fusion polypeptide, indication, target mutation, template RNA, or delivery vehicle.

Heterologous object sequence

A template RNA described herein may comprise a heterologous object sequence that the gene modifying polypeptide can use as a template for reverse transcription, to write a desired sequence into the target nucleic acid. In some embodiments, the heterologous object sequence comprises, from 5' to 3', a post-edit homology region, the mutation region, and a pre-edit homology region. Without wishing to be bound by theory, an RT performing reverse transcription on the template RNA first reverse transcribes the pre-edit homology region, then the mutation region, and then the post-edit homology region, thereby creating a DNA strand comprising the desired mutation with a homology region on either side.

In some embodiments, the heterologous object sequence is at least 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 120, 140, 160, 180, 200, 500, or 1,000 nucleotides (nts) in length, or at least 1, 1.5, 2, 2.5, 3, 3.5, 4, 4.5, 5, 5.5, 6, 6.5, 7, 7.5, 8, 8.5, 9, 9.5, or 10 kilobases in length. In some embodiments, the heterologous object sequence is no more than 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 120, 140, 160, 180, 200, 500, 1,000, or 2000 nucleotides (nts) in length, or no more than 20, 15, 10, 9, 8, 7, 6, 5, 4, or 3 kilobases in length. In some embodiments, the heterologous object sequence is 30-1000, 40-1000, 50-1000, 60-1000, 70-1000, 74-1000, 75-1000, 76-1000, 77-1000, 78-1000, 79-1000, 80-1000, 85-1000, 90-1000, 100-1000, 120-1000, 140-1000, 160-1000, 180-1000, 200-1000, 500-1000, 30-500, 40-500, 50-500, 60-500, 70-500, 74-500, 75-500, 76-500, 77-500, 78-500, 79-500, 80-500, 85-500, 90-500, 100-500, 120-500, 140-500, 160-500, 180-500, 200-500, 30-200, 40-200, 50-200, 60-200, 70-200, 74-200, 75-200, 76-200, 77-200, 78-200, 79-200, 80-200, 85-200, 90-200, 100-200, 120-200, 140-200, 160-200, 180-200, 30-100, 40-100, 50-100, 60-100, 70-100, 74-100, 75-100, 76-100, 77-100, 78-100, 79-100, 80-100, 85-100, or 90-100 nucleotides (nts) in length, or 1-20, 1-15, 1-10, 1-9, 1-8, 1-7, 1-6, 1-5, 1-4, 1-3, 1-2, 2-20, 2-15, 2-10, 2-9, 2-8, 2-7, 2-6, 2-5, 2-4, 2-3, 3-20, 3-15, 3-10, 3-9, 3-8, 3-7, 3-6, 3-5, 3-4, 4-20, 4-15, 4-10, 4-9, 4-8, 4-7, 4-6, 4-5, 5-20, 5-15, 5-10, 5-9, 5-8, 5-7, 5-6, 6-20, 6-15, 6-10, 6-9, 6-8, 6-7, 7-20, 7-15, 7-10, 7-9, 7-8, 8-20, 8-15, 8-

10, 8-9, 9-20, 9-15, 9-10, 10-15, 10-20, or 15-20 kilobases in length. In some embodiments, the heterologous object sequence is 10-100, 10-90, 10-80, 10-70, 10-60, 10-50, 10-40, 10-30, or 10-20 nt in length, e.g., 10-80, 10-50, or 10-20 nt in length, e.g., about10-20 nt in length. In some embodiments, the heterologous object sequence is 8-30, 9-25, 10-20, 11-16, or 12-15 nucleotides in length, e.g., is 11-16 nt in length. Without wishing to be bound by theory, in some embodiments, a larger insertion size, larger region of editing (e.g., the distance between a first edit/substitution and a second edit/substitution in the target region), and/or greater number of desired edits (e.g., mismatches of the heterologous object sequence to the target genome), may result in a longer optimal heterologous object sequence.

In certain embodiments, the template nucleic acid comprises a customized RNA sequence template which can be identified, designed, engineered and constructed to contain sequences altering or specifying host genome function, for example by introducing a heterologous coding region into a genome; affecting or causing exon structure/alternative splicing, e.g., leading to exon skipping of one or more exons; causing disruption of an endogenous gene, e.g., creating a genetic knockout; causing transcriptional activation of an endogenous gene; causing epigenetic regulation of an endogenous DNA; causing up-regulation of one or more operably linked genes, e.g., leading to gene activation or overexpression; causing down-regulation of one or more operably linked genes, e.g., creating a genetic knock-down; etc. In certain embodiments, a customized RNA sequence template can be engineered to contain sequences coding for exons and/or transgenes, provide binding sites for transcription factor activators, repressors, enhancers, etc., and combinations thereof. In some embodiments, a customized template can be engineered to encode a nucleic acid or peptide tag to be expressed in an endogenous RNA transcript or endogenous protein operably linked to the target site. In other embodiments, the coding sequence can be further customized with splice donor sites, splice acceptor sites, or poly-A tails.

The template nucleic acid (e.g., template RNA) of the system typically comprises an object sequence (e.g., a heterologous object sequence) for writing a desired sequence into a target DNA. The object sequence may be coding or non-coding. The template nucleic acid (e.g., template RNA) can be designed to result in insertions, mutations, or deletions at the target DNA locus. In some embodiments, the template nucleic acid (e.g., template RNA) may be designed to cause an insertion in the target DNA. For example, the template nucleic acid (e.g., template RNA) may contain a heterologous sequence, wherein the reverse transcription will result in

insertion of the heterologous sequence into the target DNA. In other embodiments, the RNA template may be designed to introduce a deletion into the target DNA. For example, the template nucleic acid (e.g., template RNA) may match the target DNA upstream and downstream of the desired deletion, wherein the reverse transcription will result in the copying of the upstream and downstream sequences from the template nucleic acid (e.g., template RNA) without the intervening sequence, e.g., causing deletion of the intervening sequence. In other embodiments, the template nucleic acid (e.g., template RNA) may be designed to introduce an edit into the target DNA. For example, the template RNA may match the target DNA sequence with the exception of one or more nucleotides, wherein the reverse transcription will result in the copying of these edits into the target DNA, e.g., resulting in mutations, e.g., transition or transversion mutations.

In some embodiments, writing of an object sequence into a target site results in the substitution of nucleotides, e.g., where the full length of the object sequence corresponds to a matching length of the target site with one or more mismatched bases. In some embodiments, a heterologous object sequence may be designed such that a combination of sequence alterations may occur, e.g., a simultaneous addition and deletion, addition and substitution, or deletion and substitution.

In some embodiments, the heterologous object sequence may contain an open reading frame or a fragment of an open reading frame. In some embodiments the heterologous object sequence has a Kozak sequence. In some embodiments the heterologous object sequence has an internal ribosome entry site. In some embodiments the heterologous object sequence has a self-cleaving peptide such as a T2A or P2A site. In some embodiments the heterologous object sequence has a start codon. In some embodiments the template RNA has a splice acceptor site. In some embodiments the template RNA has a splice donor site. Exemplary splice acceptor and splice donor sites are described in WO2016044416, incorporated herein by reference in its entirety. Exemplary splice acceptor site sequences are known to those of skill in the art. In some embodiments the template RNA has a microRNA binding site downstream of the stop codon. In some embodiments the template RNA has a polyA tail downstream of the stop codon of an open reading frame. In some embodiments the template RNA comprises one or more exons. In some embodiments the template RNA comprises one or more introns. In some embodiments the template RNA comprises a eukaryotic transcriptional terminator. In some embodiments the

template RNA comprises an enhanced translation element or a translation enhancing element. In some embodiments the RNA comprises the human T-cell leukemia virus (HTLV-1) R region. In some embodiments the RNA comprises a posttranscriptional regulatory element that enhances nuclear export, such as that of Hepatitis B Virus (HPRE) or Woodchuck Hepatitis Virus (WPRE).

In some embodiments, the heterologous object sequence may contain a non-coding sequence. For example, the template nucleic acid (e.g., template RNA) may comprise a regulatory element, e.g., a promoter or enhancer sequence or miRNA binding site. In some embodiments, integration of the object sequence at a target site will result in upregulation of an endogenous gene. In some embodiments, integration of the object sequence at a target site will result in downregulation of an endogenous gene. In some embodiments the template nucleic acid (e.g., template RNA) comprises a tissue specific promoter or enhancer, each of which may be unidirectional or bidirectional. In some embodiments the promoter is an RNA polymerase I promoter, RNA polymerase II promoter, or RNA polymerase III promoter. In some embodiments the promoter comprises a TATA element. In some embodiments the promoter comprises a B recognition element. In some embodiments the promoter has one or more binding sites for transcription factors.

In some embodiments, the template nucleic acid (e.g., template RNA) comprises a site that coordinates epigenetic modification. In some embodiments, the template nucleic acid (e.g., template RNA) comprises a chromatin insulator. For example, the template nucleic acid (e.g., template RNA) comprises a CTCF site or a site targeted for DNA methylation.

In some embodiments, the template nucleic acid (e.g., template RNA) comprises a gene expression unit composed of at least one regulatory region operably linked to an effector sequence. The effector sequence may be a sequence that is transcribed into RNA (e.g., a coding sequence or a non-coding sequence such as a sequence encoding a micro RNA).

In some embodiments, the heterologous object sequence of the template nucleic acid (e.g., template RNA) is inserted into a target genome in an endogenous intron. In some embodiments, the heterologous object sequence of the template nucleic acid (e.g., template RNA) is inserted into a target genome and thereby acts as a new exon. In some embodiments, the insertion of the heterologous object sequence into the target genome results in replacement of a natural exon or the skipping of a natural exon.

The template nucleic acid (e.g., template RNA) can be designed to result in insertions, mutations, or deletions at the target DNA locus. In some embodiments, the template nucleic acid (e.g., template RNA) may be designed to cause an insertion in the target DNA. For example, the template nucleic acid (e.g., template RNA) may contain a heterologous object sequence, wherein the reverse transcription will result in insertion of the heterologous object sequence into the target DNA. In other embodiments, the RNA template may be designed to write a deletion into the target DNA. For example, the template nucleic acid (e.g., template RNA) may match the target DNA upstream and downstream of the desired deletion, wherein the reverse transcription will result in the copying of the upstream and downstream sequences from the template nucleic acid (e.g., template RNA) without the intervening sequence, e.g., causing deletion of the intervening sequence. In other embodiments, the template nucleic acid (e.g., template RNA) may be designed to write an edit into the target DNA. For example, the template RNA may match the target DNA sequence with the exception of one or more nucleotides, wherein the reverse transcription will result in the copying of these edits into the target DNA, e.g., resulting in mutations, e.g., transition or transversion mutations.

In some embodiments, the pre-edit homology domain comprises a nucleic acid sequence having 100% sequence identity with a nucleic acid sequence comprised in a target nucleic acid molecule.

In some embodiments, the post-edit homology domain comprises a nucleic acid sequence having 100% sequence identity with a nucleic acid sequence comprised in a target nucleic acid molecule.

PBS sequence

In some embodiments, a template nucleic acid (e.g., template RNA) comprises a PBS sequence. In some embodiments, a PBS sequence is disposed 3′ of the heterologous object sequence and is complementary to a sequence adjacent to a site to be modified by a system described herein, or comprises no more than 1, 2, 3, 4, or 5 mismatches to a sequence complementary to the sequence adjacent to a site to be modified by the system/gene modifying polypeptide. In some embodiments, the PBS sequence binds within 1, 2, 3, 4, 5, 6, 7, 8, 9, or 10 nucleotides of a nick site in the target nucleic acid molecule. In some embodiments, binding of the PBS sequence to the target nucleic acid molecule permits initiation of target-primed reverse transcription (TPRT), e.g., with the 3′ homology domain acting as a primer for TPRT. In some

embodiments, the PBS sequence is 3-5, 5-10, 10-30, 10-25, 10-20, 10-19, 10-18, 10-17, 10-16, 10-15, 10-14, 10-13, 10-12, 10-11, 11-30, 11-25, 11-20, 11-19, 11-18, 11-17, 11-16, 11-15, 11-14, 11-13, 11-12, 12-30, 12-25, 12-20, 12-19, 12-18, 12-17, 12-16, 12-15, 12-14, 12-13, 13-30, 13-25, 13-20, 13-19, 13-18, 13-17, 13-16, 13-15, 13-14, 14-30, 14-25, 14-20, 14-19, 14-18, 14-17, 14-16, 14-15, 15-30, 15-25, 15-20, 15-19, 15-18, 15-17, 15-16, 16-30, 16-25, 16-20, 16-19, 16-18, 16-17, 17-30, 17-25, 17-20, 17-19, 17-18, 18-30, 18-25, 18-20, 18-19, 19-30, 19-25, 19-20, 20-30, 20-25, or 25-30 nucleotides in length, e.g., 10-17, 12-16, or 12-14 nucleotides in length. In some embodiments, the PBS sequence is 5-20, 8-16, 8-14, 8-13, 9-13, 9-12, or 10-12 nucleotides in length, e.g., 9-12 nucleotides in length.

The template nucleic acid (e.g., template RNA) may have some homology to the target DNA. In some embodiments, the template nucleic acid (e.g., template RNA) PBS sequence domain may serve as an annealing region to the target DNA, such that the target DNA is positioned to prime the reverse transcription of the template nucleic acid (e.g., template RNA). In some embodiments the template nucleic acid (e.g., template RNA) has at least 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 20, 25, 30, 35, 40, 45, 50, 60, 70, 80, 90, 100, 110, 120, 130, 140, 150, 175, 200 or more bases of exact homology to the target DNA at the 3′ end of the RNA. In some embodiments the template nucleic acid (e.g., template RNA) has at least 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 20, 25, 30, 35, 40, 45, 50, 60, 70, 80, 90, 100, 110, 120, 130, 140, 150, 175, 200 or more bases of at least 50%, 60%, 70%, 80%, 85%, 90%, 95%, 97%, 98%, 99% or 100% homology to the target DNA, e.g., at the 5′ end of the template nucleic acid (e.g., template RNA).

Exemplary template sequences

In some embodiments of the systems and methods herein, the template RNA comprises a gRNA spacer comprising the core nucleotides of a gRNA spacer sequence of Table 1A, Table 1B, Table 1C, or Table 1D. In some embodiments, the gRNA spacer additionally comprises one or more (e.g., 2, 3, or all) consecutive nucleotides starting with the 3’ end of the flanking nucleotides of the gRNA spacer. In some embodiments, the template RNA comprising a sequence of Table 11A, Table 1B, Table 1C, or Table 1D is comprised by a system that further comprises a gene modifying polypeptide having an RT domain listed in the same line of Table 11A, Table 1B, Table 1C, or Table 1D. RT domain amino acid sequences can be found, e.g., in Table 6 herein.

Table 1A: Exemplary gRNA spacer Cas pairs for correcting the pathogenic R408W mutation

Table 1A provides a gRNA database for correcting the pathogenic R408W mutation in PAH. List of spacers, PAMs, and Cas variants for generating a nick at an appropriate position to enable installation of a desired genomic edit with a gene modifying system. The spacers in this table are designed to be used with a gene modifying polypeptide comprising a nickase variant of the Cas species indicated in the table. Tables 2A, 3A, and 4A detail the other components of the system and are organized such that the ID number shown here in Column 1 ("ID") is meant to correspond to the same ID number in Tables 2A, 3A, and 4A.

ID	PAM sequence	gRNA spacer	SEQ ID NO	Cas species	distance	Overlaps mutation
1	CCC	TTGCTGCCACAATACCTTGG	17033	SpyCas9-SpRY	0	0
2	GG	AGCGAACTGAGAAGGGCCAA	17034	SpyCas9-NG	1	0
3	GG	AGCGAACTGAGAAGGGCCAA	17035	SpyCas9-xCas	1	0
4	GG	AGCGAACTGAGAAGGGCCAA	17036	SpyCas9-xCas-NG	1	0
5	GGT	AGCGAACTGAGAAGGGCCAA	17037	SpyCas9-SpG	1	0
6	GGT	AGCGAACTGAGAAGGGCCAA	17038	SpyCas9-SpRY	1	0
7	GCC	TTTGCTGCCACAATACCTTG	17039	SpyCas9-SpRY	1	0
8	GGTA	AGCGAACTGAGAAGGGCCAA	17040	SpyCas9-3var-NRTH	1	0
9	AGGTATT	CGTAGCGAACTGAGAAGGGCCA	17041	CdiCas9	2	0
10	AGGTATT	gtcGTAGCGAACTGAGAAGGGCCA	17042	PpnCas9	2	0
11	AGG	TAGCGAACTGAGAAGGGCCA	17043	ScaCas9	2	0
12	AGG	TAGCGAACTGAGAAGGGCCA	17044	ScaCas9-HiFi-Sc++	2	0
13	AGG	TAGCGAACTGAGAAGGGCCA	17045	ScaCas9-Sc++	2	0
14	AGG	TAGCGAACTGAGAAGGGCCA	17046	SpyCas9	2	0
15	AGG	TAGCGAACTGAGAAGGGCCA	17047	SpyCas9-HF1	2	0
16	AGG	TAGCGAACTGAGAAGGGCCA	17048	SpyCas9-SpG	2	0

17	AGG	TAGCGAACTGAGAAGGGCCA	17049	SpyCas9-SpRY	2	0
18	GG	CTTTGCTGCCACAATACCTT	17050	SpyCas9-NG	2	0
19	GG	CTTTGCTGCCACAATACCTT	17051	SpyCas9-xCas	2	0
20	GG	CTTTGCTGCCACAATACCTT	17052	SpyCas9-xCas-NG	2	0
21	AG	TAGCGAACTGAGAAGGGCCA	17053	SpyCas9-NG	2	0
22	AG	TAGCGAACTGAGAAGGGCCA	17054	SpyCas9-xCas	2	0
23	AG	TAGCGAACTGAGAAGGGCCA	17055	SpyCas9-xCas-NG	2	0
24	GGC	CTTTGCTGCCACAATACCTT	17056	SpyCas9-SpG	2	0
25	GGC	CTTTGCTGCCACAATACCTT	17057	SpyCas9-SpRY	2	0
26	GGCCC	gaacTTTGCTGCCACAATACCTT	17058	BlatCas9	2	0
27	AGGT	TAGCGAACTGAGAAGGGCCA	17059	SpyCas9-3var-NRRH	2	0
28	GGCC	CTTTGCTGCCACAATACCTT	17060	SpyCas9-3var-NRCH	2	0
29	tGGCCC	agGAACTTTGCTGCCACAATACCT	17061	Nme2Cas9	3	1
30	aAGG	CGTAGCGAACTGAGAAGGGCC	17062	SauriCas9	3	1
31	aAGG	CGTAGCGAACTGAGAAGGGCC	17063	SauriCas9-KKH	3	1
32	tGG	ACTTTGCTGCCACAATACCT	17064	ScaCas9	3	1
33	tGG	ACTTTGCTGCCACAATACCT	17065	ScaCas9-HiFi-Sc++	3	1
34	tGG	ACTTTGCTGCCACAATACCT	17066	ScaCas9-Sc++	3	1
35	tGG	ACTTTGCTGCCACAATACCT	17067	SpyCas9	3	1
36	tGG	ACTTTGCTGCCACAATACCT	17068	SpyCas9-HF1	3	1
37	tGG	ACTTTGCTGCCACAATACCT	17069	SpyCas9-SpG	3	1
38	tGG	ACTTTGCTGCCACAATACCT	17070	SpyCas9-SpRY	3	1
39	aAG	GTAGCGAACTGAGAAGGGCC	17071	ScaCas9	3	1
40	aAG	GTAGCGAACTGAGAAGGGCC	17072	ScaCas9-HiFi-Sc++	3	1
41	aAG	GTAGCGAACTGAGAAGGGCC	17073	ScaCas9-Sc++	3	1
42	aAG	GTAGCGAACTGAGAAGGGCC	17074	SpyCas9-SpRY	3	1
43	tG	ACTTTGCTGCCACAATACCT	17075	SpyCas9-NG	3	1

44	tG	ACTTTGCTGCCACAATACCT	17076	SpyCas9-xCas	3	1
45	tG	ACTTTGCTGCCACAATACCT	17077	SpyCas9-xCas-NG	3	1
46	tGGCCCTT	ggaaCTTTGCTGCCACAATACCT	17078	BlatCas9	3	1
47	tGGCC	ggaaCTTTGCTGCCACAATACCT	17079	BlatCas9	3	1
48	tGGCCCT	GAACTTTGCTGCCACAATACCT	17080	CdiCas9	3	1
49	tGGC	ACTTTGCTGCCACAATACCT	17081	SpyCas9-3var-NRRH	3	1
50	TtGGCC	taGGAACTTTGCTGCCACAATACC	17082	Nme2Cas9	4	1
51	CaAGG	TCGTAGCGAACTGAGAAGGGC	17083	SauCas9KKH	4	1
52	CaAGGT	TCGTAGCGAACTGAGAAGGGC	17084	SauCas9KKH	4	1
53	CaAGGT	TCGTAGCGAACTGAGAAGGGC	17085	cCas9-v17	4	1
54	CaAGGT	TCGTAGCGAACTGAGAAGGGC	17086	cCas9-v42	4	1
55	TtGG	GAACTTTGCTGCCACAATACC	17087	SauriCas9	4	1
56	TtGG	GAACTTTGCTGCCACAATACC	17088	SauriCas9-KKH	4	1
57	CaAG	TCGTAGCGAACTGAGAAGGGC	17089	SauriCas9-KKH	4	1
58	CaAG	CGTAGCGAACTGAGAAGGGC	17090	SpyCas9-QQR1	4	1
59	CaAG	tcGTAGCGAACTGAGAAGGGC	17091	iSpyMacCas9	4	1
60	TtG	AACTTTGCTGCCACAATACC	17092	ScaCas9	4	1
61	TtG	AACTTTGCTGCCACAATACC	17093	ScaCas9-HiFi-Sc++	4	1
62	TtG	AACTTTGCTGCCACAATACC	17094	ScaCas9-Sc++	4	1
63	TtG	AACTTTGCTGCCACAATACC	17095	SpyCas9-SpRY	4	1
64	CaA	CGTAGCGAACTGAGAAGGGC	17096	SpyCas9-SpRY	4	1
65	TtGGC	aggaACTTTGCTGCCACAATACC	17097	BlatCas9	4	1
66	CCaAG	GTCGTAGCGAACTGAGAAGGG	17098	SauCas9KKH	5	1
67	CTtGG	GGAACTTTGCTGCCACAATAC	17099	SauCas9KKH	5	1
68	CCa	TCGTAGCGAACTGAGAAGGG	17100	SpyCas9-SpRY	5	1
69	CTt	GAACTTTGCTGCCACAATAC	17101	SpyCas9-SpRY	5	1
70	CCaAGG	GTCGTAGCGAACTGAGAAGGG	17102	cCas9-v17	5	1

71	CCaAGG	GTCGTAGCGAACTGAGAAGGG	17103	cCas9-v42	5	1
72	GCCaA	GGTCGTAGCGAACTGAGAAGG	17104	SauCas9KKH	6	1
73	GCC	GTCGTAGCGAACTGAGAAGG	17105	SpyCas9-SpRY	6	0
74	CCT	GGAACTTTGCTGCCACAATA	17106	SpyCas9-SpRY	6	0
75	GCCaAG	GGTCGTAGCGAACTGAGAAGG	17107	cCas9-v17	6	1
76	GCCaAG	GGTCGTAGCGAACTGAGAAGG	17108	cCas9-v42	6	1
77	GG	GGTCGTAGCGAACTGAGAAG	17109	SpyCas9-NG	7	0
78	GG	GGTCGTAGCGAACTGAGAAG	17110	SpyCas9-xCas	7	0
79	GG	GGTCGTAGCGAACTGAGAAG	17111	SpyCas9-xCas-NG	7	0
80	GGC	GGTCGTAGCGAACTGAGAAG	17112	SpyCas9-SpG	7	0
81	GGC	GGTCGTAGCGAACTGAGAAG	17113	SpyCas9-SpRY	7	0
82	ACC	AGGAACTTTGCTGCCACAAT	17114	SpyCas9-SpRY	7	0
83	GGCC	GGTCGTAGCGAACTGAGAAG	17115	SpyCas9-3var-NRCH	7	0
84	GGG	GGGTCGTAGCGAACTGAGAA	17116	ScaCas9	8	0
85	GGG	GGGTCGTAGCGAACTGAGAA	17117	ScaCas9-HiFi-Sc++	8	0
86	GGG	GGGTCGTAGCGAACTGAGAA	17118	ScaCas9-Sc++	8	0
87	GGG	GGGTCGTAGCGAACTGAGAA	17119	SpyCas9	8	0
88	GGG	GGGTCGTAGCGAACTGAGAA	17120	SpyCas9-HF1	8	0
89	GGG	GGGTCGTAGCGAACTGAGAA	17121	SpyCas9-SpG	8	0
90	GGG	GGGTCGTAGCGAACTGAGAA	17122	SpyCas9-SpRY	8	0
91	GG	GGGTCGTAGCGAACTGAGAA	17123	SpyCas9-NG	8	0
92	GG	GGGTCGTAGCGAACTGAGAA	17124	SpyCas9-xCas	8	0
93	GG	GGGTCGTAGCGAACTGAGAA	17125	SpyCas9-xCas-NG	8	0
94	TAC	TAGGAACTTTGCTGCCACAA	17126	SpyCas9-SpRY	8	0
95	GGGCCaAG	tatgGGTCGTAGCGAACTGAGAA	17127	BlatCas9	8	1
96	GGGCC	tatgGGTCGTAGCGAACTGAGAA	17128	BlatCas9	8	0
97	GGGC	GGGTCGTAGCGAACTGAGAA	17129	SpyCas9-3var-NRRH	8	0

98	TACC	TAGGAACTTTGCTGCCACAA	17130	SpyCas9-3var-NRCH	8	0
99	AGGGCC	tgTATGGGTCGTAGCGAACTGAGA	17131	Nme2Cas9	9	0
100	AGGG	ATGGGTCGTAGCGAACTGAGA	17132	SauriCas9	9	0
101	AGGG	ATGGGTCGTAGCGAACTGAGA	17133	SauriCas9-KKH	9	0
102	AGG	TGGGTCGTAGCGAACTGAGA	17134	ScaCas9	9	0
103	AGG	TGGGTCGTAGCGAACTGAGA	17135	ScaCas9-HiFi-Sc++	9	0
104	AGG	TGGGTCGTAGCGAACTGAGA	17136	ScaCas9-Sc++	9	0
105	AGG	TGGGTCGTAGCGAACTGAGA	17137	SpyCas9	9	0
106	AGG	TGGGTCGTAGCGAACTGAGA	17138	SpyCas9-HF1	9	0
107	AGG	TGGGTCGTAGCGAACTGAGA	17139	SpyCas9-SpG	9	0
108	AGG	TGGGTCGTAGCGAACTGAGA	17140	SpyCas9-SpRY	9	0
109	AG	TGGGTCGTAGCGAACTGAGA	17141	SpyCas9-NG	9	0
110	AG	TGGGTCGTAGCGAACTGAGA	17142	SpyCas9-xCas	9	0
111	AG	TGGGTCGTAGCGAACTGAGA	17143	SpyCas9-xCas-NG	9	0
112	ATA	TTAGGAACTTTGCTGCCACA	17144	SpyCas9-SpRY	9	0
113	AGGGCCaA	gtatGGGTCGTAGCGAACTGAGA	17145	BlatCas9	9	1
114	AGGGCCaA	gtatGGGTCGTAGCGAACTGAGA	17146	BlatCas9	9	1
115	ATACCTtG	gtctTAGGAACTTTGCTGCCACA	17147	BlatCas9	9	1
116	AGGGC	gtatGGGTCGTAGCGAACTGAGA	17148	BlatCas9	9	0
117	ATACC	gtctTAGGAACTTTGCTGCCACA	17149	BlatCas9	9	0
118	ATACCTt	TCTTAGGAACTTTGCTGCCACA	17150	CdiCas9	9	1
119	AATACC	tgGTCTTAGGAACTTTGCTGCCAC	17151	Nme2Cas9	10	0
120	AAGGG	tgTATGGGTCGTAGCGAACTGAG	17152	SauCas9	10	0
121	AAGGG	TATGGGTCGTAGCGAACTGAG	17153	SauCas9KKH	10	0
122	AAGG	TATGGGTCGTAGCGAACTGAG	17154	SauriCas9	10	0
123	AAGG	TATGGGTCGTAGCGAACTGAG	17155	SauriCas9-KKH	10	0
124	AAG	ATGGGTCGTAGCGAACTGAG	17156	ScaCas9	10	0

125	AAG	ATGGGTCGTAGCGAACTGAG	17157	ScaCas9-HiFi-Sc++	10	0
126	AAG	ATGGGTCGTAGCGAACTGAG	17158	ScaCas9-Sc++	10	0
127	AAG	ATGGGTCGTAGCGAACTGAG	17159	SpyCas9-SpRY	10	0
128	AAT	CTTAGGAACTTTGCTGCCAC	17160	SpyCas9-SpRY	10	0
129	AATACCTt	ggtcTTAGGAACTTTGCTGCCAC	17161	BlatCas9	10	1
130	AATAC	ggtcTTAGGAACTTTGCTGCCAC	17162	BlatCas9	10	0
131	AAGGGC	TATGGGTCGTAGCGAACTGAG	17163	cCas9-v17	10	0
132	AAGGGC	TATGGGTCGTAGCGAACTGAG	17164	cCas9-v42	10	0
133	AATA	CTTAGGAACTTTGCTGCCAC	17165	SpyCas9-3var-NRTH	10	0
134	GAAGG	GTATGGGTCGTAGCGAACTGA	17166	SauCas9KKH	11	0
135	GAAG	GTATGGGTCGTAGCGAACTGA	17167	SauriCas9-KKH	11	0
136	GAAG	TATGGGTCGTAGCGAACTGA	17168	SpyCas9-QQR1	11	0
137	GAAG	gtATGGGTCGTAGCGAACTGA	17169	iSpyMacCas9	11	0
138	GAA	TATGGGTCGTAGCGAACTGA	17170	SpyCas9-SpRY	11	0
139	GAA	TATGGGTCGTAGCGAACTGA	17171	SpyCas9-xCas	11	0
140	CAA	TCTTAGGAACTTTGCTGCCA	17172	SpyCas9-SpRY	11	0
141	GAAGGG	GTATGGGTCGTAGCGAACTGA	17173	cCas9-v17	11	0
142	GAAGGG	GTATGGGTCGTAGCGAACTGA	17174	cCas9-v42	11	0
143	CAATACC	GGTCTTAGGAACTTTGCTGCCA	17175	CdiCas9	11	0
144	CAAT	TCTTAGGAACTTTGCTGCCA	17176	SpyCas9-3var-NRRH	11	0
145	CAAT	gtCTTAGGAACTTTGCTGCCA	17177	iSpyMacCas9	11	0
146	AGAAG	TGTATGGGTCGTAGCGAACTG	17178	SauCas9KKH	12	0
147	AG	GTATGGGTCGTAGCGAACTG	17179	SpyCas9-NG	12	0
148	AG	GTATGGGTCGTAGCGAACTG	17180	SpyCas9-xCas	12	0
149	AG	GTATGGGTCGTAGCGAACTG	17181	SpyCas9-xCas-NG	12	0
150	AGA	GTATGGGTCGTAGCGAACTG	17182	SpyCas9-SpG	12	0
151	AGA	GTATGGGTCGTAGCGAACTG	17183	SpyCas9-SpRY	12	0

152	ACA	GTCTTAGGAACTTTGCTGCC	17184	SpyCas9-SpRY	12	0
153	AGAAGG	TGTATGGGTCGTAGCGAACTG	17185	cCas9-v17	12	0
154	AGAAGG	TGTATGGGTCGTAGCGAACTG	17186	cCas9-v42	12	0
155	ACAATAC	TGGTCTTAGGAACTTTGCTGCC	17187	CdiCas9	12	0
156	AGAA	GTATGGGTCGTAGCGAACTG	17188	SpyCas9-3var-NRRH	12	0
157	AGAA	GTATGGGTCGTAGCGAACTG	17189	SpyCas9-VQR	12	0
158	GAGAA	ggGTGTATGGGTCGTAGCGAACT	17190	SauCas9	13	0
159	GAGAA	GTGTATGGGTCGTAGCGAACT	17191	SauCas9KKH	13	0
160	CACAA	TGGTCTTAGGAACTTTGCTGC	17192	SauCas9KKH	13	0
161	CACAAT	TGGTCTTAGGAACTTTGCTGC	17193	SauCas9KKH	13	0
162	CACAAT	TGGTCTTAGGAACTTTGCTGC	17194	cCas9-v17	13	0
163	CACAAT	TGGTCTTAGGAACTTTGCTGC	17195	cCas9-v42	13	0
164	GAG	TGTATGGGTCGTAGCGAACT	17196	ScaCas9	13	0
165	GAG	TGTATGGGTCGTAGCGAACT	17197	ScaCas9-HiFi-Sc++	13	0
166	GAG	TGTATGGGTCGTAGCGAACT	17198	ScaCas9-Sc++	13	0
167	GAG	TGTATGGGTCGTAGCGAACT	17199	SpyCas9-SpRY	13	0
168	CAC	GGTCTTAGGAACTTTGCTGC	17200	SpyCas9-SpRY	13	0
169	GAGAAG	GTGTATGGGTCGTAGCGAACT	17201	cCas9-v17	13	0
170	GAGAAG	GTGTATGGGTCGTAGCGAACT	17202	cCas9-v42	13	0
171	CACAATAC	ttTGGTCTTAGGAACTTTGCTGC	17203	CjeCas9	13	0
172	GAGA	TGTATGGGTCGTAGCGAACT	17204	SpyCas9-3var-NRRH	13	0
173	CACA	GGTCTTAGGAACTTTGCTGC	17205	SpyCas9-3var-NRCH	13	0
174	TGAGA	GGTGTATGGGTCGTAGCGAAC	17206	SauCas9KKH	14	0
175	TGAG	GGTGTATGGGTCGTAGCGAAC	17207	SauriCas9-KKH	14	0
176	TGAG	GTGTATGGGTCGTAGCGAAC	17208	SpyCas9-VQR	14	0
177	TG	GTGTATGGGTCGTAGCGAAC	17209	SpyCas9-NG	14	0
178	TG	GTGTATGGGTCGTAGCGAAC	17210	SpyCas9-xCas	14	0

179	TG	GTGTATGGGTCGTAGCGAAC	17211	SpyCas9-xCas-NG	14	0
180	TGA	GTGTATGGGTCGTAGCGAAC	17212	SpyCas9-SpG	14	0
181	TGA	GTGTATGGGTCGTAGCGAAC	17213	SpyCas9-SpRY	14	0
182	CCA	TGGTCTTAGGAACTTTGCTG	17214	SpyCas9-SpRY	14	0
183	TGAGAA	GGTGTATGGGTCGTAGCGAAC	17215	cCas9-v17	14	0
184	TGAGAA	GGTGTATGGGTCGTAGCGAAC	17216	cCas9-v42	14	0
185	CCACAAT	TTTGGTCTTAGGAACTTTGCTG	17217	CdiCas9	14	0
186	CCACAA	TGGTCTTAGGAACTTTGCTG	17218	St1Cas9-CNRZ1066	14	0
187	CTGAG	ttGGGTGTATGGGTCGTAGCGAA	17219	SauCas9	15	0
188	CTGAG	GGGTGTATGGGTCGTAGCGAA	17220	SauCas9KKH	15	0
189	CTG	GGTGTATGGGTCGTAGCGAA	17221	ScaCas9	15	0
190	CTG	GGTGTATGGGTCGTAGCGAA	17222	ScaCas9-HiFi-Sc++	15	0
191	CTG	GGTGTATGGGTCGTAGCGAA	17223	ScaCas9-Sc++	15	0
192	CTG	GGTGTATGGGTCGTAGCGAA	17224	SpyCas9-SpRY	15	0
193	GCC	TTGGTCTTAGGAACTTTGCT	17225	SpyCas9-SpRY	15	0
194	GCCACAAT	gtttTGGTCTTAGGAACTTTGCT	17226	BlatCas9	15	0
195	GCCAC	gtttTGGTCTTAGGAACTTTGCT	17227	BlatCas9	15	0
196	CTGAGA	GGGTGTATGGGTCGTAGCGAA	17228	cCas9-v17	15	0
197	CTGAGA	GGGTGTATGGGTCGTAGCGAA	17229	cCas9-v42	15	0
198	ACTGA	TGGGTGTATGGGTCGTAGCGA	17230	SauCas9KKH	16	0
199	TG	TTTGGTCTTAGGAACTTTGC	17231	SpyCas9-NG	16	0
200	TG	TTTGGTCTTAGGAACTTTGC	17232	SpyCas9-xCas	16	0
201	TG	TTTGGTCTTAGGAACTTTGC	17233	SpyCas9-xCas-NG	16	0
202	TGC	TTTGGTCTTAGGAACTTTGC	17234	SpyCas9-SpG	16	0
203	TGC	TTTGGTCTTAGGAACTTTGC	17235	SpyCas9-SpRY	16	0
204	ACT	GGGTGTATGGGTCGTAGCGA	17236	SpyCas9-SpRY	16	0
205	TGCC	TTTGGTCTTAGGAACTTTGC	17237	SpyCas9-3var-NRCH	16	0

206	CTG	TTTTGGTCTTAGGAACTTTG	17238	ScaCas9	17	0
207	CTG	TTTTGGTCTTAGGAACTTTG	17239	ScaCas9-HiFi-Sc++	17	0
208	CTG	TTTTGGTCTTAGGAACTTTG	17240	ScaCas9-Sc++	17	0
209	CTG	TTTTGGTCTTAGGAACTTTG	17241	SpyCas9-SpRY	17	0
210	AAC	TGGGTGTATGGGTCGTAGCG	17242	SpyCas9-SpRY	17	0
211	CTGCC	tggtTTTGGTCTTAGGAACTTTG	17243	BlatCas9	17	0
212	CTGCCAC	GGTTTTGGTCTTAGGAACTTTG	17244	CdiCas9	17	0
213	AACT	TGGGTGTATGGGTCGTAGCG	17245	SpyCas9-3var-NRCH	17	0
214	GCTGCC	tgTGGTTTTGGTCTTAGGAACTTT	17246	Nme2Cas9	18	0
215	GAA	TTGGGTGTATGGGTCGTAGC	17247	SpyCas9-SpRY	18	0
216	GAA	TTGGGTGTATGGGTCGTAGC	17248	SpyCas9-xCas	18	0
217	GCT	GTTTTGGTCTTAGGAACTTT	17249	SpyCas9-SpRY	18	0
218	GCTGC	gtggTTTTGGTCTTAGGAACTTT	17250	BlatCas9	18	0
219	GAAC	TTGGGTGTATGGGTCGTAGC	17251	SpyCas9-3var-NRRH	18	0
220	GAAC	ttTGGGTGTATGGGTCGTAGC	17252	iSpyMacCas9	18	0
221	CG	TTTGGGTGTATGGGTCGTAG	17253	SpyCas9-NG	19	0
222	CG	TTTGGGTGTATGGGTCGTAG	17254	SpyCas9-xCas	19	0
223	CG	TTTGGGTGTATGGGTCGTAG	17255	SpyCas9-xCas-NG	19	0
224	TG	GGTTTTGGTCTTAGGAACTT	17256	SpyCas9-NG	19	0
225	TG	GGTTTTGGTCTTAGGAACTT	17257	SpyCas9-xCas	19	0
226	TG	GGTTTTGGTCTTAGGAACTT	17258	SpyCas9-xCas-NG	19	0
227	CGA	TTTGGGTGTATGGGTCGTAG	17259	SpyCas9-SpG	19	0
228	CGA	TTTGGGTGTATGGGTCGTAG	17260	SpyCas9-SpRY	19	0
229	TGC	GGTTTTGGTCTTAGGAACTT	17261	SpyCas9-SpG	19	0
230	TGC	GGTTTTGGTCTTAGGAACTT	17262	SpyCas9-SpRY	19	0
231	CGAACTGA	tcctTTGGGTGTATGGGTCGTAG	17263	BlatCas9	19	0
232	CGAAC	tcctTTGGGTGTATGGGTCGTAG	17264	BlatCas9	19	0

233	CGAACT	CTTTGGGTGTATGGGTCGTAG	17265	cCas9-v16	19	0
234	CGAACT	CTTTGGGTGTATGGGTCGTAG	17266	cCas9-v21	19	0
235	CGAA	TTTGGGTGTATGGGTCGTAG	17267	SpyCas9-3var-NRRH	19	0
236	CGAA	TTTGGGTGTATGGGTCGTAG	17268	SpyCas9-VQR	19	0
237	TGCT	GGTTTTGGTCTTAGGAACTT	17269	SpyCas9-3var-NRCH	19	0
238	GCGAA	atCCTTTGGGTGTATGGGTCGTA	17270	SauCas9	20	0
239	GCGAA	CCTTTGGGTGTATGGGTCGTA	17271	SauCas9KKH	20	0
240	GCG	CTTTGGGTGTATGGGTCGTA	17272	ScaCas9	20	0
241	GCG	CTTTGGGTGTATGGGTCGTA	17273	ScaCas9-HiFi-Sc++	20	0
242	GCG	CTTTGGGTGTATGGGTCGTA	17274	ScaCas9-Sc++	20	0
243	GCG	CTTTGGGTGTATGGGTCGTA	17275	SpyCas9-SpRY	20	0
244	TTG	TGGTTTTGGTCTTAGGAACT	17276	ScaCas9	20	0
245	TTG	TGGTTTTGGTCTTAGGAACT	17277	ScaCas9-HiFi-Sc++	20	0
246	TTG	TGGTTTTGGTCTTAGGAACT	17278	ScaCas9-Sc++	20	0
247	TTG	TGGTTTTGGTCTTAGGAACT	17279	SpyCas9-SpRY	20	0
248	GCGAAC	CCTTTGGGTGTATGGGTCGTA	17280	cCas9-v17	20	0
249	GCGAAC	CCTTTGGGTGTATGGGTCGTA	17281	cCas9-v42	20	0
250	GCGAACT	TCCTTTGGGTGTATGGGTCGTA	17282	CdiCas9	20	0
251	AGCGA	TCCTTTGGGTGTATGGGTCGT	17283	SauCas9KKH	21	0
252	AG	CCTTTGGGTGTATGGGTCGT	17284	SpyCas9-NG	21	0
253	AG	CCTTTGGGTGTATGGGTCGT	17285	SpyCas9-xCas	21	0
254	AG	CCTTTGGGTGTATGGGTCGT	17286	SpyCas9-xCas-NG	21	0
255	AGC	CCTTTGGGTGTATGGGTCGT	17287	SpyCas9-SpG	21	0
256	AGC	CCTTTGGGTGTATGGGTCGT	17288	SpyCas9-SpRY	21	0
257	TTT	GTGGTTTTGGTCTTAGGAAC	17289	SpyCas9-SpRY	21	0
258	TTTGC	cctgTGGTTTTGGTCTTAGGAAC	17290	BlatCas9	21	0
259	AGCGAA	TCCTTTGGGTGTATGGGTCGT	17291	cCas9-v17	21	0

260	AGCGAA	TCCTTTGGGTGTATGGGTCGT	17292	cCas9-v42	21	0
261	AGCG	CCTTTGGGTGTATGGGTCGT	17293	SpyCas9-VRER	21	0
262	TAG	TCCTTTGGGTGTATGGGTCG	17294	ScaCas9	22	0
263	TAG	TCCTTTGGGTGTATGGGTCG	17295	ScaCas9-HiFi-Sc++	22	0
264	TAG	TCCTTTGGGTGTATGGGTCG	17296	ScaCas9-Sc++	22	0
265	TAG	TCCTTTGGGTGTATGGGTCG	17297	SpyCas9-SpRY	22	0
266	CTT	TGTGGTTTTGGTCTTAGGAA	17298	SpyCas9-SpRY	22	0
267	TAGC	TCCTTTGGGTGTATGGGTCG	17299	SpyCas9-3var-NRRH	22	0
268	GTAG	AATCCTTTGGGTGTATGGGTC	17300	SauriCas9-KKH	23	0
269	GTA	ATCCTTTGGGTGTATGGGTC	17301	SpyCas9-SpRY	23	0
270	ACT	CTGTGGTTTTGGTCTTAGGA	17302	SpyCas9-SpRY	23	0
271	GTAGCGAA	tcaaTCCTTTGGGTGTATGGGTC	17303	BlatCas9	23	0
272	GTAGCGAA	tcaaTCCTTTGGGTGTATGGGTC	17304	BlatCas9	23	0
273	GTAGCGAA	tcAATCCTTTGGGTGTATGGGTC	17305	GeoCas9	23	0
274	GTAGC	tcaaTCCTTTGGGTGTATGGGTC	17306	BlatCas9	23	0
275	CGTAG	CAATCCTTTGGGTGTATGGGT	17307	SauCas9KKH	24	0
276	CG	AATCCTTTGGGTGTATGGGT	17308	SpyCas9-NG	24	0
277	CG	AATCCTTTGGGTGTATGGGT	17309	SpyCas9-xCas	24	0
278	CG	AATCCTTTGGGTGTATGGGT	17310	SpyCas9-xCas-NG	24	0
279	CGT	AATCCTTTGGGTGTATGGGT	17311	SpyCas9-SpG	24	0
280	CGT	AATCCTTTGGGTGTATGGGT	17312	SpyCas9-SpRY	24	0
281	AAC	CCTGTGGTTTTGGTCTTAGG	17313	SpyCas9-SpRY	24	0
282	CGTA	AATCCTTTGGGTGTATGGGT	17314	SpyCas9-3var-NRTH	24	0
283	AACT	CCTGTGGTTTTGGTCTTAGG	17315	SpyCas9-3var-NRCH	24	0
284	TCG	CAATCCTTTGGGTGTATGGG	17316	ScaCas9	25	0
285	TCG	CAATCCTTTGGGTGTATGGG	17317	ScaCas9-HiFi-Sc++	25	0
286	TCG	CAATCCTTTGGGTGTATGGG	17318	ScaCas9-Sc++	25	0

287	TCG	CAATCCTTTGGGTGTATGGG	17319	SpyCas9-SpRY	25	0
288	GAA	GCCTGTGGTTTTGGTCTTAG	17320	SpyCas9-SpRY	25	0
289	GAA	GCCTGTGGTTTTGGTCTTAG	17321	SpyCas9-xCas	25	0
290	GAACTTT	AAGCCTGTGGTTTTGGTCTTAG	17322	CdiCas9	25	0
291	GAAC	GCCTGTGGTTTTGGTCTTAG	17323	SpyCas9-3var-NRRH	25	0
292	GAAC	agCCTGTGGTTTTGGTCTTAG	17324	iSpyMacCas9	25	0
293	GG	AGCCTGTGGTTTTGGTCTTA	17325	SpyCas9-NG	26	0
294	GG	AGCCTGTGGTTTTGGTCTTA	17326	SpyCas9-xCas	26	0
295	GG	AGCCTGTGGTTTTGGTCTTA	17327	SpyCas9-xCas-NG	26	0
296	GGA	AGCCTGTGGTTTTGGTCTTA	17328	SpyCas9-SpG	26	0
297	GGA	AGCCTGTGGTTTTGGTCTTA	17329	SpyCas9-SpRY	26	0
298	GTC	TCAATCCTTTGGGTGTATGG	17330	SpyCas9-SpRY	26	0
299	GGAACTTT	tcaaGCCTGTGGTTTTGGTCTTA	17331	BlatCas9	26	0
300	GGAAC	tcaaGCCTGTGGTTTTGGTCTTA	17332	BlatCas9	26	0
301	GGAACT	AAGCCTGTGGTTTTGGTCTTA	17333	cCas9-v16	26	0
302	GGAACT	AAGCCTGTGGTTTTGGTCTTA	17334	cCas9-v21	26	0
303	GGAACTT	CAAGCCTGTGGTTTTGGTCTTA	17335	CdiCas9	26	0
304	GGAA	AGCCTGTGGTTTTGGTCTTA	17336	SpyCas9-3var-NRRH	26	0
305	GGAA	AGCCTGTGGTTTTGGTCTTA	17337	SpyCas9-VQR	26	0
306	AGGAA	ctCAAGCCTGTGGTTTTGGTCTT	17338	SauCas9	27	0
307	AGGAA	CAAGCCTGTGGTTTTGGTCTT	17339	SauCas9KKH	27	0
308	AGG	AAGCCTGTGGTTTTGGTCTT	17340	ScaCas9	27	0
309	AGG	AAGCCTGTGGTTTTGGTCTT	17341	ScaCas9-HiFi-Sc++	27	0
310	AGG	AAGCCTGTGGTTTTGGTCTT	17342	ScaCas9-Sc++	27	0
311	AGG	AAGCCTGTGGTTTTGGTCTT	17343	SpyCas9	27	0
312	AGG	AAGCCTGTGGTTTTGGTCTT	17344	SpyCas9-HF1	27	0
313	AGG	AAGCCTGTGGTTTTGGTCTT	17345	SpyCas9-SpG	27	0

314	AGG	AAGCCTGTGGTTTTGGTCTT	17346	SpyCas9-SpRY	27	0
315	GG	CTCAATCCTTTGGGTGTATG	17347	SpyCas9-NG	27	0
316	GG	CTCAATCCTTTGGGTGTATG	17348	SpyCas9-xCas	27	0
317	GG	CTCAATCCTTTGGGTGTATG	17349	SpyCas9-xCas-NG	27	0
318	AG	AAGCCTGTGGTTTTGGTCTT	17350	SpyCas9-NG	27	0
319	AG	AAGCCTGTGGTTTTGGTCTT	17351	SpyCas9-xCas	27	0
320	AG	AAGCCTGTGGTTTTGGTCTT	17352	SpyCas9-xCas-NG	27	0
321	GGT	CTCAATCCTTTGGGTGTATG	17353	SpyCas9-SpG	27	0
322	GGT	CTCAATCCTTTGGGTGTATG	17354	SpyCas9-SpRY	27	0
323	AGGAAC	CAAGCCTGTGGTTTTGGTCTT	17355	cCas9-v17	27	0
324	AGGAAC	CAAGCCTGTGGTTTTGGTCTT	17356	cCas9-v42	27	0
325	AGGAACT	TCAAGCCTGTGGTTTTGGTCTT	17357	CdiCas9	27	0
326	AGGA	AAGCCTGTGGTTTTGGTCTT	17358	SpyCas9-3var-NRRH	27	0
327	GGTC	CTCAATCCTTTGGGTGTATG	17359	SpyCas9-3var-NRTH	27	0
328	TAGGA	acTCAAGCCTGTGGTTTTGGTCT	17360	SauCas9	28	0
329	TAGGA	TCAAGCCTGTGGTTTTGGTCT	17361	SauCas9KKH	28	0
330	TAGG	TCAAGCCTGTGGTTTTGGTCT	17362	SauriCas9	28	0
331	TAGG	TCAAGCCTGTGGTTTTGGTCT	17363	SauriCas9-KKH	28	0
332	GGG	CCTCAATCCTTTGGGTGTAT	17364	ScaCas9	28	0
333	GGG	CCTCAATCCTTTGGGTGTAT	17365	ScaCas9-HiFi-Sc++	28	0
334	GGG	CCTCAATCCTTTGGGTGTAT	17366	ScaCas9-Sc++	28	0
335	GGG	CCTCAATCCTTTGGGTGTAT	17367	SpyCas9	28	0
336	GGG	CCTCAATCCTTTGGGTGTAT	17368	SpyCas9-HF1	28	0
337	GGG	CCTCAATCCTTTGGGTGTAT	17369	SpyCas9-SpG	28	0
338	GGG	CCTCAATCCTTTGGGTGTAT	17370	SpyCas9-SpRY	28	0
339	TAG	CAAGCCTGTGGTTTTGGTCT	17371	ScaCas9	28	0
340	TAG	CAAGCCTGTGGTTTTGGTCT	17372	ScaCas9-HiFi-Sc++	28	0

341	TAG	CAAGCCTGTGGTTTTGGTCT	17373	ScaCas9-Sc++	28	0
342	TAG	CAAGCCTGTGGTTTTGGTCT	17374	SpyCas9-SpRY	28	0
343	GG	CCTCAATCCTTTGGGTGTAT	17375	SpyCas9-NG	28	0
344	GG	CCTCAATCCTTTGGGTGTAT	17376	SpyCas9-xCas	28	0
345	GG	CCTCAATCCTTTGGGTGTAT	17377	SpyCas9-xCas-NG	28	0
346	GGGTCGTA	agacCTCAATCCTTTGGGTGTAT	17378	BlatCas9	28	0
347	GGGTC	agacCTCAATCCTTTGGGTGTAT	17379	BlatCas9	28	0
348	TAGGAA	TCAAGCCTGTGGTTTTGGTCT	17380	cCas9-v17	28	0
349	TAGGAA	TCAAGCCTGTGGTTTTGGTCT	17381	cCas9-v42	28	0
350	GGGT	CCTCAATCCTTTGGGTGTAT	17382	SpyCas9-3var-NRRH	28	0
351	TTAGG	CTCAAGCCTGTGGTTTTGGTC	17383	SauCas9KKH	29	0
352	TGGG	GACCTCAATCCTTTGGGTGTA	17384	SauriCas9	29	0
353	TGGG	GACCTCAATCCTTTGGGTGTA	17385	SauriCas9-KKH	29	0
354	TTAG	CTCAAGCCTGTGGTTTTGGTC	17386	SauriCas9-KKH	29	0
355	TGG	ACCTCAATCCTTTGGGTGTA	17387	ScaCas9	29	0
356	TGG	ACCTCAATCCTTTGGGTGTA	17388	ScaCas9-HiFi-Sc++	29	0
357	TGG	ACCTCAATCCTTTGGGTGTA	17389	ScaCas9-Sc++	29	0
358	TGG	ACCTCAATCCTTTGGGTGTA	17390	SpyCas9	29	0
359	TGG	ACCTCAATCCTTTGGGTGTA	17391	SpyCas9-HF1	29	0
360	TGG	ACCTCAATCCTTTGGGTGTA	17392	SpyCas9-SpG	29	0
361	TGG	ACCTCAATCCTTTGGGTGTA	17393	SpyCas9-SpRY	29	0
362	TG	ACCTCAATCCTTTGGGTGTA	17394	SpyCas9-NG	29	0
363	TG	ACCTCAATCCTTTGGGTGTA	17395	SpyCas9-xCas	29	0
364	TG	ACCTCAATCCTTTGGGTGTA	17396	SpyCas9-xCas-NG	29	0
365	TTA	TCAAGCCTGTGGTTTTGGTC	17397	SpyCas9-SpRY	29	0
366	TTAGGAA	TCAAGCCTGTGGTTTTGGTC	17398	St1Cas9	29	0
367	TTAGGA	CTCAAGCCTGTGGTTTTGGTC	17399	cCas9-v17	29	0

368	TTAGGA	CTCAAGCCTGTGGTTTTGGTC	17400	cCas9-v42	29	0
369	ATGGG	caAGACCTCAATCCTTTGGGTGT	17401	SauCas9	30	0
370	ATGGG	AGACCTCAATCCTTTGGGTGT	17402	SauCas9KKH	30	0
371	ATGGGT	caAGACCTCAATCCTTTGGGTGT	17403	SauCas9	30	0
372	ATGGGT	AGACCTCAATCCTTTGGGTGT	17404	SauCas9KKH	30	0
373	ATGGGT	AGACCTCAATCCTTTGGGTGT	17405	cCas9-v17	30	0
374	ATGGGT	AGACCTCAATCCTTTGGGTGT	17406	cCas9-v42	30	0
375	CTTAG	ACTCAAGCCTGTGGTTTTGGT	17407	SauCas9KKH	30	0
376	ATGG	AGACCTCAATCCTTTGGGTGT	17408	SauriCas9	30	0
377	ATGG	AGACCTCAATCCTTTGGGTGT	17409	SauriCas9-KKH	30	0
378	ATG	GACCTCAATCCTTTGGGTGT	17410	ScaCas9	30	0
379	ATG	GACCTCAATCCTTTGGGTGT	17411	ScaCas9-HiFi-Sc++	30	0
380	ATG	GACCTCAATCCTTTGGGTGT	17412	ScaCas9-Sc++	30	0
381	ATG	GACCTCAATCCTTTGGGTGT	17413	SpyCas9-SpRY	30	0
382	CTT	CTCAAGCCTGTGGTTTTGGT	17414	SpyCas9-SpRY	30	0
383	TATGG	AAGACCTCAATCCTTTGGGTG	17415	SauCas9KKH	31	0
384	TAT	AGACCTCAATCCTTTGGGTG	17416	SpyCas9-SpRY	31	0
385	TCT	ACTCAAGCCTGTGGTTTTGG	17417	SpyCas9-SpRY	31	0
386	GTA	AAGACCTCAATCCTTTGGGT	17418	SpyCas9-SpRY	32	0
387	GTC	CACTCAAGCCTGTGGTTTTG	17419	SpyCas9-SpRY	32	0
388	TG	CAAGACCTCAATCCTTTGGG	17420	SpyCas9-NG	33	0
389	TG	CAAGACCTCAATCCTTTGGG	17421	SpyCas9-xCas	33	0
390	TG	CAAGACCTCAATCCTTTGGG	17422	SpyCas9-xCas-NG	33	0
391	GG	TCACTCAAGCCTGTGGTTTT	17423	SpyCas9-NG	33	0
392	GG	TCACTCAAGCCTGTGGTTTT	17424	SpyCas9-xCas	33	0
393	GG	TCACTCAAGCCTGTGGTTTT	17425	SpyCas9-xCas-NG	33	0
394	TGT	CAAGACCTCAATCCTTTGGG	17426	SpyCas9-SpG	33	0

395	TGT	CAAGACCTCAATCCTTTGGG	17427	SpyCas9-SpRY	33	0
396	GGT	TCACTCAAGCCTGTGGTTTT	17428	SpyCas9-SpG	33	0
397	GGT	TCACTCAAGCCTGTGGTTTT	17429	SpyCas9-SpRY	33	0
398	TGTA	CAAGACCTCAATCCTTTGGG	17430	SpyCas9-3var-NRTH	33	0
399	GGTC	TCACTCAAGCCTGTGGTTTT	17431	SpyCas9-3var-NRTH	33	0
400	GTG	CCAAGACCTCAATCCTTTGG	17432	ScaCas9	34	0
401	GTG	CCAAGACCTCAATCCTTTGG	17433	ScaCas9-HiFi-Sc++	34	0
402	GTG	CCAAGACCTCAATCCTTTGG	17434	ScaCas9-Sc++	34	0
403	GTG	CCAAGACCTCAATCCTTTGG	17435	SpyCas9-SpRY	34	0
404	TGG	TTCACTCAAGCCTGTGGTTT	17436	ScaCas9	34	0
405	TGG	TTCACTCAAGCCTGTGGTTT	17437	ScaCas9-HiFi-Sc++	34	0
406	TGG	TTCACTCAAGCCTGTGGTTT	17438	ScaCas9-Sc++	34	0
407	TGG	TTCACTCAAGCCTGTGGTTT	17439	SpyCas9	34	0
408	TGG	TTCACTCAAGCCTGTGGTTT	17440	SpyCas9-HF1	34	0
409	TGG	TTCACTCAAGCCTGTGGTTT	17441	SpyCas9-SpG	34	0
410	TGG	TTCACTCAAGCCTGTGGTTT	17442	SpyCas9-SpRY	34	0
411	TG	TTCACTCAAGCCTGTGGTTT	17443	SpyCas9-NG	34	0
412	TG	TTCACTCAAGCCTGTGGTTT	17444	SpyCas9-xCas	34	0
413	TG	TTCACTCAAGCCTGTGGTTT	17445	SpyCas9-xCas-NG	34	0
414	TGGTCTTA	ccctTCACTCAAGCCTGTGGTTT	17446	BlatCas9	34	0
415	TGGTC	ccctTCACTCAAGCCTGTGGTTT	17447	BlatCas9	34	0
416	TGGTCTT	CCTTCACTCAAGCCTGTGGTTT	17448	CdiCas9	34	0
417	TGGT	TTCACTCAAGCCTGTGGTTT	17449	SpyCas9-3var-NRRH	34	0
418	TTGG	CCTTCACTCAAGCCTGTGGTT	17450	SauriCas9	35	0
419	TTGG	CCTTCACTCAAGCCTGTGGTT	17451	SauriCas9-KKH	35	0
420	TTG	CTTCACTCAAGCCTGTGGTT	17452	ScaCas9	35	0
421	TTG	CTTCACTCAAGCCTGTGGTT	17453	ScaCas9-HiFi-Sc++	35	0

422	TTG	CTTCACTCAAGCCTGTGGTT	17454	ScaCas9-Sc++	35	0
423	TTG	CTTCACTCAAGCCTGTGGTT	17455	SpyCas9-SpRY	35	0
424	GG	TCCAAGACCTCAATCCTTTG	17456	SpyCas9-NG	35	0
425	GG	TCCAAGACCTCAATCCTTTG	17457	SpyCas9-xCas	35	0
426	GG	TCCAAGACCTCAATCCTTTG	17458	SpyCas9-xCas-NG	35	0
427	GGT	TCCAAGACCTCAATCCTTTG	17459	SpyCas9-SpG	35	0
428	GGT	TCCAAGACCTCAATCCTTTG	17460	SpyCas9-SpRY	35	0
429	TTTGG	CCCTTCACTCAAGCCTGTGGT	17461	SauCas9KKH	36	0
430	TTTGGT	CCCTTCACTCAAGCCTGTGGT	17462	SauCas9KKH	36	0
431	GGG	GTCCAAGACCTCAATCCTTT	17463	ScaCas9	36	0
432	GGG	GTCCAAGACCTCAATCCTTT	17464	ScaCas9-HiFi-Sc++	36	0
433	GGG	GTCCAAGACCTCAATCCTTT	17465	ScaCas9-Sc++	36	0
434	GGG	GTCCAAGACCTCAATCCTTT	17466	SpyCas9	36	0
435	GGG	GTCCAAGACCTCAATCCTTT	17467	SpyCas9-HF1	36	0
436	GGG	GTCCAAGACCTCAATCCTTT	17468	SpyCas9-SpG	36	0
437	GGG	GTCCAAGACCTCAATCCTTT	17469	SpyCas9-SpRY	36	0
438	GG	GTCCAAGACCTCAATCCTTT	17470	SpyCas9-NG	36	0
439	GG	GTCCAAGACCTCAATCCTTT	17471	SpyCas9-xCas	36	0
440	GG	GTCCAAGACCTCAATCCTTT	17472	SpyCas9-xCas-NG	36	0
441	TTT	CCTTCACTCAAGCCTGTGGT	17473	SpyCas9-SpRY	36	0
442	TTTGGTCT	gtgcCCTTCACTCAAGCCTGTGGT	17474	NmeCas9	36	0
443	GGGT	GTCCAAGACCTCAATCCTTT	17475	SpyCas9-3var-NRRH	36	0
444	TGGG	TTGTCCAAGACCTCAATCCTT	17476	SauriCas9	37	0
445	TGGG	TTGTCCAAGACCTCAATCCTT	17477	SauriCas9-KKH	37	0
446	TGG	TGTCCAAGACCTCAATCCTT	17478	ScaCas9	37	0
447	TGG	TGTCCAAGACCTCAATCCTT	17479	ScaCas9-HiFi-Sc++	37	0
448	TGG	TGTCCAAGACCTCAATCCTT	17480	ScaCas9-Sc++	37	0

449	TGG	TGTCCAAGACCTCAATCCTT	17481	SpyCas9	37	0
450	TGG	TGTCCAAGACCTCAATCCTT	17482	SpyCas9-HF1	37	0
451	TGG	TGTCCAAGACCTCAATCCTT	17483	SpyCas9-SpG	37	0
452	TGG	TGTCCAAGACCTCAATCCTT	17484	SpyCas9-SpRY	37	0
453	TG	TGTCCAAGACCTCAATCCTT	17485	SpyCas9-NG	37	0
454	TG	TGTCCAAGACCTCAATCCTT	17486	SpyCas9-xCas	37	0
455	TG	TGTCCAAGACCTCAATCCTT	17487	SpyCas9-xCas-NG	37	0
456	TTT	CCCTTCACTCAAGCCTGTGG	17488	SpyCas9-SpRY	37	0
457	TGGGTG	TTGTCCAAGACCTCAATCCTT	17489	cCas9-v16	37	0
458	TGGGTG	TTGTCCAAGACCTCAATCCTT	17490	cCas9-v21	37	0
459	TTGGG	gtATTGTCCAAGACCTCAATCCT	17491	SauCas9	38	0
460	TTGGG	ATTGTCCAAGACCTCAATCCT	17492	SauCas9KKH	38	0
461	TTGGGT	gtATTGTCCAAGACCTCAATCCT	17493	SauCas9	38	0
462	TTGGGT	ATTGTCCAAGACCTCAATCCT	17494	SauCas9KKH	38	0
463	TTGGGT	ATTGTCCAAGACCTCAATCCT	17495	cCas9-v17	38	0
464	TTGGGT	ATTGTCCAAGACCTCAATCCT	17496	cCas9-v42	38	0
465	TTGG	ATTGTCCAAGACCTCAATCCT	17497	SauriCas9	38	0
466	TTGG	ATTGTCCAAGACCTCAATCCT	17498	SauriCas9-KKH	38	0
467	TTG	TTGTCCAAGACCTCAATCCT	17499	ScaCas9	38	0
468	TTG	TTGTCCAAGACCTCAATCCT	17500	ScaCas9-HiFi-Sc++	38	0
469	TTG	TTGTCCAAGACCTCAATCCT	17501	ScaCas9-Sc++	38	0
470	TTG	TTGTCCAAGACCTCAATCCT	17502	SpyCas9-SpRY	38	0
471	GTT	GCCCTTCACTCAAGCCTGTG	17503	SpyCas9-SpRY	38	0
472	TTTGG	TATTGTCCAAGACCTCAATCC	17504	SauCas9KKH	39	0
473	GG	TGCCCTTCACTCAAGCCTGT	17505	SpyCas9-NG	39	0
474	GG	TGCCCTTCACTCAAGCCTGT	17506	SpyCas9-xCas	39	0
475	GG	TGCCCTTCACTCAAGCCTGT	17507	SpyCas9-xCas-NG	39	0

476	GGT	TGCCCTTCACTCAAGCCTGT	17508	SpyCas9-SpG	39	0
477	GGT	TGCCCTTCACTCAAGCCTGT	17509	SpyCas9-SpRY	39	0
478	TTT	ATTGTCCAAGACCTCAATCC	17510	SpyCas9-SpRY	39	0
479	GGTT	TGCCCTTCACTCAAGCCTGT	17511	SpyCas9-3var-NRTH	39	0
480	TGG	GTGCCCTTCACTCAAGCCTG	17512	ScaCas9	40	0
481	TGG	GTGCCCTTCACTCAAGCCTG	17513	ScaCas9-HiFi-Sc++	40	0
482	TGG	GTGCCCTTCACTCAAGCCTG	17514	ScaCas9-Sc++	40	0
483	TGG	GTGCCCTTCACTCAAGCCTG	17515	SpyCas9	40	0
484	TGG	GTGCCCTTCACTCAAGCCTG	17516	SpyCas9-HF1	40	0
485	TGG	GTGCCCTTCACTCAAGCCTG	17517	SpyCas9-SpG	40	0
486	TGG	GTGCCCTTCACTCAAGCCTG	17518	SpyCas9-SpRY	40	0
487	TG	GTGCCCTTCACTCAAGCCTG	17519	SpyCas9-NG	40	0
488	TG	GTGCCCTTCACTCAAGCCTG	17520	SpyCas9-xCas	40	0
489	TG	GTGCCCTTCACTCAAGCCTG	17521	SpyCas9-xCas-NG	40	0
490	CTT	TATTGTCCAAGACCTCAATC	17522	SpyCas9-SpRY	40	0
491	TGGTTTT	TGGTGCCCTTCACTCAAGCCTG	17523	CdiCas9	40	0
492	TGGT	GTGCCCTTCACTCAAGCCTG	17524	SpyCas9-3var-NRRH	40	0
493	GTGG	TGGTGCCCTTCACTCAAGCCT	17525	SauriCas9	41	0
494	GTGG	TGGTGCCCTTCACTCAAGCCT	17526	SauriCas9-KKH	41	0
495	GTG	GGTGCCCTTCACTCAAGCCT	17527	ScaCas9	41	0
496	GTG	GGTGCCCTTCACTCAAGCCT	17528	ScaCas9-HiFi-Sc++	41	0
497	GTG	GGTGCCCTTCACTCAAGCCT	17529	ScaCas9-Sc++	41	0
498	GTG	GGTGCCCTTCACTCAAGCCT	17530	SpyCas9-SpRY	41	0
499	CCT	GTATTGTCCAAGACCTCAAT	17531	SpyCas9-SpRY	41	0
500	GTGGTT	TGGTGCCCTTCACTCAAGCCT	17532	cCas9-v16	41	0
501	GTGGTT	TGGTGCCCTTCACTCAAGCCT	17533	cCas9-v21	41	0
502	TGTGGTT	caaATGGTGCCCTTCACTCAAGCC	17534	PpnCas9	42	0

503	TGTGG	ATGGTGCCCTTCACTCAAGCC	17535	SauCas9KKH	42	0
504	TGTGGT	ATGGTGCCCTTCACTCAAGCC	17536	SauCas9KKH	42	0
505	TG	TGGTGCCCTTCACTCAAGCC	17537	SpyCas9-NG	42	0
506	TG	TGGTGCCCTTCACTCAAGCC	17538	SpyCas9-xCas	42	0
507	TG	TGGTGCCCTTCACTCAAGCC	17539	SpyCas9-xCas-NG	42	0
508	TGT	TGGTGCCCTTCACTCAAGCC	17540	SpyCas9-SpG	42	0
509	TGT	TGGTGCCCTTCACTCAAGCC	17541	SpyCas9-SpRY	42	0
510	TCC	GGTATTGTCCAAGACCTCAA	17542	SpyCas9-SpRY	42	0
511	TGTGGTTT	caaaTGGTGCCCTTCACTCAAGCC	17543	NmeCas9	42	0
512	CTG	ATGGTGCCCTTCACTCAAGC	17544	ScaCas9	43	0
513	CTG	ATGGTGCCCTTCACTCAAGC	17545	ScaCas9-HiFi-Sc++	43	0
514	CTG	ATGGTGCCCTTCACTCAAGC	17546	ScaCas9-Sc++	43	0
515	CTG	ATGGTGCCCTTCACTCAAGC	17547	SpyCas9-SpRY	43	0
516	ATC	GGGTATTGTCCAAGACCTCA	17548	SpyCas9-SpRY	43	0
517	AAT	TGGGTATTGTCCAAGACCTC	17549	SpyCas9-SpRY	44	0
518	CCT	AATGGTGCCCTTCACTCAAG	17550	SpyCas9-SpRY	44	0
519	AATCCTTT	tgctGGGTATTGTCCAAGACCTC	17551	BlatCas9	44	0
520	AATCC	tgctGGGTATTGTCCAAGACCTC	17552	BlatCas9	44	0
521	AATC	TGGGTATTGTCCAAGACCTC	17553	SpyCas9-3var-NRTH	44	0
522	CAATCC	gcTGCTGGGTATTGTCCAAGACCT	17554	Nme2Cas9	45	0
523	CAA	CTGGGTATTGTCCAAGACCT	17555	SpyCas9-SpRY	45	0
524	GCC	AAATGGTGCCCTTCACTCAA	17556	SpyCas9-SpRY	45	0
525	CAATCCTT	ctgcTGGGTATTGTCCAAGACCT	17557	BlatCas9	45	0
526	CAATC	ctgcTGGGTATTGTCCAAGACCT	17558	BlatCas9	45	0
527	CAATCCT	TGCTGGGTATTGTCCAAGACCT	17559	CdiCas9	45	0
528	CAAT	CTGGGTATTGTCCAAGACCT	17560	SpyCas9-3var-NRRH	45	0
529	CAAT	gcTGGGTATTGTCCAAGACCT	17561	iSpyMacCas9	45	0

530	AG	CAAATGGTGCCCTTCACTCA	17562	SpyCas9-NG	46	0
531	AG	CAAATGGTGCCCTTCACTCA	17563	SpyCas9-xCas	46	0
532	AG	CAAATGGTGCCCTTCACTCA	17564	SpyCas9-xCas-NG	46	0
533	AGC	CAAATGGTGCCCTTCACTCA	17565	SpyCas9-SpG	46	0
534	AGC	CAAATGGTGCCCTTCACTCA	17566	SpyCas9-SpRY	46	0
535	TCA	GCTGGGTATTGTCCAAGACC	17567	SpyCas9-SpRY	46	0
536	TCAATCC	CTGCTGGGTATTGTCCAAGACC	17568	CdiCas9	46	0
537	AGCC	CAAATGGTGCCCTTCACTCA	17569	SpyCas9-3var-NRCH	46	0
538	CTCAA	CTGCTGGGTATTGTCCAAGAC	17570	SauCas9KKH	47	0
539	CTCAAT	CTGCTGGGTATTGTCCAAGAC	17571	SauCas9KKH	47	0
540	CTCAAT	CTGCTGGGTATTGTCCAAGAC	17572	cCas9-v17	47	0
541	CTCAAT	CTGCTGGGTATTGTCCAAGAC	17573	cCas9-v42	47	0
542	AAG	CCAAATGGTGCCCTTCACTC	17574	ScaCas9	47	0
543	AAG	CCAAATGGTGCCCTTCACTC	17575	ScaCas9-HiFi-Sc++	47	0
544	AAG	CCAAATGGTGCCCTTCACTC	17576	ScaCas9-Sc++	47	0
545	AAG	CCAAATGGTGCCCTTCACTC	17577	SpyCas9-SpRY	47	0
546	CTC	TGCTGGGTATTGTCCAAGAC	17578	SpyCas9-SpRY	47	0
547	AAGCCTGT	tctcCAAATGGTGCCCTTCACTC	17579	BlatCas9	47	0
548	AAGCC	tctcCAAATGGTGCCCTTCACTC	17580	BlatCas9	47	0
549	AAGC	CCAAATGGTGCCCTTCACTC	17581	SpyCas9-3var-NRRH	47	0
550	CAAGCC	ttTCTCCAAATGGTGCCCTTCACT	17582	Nme2Cas9	48	0
551	CAAG	CTCCAAATGGTGCCCTTCACT	17583	SauriCas9-KKH	48	0
552	CAAG	TCCAAATGGTGCCCTTCACT	17584	SpyCas9-QQR1	48	0
553	CAAG	ctCCAAATGGTGCCCTTCACT	17585	iSpyMacCas9	48	0
554	CAA	TCCAAATGGTGCCCTTCACT	17586	SpyCas9-SpRY	48	0
555	CCT	CTGCTGGGTATTGTCCAAGA	17587	SpyCas9-SpRY	48	0
556	CAAGCCTG	ttctCCAAATGGTGCCCTTCACT	17588	BlatCas9	48	0

557	CAAGC	ttctCCAAATGGTGCCCTTCACT	17589	BlatCas9	48	0
558	TCAAG	TCTCCAAATGGTGCCCTTCAC	17590	SauCas9KKH	49	0
559	ACC	GCTGCTGGGTATTGTCCAAG	17591	SpyCas9-SpRY	49	0
560	TCA	CTCCAAATGGTGCCCTTCAC	17592	SpyCas9-SpRY	49	0
561	ACCTCAAT	taagCTGCTGGGTATTGTCCAAG	17593	BlatCas9	49	0
562	ACCTC	taagCTGCTGGGTATTGTCCAAG	17594	BlatCas9	49	0
563	TCAAGC	TCTCCAAATGGTGCCCTTCAC	17595	cCas9-v17	49	0
564	TCAAGC	TCTCCAAATGGTGCCCTTCAC	17596	cCas9-v42	49	0
565	CTCAA	TTCTCCAAATGGTGCCCTTCA	17597	SauCas9KKH	50	0
566	GAC	AGCTGCTGGGTATTGTCCAA	17598	SpyCas9-SpRY	50	0
567	CTC	TCTCCAAATGGTGCCCTTCA	17599	SpyCas9-SpRY	50	0
568	CTCAAG	TTCTCCAAATGGTGCCCTTCA	17600	cCas9-v17	50	0
569	CTCAAG	TTCTCCAAATGGTGCCCTTCA	17601	cCas9-v42	50	0
570	GACC	AGCTGCTGGGTATTGTCCAA	17602	SpyCas9-3var-NRCH	50	0
571	AG	AAGCTGCTGGGTATTGTCCA	17603	SpyCas9-NG	51	0
572	AG	AAGCTGCTGGGTATTGTCCA	17604	SpyCas9-xCas	51	0
573	AG	AAGCTGCTGGGTATTGTCCA	17605	SpyCas9-xCas-NG	51	0
574	AGA	AAGCTGCTGGGTATTGTCCA	17606	SpyCas9-SpG	51	0
575	AGA	AAGCTGCTGGGTATTGTCCA	17607	SpyCas9-SpRY	51	0
576	ACT	TTCTCCAAATGGTGCCCTTC	17608	SpyCas9-SpRY	51	0
577	AGACC	cttaAGCTGCTGGGTATTGTCCA	17609	BlatCas9	51	0
578	AGACCTC	TTAAGCTGCTGGGTATTGTCCA	17610	CdiCas9	51	0
579	AGAC	AAGCTGCTGGGTATTGTCCA	17611	SpyCas9-3var-NRRH	51	0
580	AGAC	AAGCTGCTGGGTATTGTCCA	17612	SpyCas9-VQR	51	0
581	AAGACC	atCTTAAGCTGCTGGGTATTGTCC	17613	Nme2Cas9	52	0
582	AAG	TAAGCTGCTGGGTATTGTCC	17614	ScaCas9	52	0
583	AAG	TAAGCTGCTGGGTATTGTCC	17615	ScaCas9-HiFi-Sc++	52	0

584	AAG	TAAGCTGCTGGGTATTGTCC	17616	ScaCas9-Sc++	52	0
585	AAG	TAAGCTGCTGGGTATTGTCC	17617	SpyCas9-SpRY	52	0
586	CAC	TTTCTCCAAATGGTGCCCTT	17618	SpyCas9-SpRY	52	0
587	CACTCAAG	acctTTCTCCAAATGGTGCCCTT	17619	BlatCas9	52	0
588	AAGAC	tcttAAGCTGCTGGGTATTGTCC	17620	BlatCas9	52	0
589	CACTC	acctTTCTCCAAATGGTGCCCTT	17621	BlatCas9	52	0
590	AAGACCT	CTTAAGCTGCTGGGTATTGTCC	17622	CdiCas9	52	0
591	AAGA	TAAGCTGCTGGGTATTGTCC	17623	SpyCas9-3var-NRRH	52	0
592	CACT	TTTCTCCAAATGGTGCCCTT	17624	SpyCas9-3var-NRCH	52	0
593	CAAGA	CTTAAGCTGCTGGGTATTGTC	17625	SauCas9KKH	53	0
594	CAAG	CTTAAGCTGCTGGGTATTGTC	17626	SauriCas9-KKH	53	0
595	CAAG	TTAAGCTGCTGGGTATTGTC	17627	SpyCas9-QQR1	53	0
596	CAAG	ctTAAGCTGCTGGGTATTGTC	17628	iSpyMacCas9	53	0
597	CAA	TTAAGCTGCTGGGTATTGTC	17629	SpyCas9-SpRY	53	0
598	TCA	CTTTCTCCAAATGGTGCCCT	17630	SpyCas9-SpRY	53	0
599	CAAGAC	CTTAAGCTGCTGGGTATTGTC	17631	cCas9-v17	53	0
600	CAAGAC	CTTAAGCTGCTGGGTATTGTC	17632	cCas9-v42	53	0
601	CCAAG	TCTTAAGCTGCTGGGTATTGT	17633	SauCas9KKH	54	0
602	CCA	CTTAAGCTGCTGGGTATTGT	17634	SpyCas9-SpRY	54	0
603	TTC	CCTTTCTCCAAATGGTGCCC	17635	SpyCas9-SpRY	54	0
604	TTCAC	ctacCTTTCTCCAAATGGTGCCC	17636	BlatCas9	54	0
605	TTCACT	ACCTTTCTCCAAATGGTGCCC	17637	cCas9-v16	54	0
606	TTCACT	ACCTTTCTCCAAATGGTGCCC	17638	cCas9-v21	54	0
607	CCAAGA	TCTTAAGCTGCTGGGTATTGT	17639	cCas9-v17	54	0
608	CCAAGA	TCTTAAGCTGCTGGGTATTGT	17640	cCas9-v42	54	0
609	TCCAA	ATCTTAAGCTGCTGGGTATTG	17641	SauCas9KKH	55	0
610	TCC	TCTTAAGCTGCTGGGTATTG	17642	SpyCas9-SpRY	55	0

611	CTT	ACCTTTCTCCAAATGGTGCC	17643	SpyCas9-SpRY	55	0
612	TCCAAG	ATCTTAAGCTGCTGGGTATTG	17644	cCas9-v17	55	0
613	TCCAAG	ATCTTAAGCTGCTGGGTATTG	17645	cCas9-v42	55	0
614	GTC	ATCTTAAGCTGCTGGGTATT	17646	SpyCas9-SpRY	56	0
615	CCT	TACCTTTCTCCAAATGGTGC	17647	SpyCas9-SpRY	56	0
616	CCTTC	gactACCTTTCTCCAAATGGTGC	17648	BlatCas9	56	0
617	TG	AATCTTAAGCTGCTGGGTAT	17649	SpyCas9-NG	57	0
618	TG	AATCTTAAGCTGCTGGGTAT	17650	SpyCas9-xCas	57	0
619	TG	AATCTTAAGCTGCTGGGTAT	17651	SpyCas9-xCas-NG	57	0
620	TGT	AATCTTAAGCTGCTGGGTAT	17652	SpyCas9-SpG	57	0
621	TGT	AATCTTAAGCTGCTGGGTAT	17653	SpyCas9-SpRY	57	0
622	CCC	CTACCTTTCTCCAAATGGTG	17654	SpyCas9-SpRY	57	0
623	TGTCCAAG	caaaATCTTAAGCTGCTGGGTAT	17655	BlatCas9	57	0
624	TGTCC	caaaATCTTAAGCTGCTGGGTAT	17656	BlatCas9	57	0
625	TGTC	AATCTTAAGCTGCTGGGTAT	17657	SpyCas9-3var-NRTH	57	0
626	TTGTCC	gcCAAAATCTTAAGCTGCTGGGTA	17658	Nme2Cas9	58	0
627	TTG	AAATCTTAAGCTGCTGGGTA	17659	ScaCas9	58	0
628	TTG	AAATCTTAAGCTGCTGGGTA	17660	ScaCas9-HiFi-Sc++	58	0
629	TTG	AAATCTTAAGCTGCTGGGTA	17661	ScaCas9-Sc++	58	0
630	TTG	AAATCTTAAGCTGCTGGGTA	17662	SpyCas9-SpRY	58	0
631	GCC	ACTACCTTTCTCCAAATGGT	17663	SpyCas9-SpRY	58	0
632	TTGTCCAA	ccaaAATCTTAAGCTGCTGGGTA	17664	BlatCas9	58	0
633	TTGTCCAA	ccaaAATCTTAAGCTGCTGGGTA	17665	BlatCas9	58	0
634	TTGTC	ccaaAATCTTAAGCTGCTGGGTA	17666	BlatCas9	58	0
635	TG	GACTACCTTTCTCCAAATGG	17667	SpyCas9-NG	59	0
636	TG	GACTACCTTTCTCCAAATGG	17668	SpyCas9-xCas	59	0
637	TG	GACTACCTTTCTCCAAATGG	17669	SpyCas9-xCas-NG	59	0

638	TGC	GACTACCTTTCTCCAAATGG	17670	SpyCas9-SpG	59	0
639	TGC	GACTACCTTTCTCCAAATGG	17671	SpyCas9-SpRY	59	0
640	ATT	AAAATCTTAAGCTGCTGGGT	17672	SpyCas9-SpRY	59	0
641	TGCCC	taagACTACCTTTCTCCAAATGG	17673	BlatCas9	59	0
642	TGCC	GACTACCTTTCTCCAAATGG	17674	SpyCas9-3var-NRCH	59	0
643	GTGCCC	ctTAAGACTACCTTTCTCCAAATG	17675	Nme2Cas9	60	0
644	GTG	AGACTACCTTTCTCCAAATG	17676	ScaCas9	60	0
645	GTG	AGACTACCTTTCTCCAAATG	17677	ScaCas9-HiFi-Sc++	60	0
646	GTG	AGACTACCTTTCTCCAAATG	17678	ScaCas9-Sc++	60	0
647	GTG	AGACTACCTTTCTCCAAATG	17679	SpyCas9-SpRY	60	0
648	TAT	CAAAATCTTAAGCTGCTGGG	17680	SpyCas9-SpRY	60	0
649	GTGCCCTT	ttaaGACTACCTTTCTCCAAATG	17681	BlatCas9	60	0
650	GTGCC	ttaaGACTACCTTTCTCCAAATG	17682	BlatCas9	60	0
651	GTGCCCT	TAAGACTACCTTTCTCCAAATG	17683	CdiCas9	60	0
652	TATT	CAAAATCTTAAGCTGCTGGG	17684	SpyCas9-3var-NRTH	60	0
653	GGTGCC	tcTTAAGACTACCTTTCTCCAAAT	17685	Nme2Cas9	61	0
654	GG	AAGACTACCTTTCTCCAAAT	17686	SpyCas9-NG	61	0
655	GG	AAGACTACCTTTCTCCAAAT	17687	SpyCas9-xCas	61	0
656	GG	AAGACTACCTTTCTCCAAAT	17688	SpyCas9-xCas-NG	61	0
657	GGT	AAGACTACCTTTCTCCAAAT	17689	SpyCas9-SpG	61	0
658	GGT	AAGACTACCTTTCTCCAAAT	17690	SpyCas9-SpRY	61	0
659	GTA	CCAAAATCTTAAGCTGCTGG	17691	SpyCas9-SpRY	61	0
660	GGTGC	cttaAGACTACCTTTCTCCAAAT	17692	BlatCas9	61	0
661	TGG	TAAGACTACCTTTCTCCAAA	17693	ScaCas9	62	0
662	TGG	TAAGACTACCTTTCTCCAAA	17694	ScaCas9-HiFi-Sc++	62	0
663	TGG	TAAGACTACCTTTCTCCAAA	17695	ScaCas9-Sc++	62	0
664	TGG	TAAGACTACCTTTCTCCAAA	17696	SpyCas9	62	0

665	TGG	TAAGACTACCTTTCTCCAAA	17697	SpyCas9-HF1	62	0
666	TGG	TAAGACTACCTTTCTCCAAA	17698	SpyCas9-SpG	62	0
667	TGG	TAAGACTACCTTTCTCCAAA	17699	SpyCas9-SpRY	62	0
668	GG	GCCAAAATCTTAAGCTGCTG	17700	SpyCas9-NG	62	0
669	GG	GCCAAAATCTTAAGCTGCTG	17701	SpyCas9-xCas	62	0
670	GG	GCCAAAATCTTAAGCTGCTG	17702	SpyCas9-xCas-NG	62	0
671	TG	TAAGACTACCTTTCTCCAAA	17703	SpyCas9-NG	62	0
672	TG	TAAGACTACCTTTCTCCAAA	17704	SpyCas9-xCas	62	0
673	TG	TAAGACTACCTTTCTCCAAA	17705	SpyCas9-xCas-NG	62	0
674	GGT	GCCAAAATCTTAAGCTGCTG	17706	SpyCas9-SpG	62	0
675	GGT	GCCAAAATCTTAAGCTGCTG	17707	SpyCas9-SpRY	62	0
676	TGGT	TAAGACTACCTTTCTCCAAA	17708	SpyCas9-3var-NRRH	62	0
677	GGTA	GCCAAAATCTTAAGCTGCTG	17709	SpyCas9-3var-NRTH	62	0
678	GGGTATT	TCAGCCAAAATCTTAAGCTGCT	17710	CdiCas9	63	0
679	GGGTATT	aatCAGCCAAAATCTTAAGCTGCT	17711	PpnCas9	63	0
680	ATGG	CTTAAGACTACCTTTCTCCAA	17712	SauriCas9	63	0
681	ATGG	CTTAAGACTACCTTTCTCCAA	17713	SauriCas9-KKH	63	0
682	GGG	AGCCAAAATCTTAAGCTGCT	17714	ScaCas9	63	0
683	GGG	AGCCAAAATCTTAAGCTGCT	17715	ScaCas9-HiFi-Sc++	63	0
684	GGG	AGCCAAAATCTTAAGCTGCT	17716	ScaCas9-Sc++	63	0
685	GGG	AGCCAAAATCTTAAGCTGCT	17717	SpyCas9	63	0
686	GGG	AGCCAAAATCTTAAGCTGCT	17718	SpyCas9-HF1	63	0
687	GGG	AGCCAAAATCTTAAGCTGCT	17719	SpyCas9-SpG	63	0
688	GGG	AGCCAAAATCTTAAGCTGCT	17720	SpyCas9-SpRY	63	0
689	ATG	TTAAGACTACCTTTCTCCAA	17721	ScaCas9	63	0
690	ATG	TTAAGACTACCTTTCTCCAA	17722	ScaCas9-HiFi-Sc++	63	0
691	ATG	TTAAGACTACCTTTCTCCAA	17723	ScaCas9-Sc++	63	0

692	ATG	TTAAGACTACCTTTCTCCAA	17724	SpyCas9-SpRY	63	0
693	GG	AGCCAAAATCTTAAGCTGCT	17725	SpyCas9-NG	63	0
694	GG	AGCCAAAATCTTAAGCTGCT	17726	SpyCas9-xCas	63	0
695	GG	AGCCAAAATCTTAAGCTGCT	17727	SpyCas9-xCas-NG	63	0
696	ATGGTG	CTTAAGACTACCTTTCTCCAA	17728	cCas9-v16	63	0
697	ATGGTG	CTTAAGACTACCTTTCTCCAA	17729	cCas9-v21	63	0
698	GGGT	AGCCAAAATCTTAAGCTGCT	17730	SpyCas9-3var-NRRH	63	0
699	AATGG	TCTTAAGACTACCTTTCTCCA	17731	SauCas9KKH	64	0
700	AATGGT	TCTTAAGACTACCTTTCTCCA	17732	SauCas9KKH	64	0
701	TGGG	TCAGCCAAAATCTTAAGCTGC	17733	SauriCas9	64	0
702	TGGG	TCAGCCAAAATCTTAAGCTGC	17734	SauriCas9-KKH	64	0
703	TGG	CAGCCAAAATCTTAAGCTGC	17735	ScaCas9	64	0
704	TGG	CAGCCAAAATCTTAAGCTGC	17736	ScaCas9-HiFi-Sc++	64	0
705	TGG	CAGCCAAAATCTTAAGCTGC	17737	ScaCas9-Sc++	64	0
706	TGG	CAGCCAAAATCTTAAGCTGC	17738	SpyCas9	64	0
707	TGG	CAGCCAAAATCTTAAGCTGC	17739	SpyCas9-HF1	64	0
708	TGG	CAGCCAAAATCTTAAGCTGC	17740	SpyCas9-SpG	64	0
709	TGG	CAGCCAAAATCTTAAGCTGC	17741	SpyCas9-SpRY	64	0
710	TG	CAGCCAAAATCTTAAGCTGC	17742	SpyCas9-NG	64	0
711	TG	CAGCCAAAATCTTAAGCTGC	17743	SpyCas9-xCas	64	0
712	TG	CAGCCAAAATCTTAAGCTGC	17744	SpyCas9-xCas-NG	64	0
713	AAT	CTTAAGACTACCTTTCTCCA	17745	SpyCas9-SpRY	64	0
714	CTGGG	gaATCAGCCAAAATCTTAAGCTG	17746	SauCas9	65	0
715	CTGGG	ATCAGCCAAAATCTTAAGCTG	17747	SauCas9KKH	65	0
716	CTGGGT	gaATCAGCCAAAATCTTAAGCTG	17748	SauCas9	65	0
717	CTGGGT	ATCAGCCAAAATCTTAAGCTG	17749	SauCas9KKH	65	0
718	CTGGGT	ATCAGCCAAAATCTTAAGCTG	17750	cCas9-v17	65	0

719	CTGGGT	ATCAGCCAAAATCTTAAGCTG	17751	cCas9-v42	65	0
720	CTGG	ATCAGCCAAAATCTTAAGCTG	17752	SauriCas9	65	0
721	CTGG	ATCAGCCAAAATCTTAAGCTG	17753	SauriCas9-KKH	65	0
722	CTG	TCAGCCAAAATCTTAAGCTG	17754	ScaCas9	65	0
723	CTG	TCAGCCAAAATCTTAAGCTG	17755	ScaCas9-HiFi-Sc++	65	0
724	CTG	TCAGCCAAAATCTTAAGCTG	17756	ScaCas9-Sc++	65	0
725	CTG	TCAGCCAAAATCTTAAGCTG	17757	SpyCas9-SpRY	65	0
726	AAA	TCTTAAGACTACCTTTCTCC	17758	SpyCas9-SpRY	65	0
727	AAAT	TCTTAAGACTACCTTTCTCC	17759	SpyCas9-3var-NRRH	65	0
728	AAAT	ctCTTAAGACTACCTTTCTCC	17760	iSpyMacCas9	65	0
729	GCTGG	AATCAGCCAAAATCTTAAGCT	17761	SauCas9KKH	66	0
730	CAA	CTCTTAAGACTACCTTTCTC	17762	SpyCas9-SpRY	66	0
731	GCT	ATCAGCCAAAATCTTAAGCT	17763	SpyCas9-SpRY	66	0
732	CAAA	CTCTTAAGACTACCTTTCTC	17764	SpyCas9-3var-NRRH	66	0
733	CAAA	tcTCTTAAGACTACCTTTCTC	17765	iSpyMacCas9	66	0
734	CCAAA	CTCTCTTAAGACTACCTTTCT	17766	SauCas9KKH	67	0
735	CCAAAT	CTCTCTTAAGACTACCTTTCT	17767	SauCas9KKH	67	0
736	CCAAAT	CTCTCTTAAGACTACCTTTCT	17768	cCas9-v17	67	0
737	CCAAAT	CTCTCTTAAGACTACCTTTCT	17769	cCas9-v42	67	0
738	TG	AATCAGCCAAAATCTTAAGC	17770	SpyCas9-NG	67	0
739	TG	AATCAGCCAAAATCTTAAGC	17771	SpyCas9-xCas	67	0
740	TG	AATCAGCCAAAATCTTAAGC	17772	SpyCas9-xCas-NG	67	0
741	TGC	AATCAGCCAAAATCTTAAGC	17773	SpyCas9-SpG	67	0
742	TGC	AATCAGCCAAAATCTTAAGC	17774	SpyCas9-SpRY	67	0
743	CCA	TCTCTTAAGACTACCTTTCT	17775	SpyCas9-SpRY	67	0
744	TGCT	AATCAGCCAAAATCTTAAGC	17776	SpyCas9-3var-NRCH	67	0
745	TCCAA	ACTCTCTTAAGACTACCTTTC	17777	SauCas9KKH	68	0

746	CTG	GAATCAGCCAAAATCTTAAG	17778	ScaCas9	68	0
747	CTG	GAATCAGCCAAAATCTTAAG	17779	ScaCas9-HiFi-Sc++	68	0
748	CTG	GAATCAGCCAAAATCTTAAG	17780	ScaCas9-Sc++	68	0
749	CTG	GAATCAGCCAAAATCTTAAG	17781	SpyCas9-SpRY	68	0
750	TCC	CTCTCTTAAGACTACCTTTC	17782	SpyCas9-SpRY	68	0
751	TCCAAA	ACTCTCTTAAGACTACCTTTC	17783	cCas9-v17	68	0
752	TCCAAA	ACTCTCTTAAGACTACCTTTC	17784	cCas9-v42	68	0
753	GCT	GGAATCAGCCAAAATCTTAA	17785	SpyCas9-SpRY	69	0
754	CTC	ACTCTCTTAAGACTACCTTT	17786	SpyCas9-SpRY	69	0
755	GCTGCTGG	aatgGAATCAGCCAAAATCTTAA	17787	BlatCas9	69	0
756	GCTGC	aatgGAATCAGCCAAAATCTTAA	17788	BlatCas9	69	0
757	AG	TGGAATCAGCCAAAATCTTA	17789	SpyCas9-NG	70	0
758	AG	TGGAATCAGCCAAAATCTTA	17790	SpyCas9-xCas	70	0
759	AG	TGGAATCAGCCAAAATCTTA	17791	SpyCas9-xCas-NG	70	0
760	AGC	TGGAATCAGCCAAAATCTTA	17792	SpyCas9-SpG	70	0
761	AGC	TGGAATCAGCCAAAATCTTA	17793	SpyCas9-SpRY	70	0
762	TCT	AACTCTCTTAAGACTACCTT	17794	SpyCas9-SpRY	70	0
763	TCTCCAAA	gagaACTCTCTTAAGACTACCTT	17795	BlatCas9	70	0
764	TCTCCAAA	gagaACTCTCTTAAGACTACCTT	17796	BlatCas9	70	0
765	TCTCCAAA	gaGAACTCTCTTAAGACTACCTT	17797	GeoCas9	70	0
766	TCTCC	gagaACTCTCTTAAGACTACCTT	17798	BlatCas9	70	0
767	AGCT	TGGAATCAGCCAAAATCTTA	17799	SpyCas9-3var-NRCH	70	0
768	TTCTCC	ctGAGAACTCTCTTAAGACTACCT	17800	Nme2Cas9	71	0
769	AAG	ATGGAATCAGCCAAAATCTT	17801	ScaCas9	71	0
770	AAG	ATGGAATCAGCCAAAATCTT	17802	ScaCas9-HiFi-Sc++	71	0
771	AAG	ATGGAATCAGCCAAAATCTT	17803	ScaCas9-Sc++	71	0
772	AAG	ATGGAATCAGCCAAAATCTT	17804	SpyCas9-SpRY	71	0

773	TTC	GAACTCTCTTAAGACTACCT	17805	SpyCas9-SpRY	71	0
774	TTCTCCAA	tgagAACTCTCTTAAGACTACCT	17806	BlatCas9	71	0
775	TTCTCCAA	tgagAACTCTCTTAAGACTACCT	17807	BlatCas9	71	0
776	TTCTC	tgagAACTCTCTTAAGACTACCT	17808	BlatCas9	71	0
777	AAGC	ATGGAATCAGCCAAAATCTT	17809	SpyCas9-3var-NRRH	71	0
778	TAAG	TAATGGAATCAGCCAAAATCT	17810	SauriCas9-KKH	72	0
779	TAAG	AATGGAATCAGCCAAAATCT	17811	SpyCas9-QQR1	72	0
780	TAAG	taATGGAATCAGCCAAAATCT	17812	iSpyMacCas9	72	0
781	TAA	AATGGAATCAGCCAAAATCT	17813	SpyCas9-SpRY	72	0
782	TTT	AGAACTCTCTTAAGACTACC	17814	SpyCas9-SpRY	72	0
783	TAAGC	gttaATGGAATCAGCCAAAATCT	17815	BlatCas9	72	0
784	TAAGCT	TAATGGAATCAGCCAAAATCT	17816	cCas9-v16	72	0
785	TAAGCT	TAATGGAATCAGCCAAAATCT	17817	cCas9-v21	72	0
786	TTAAG	TTAATGGAATCAGCCAAAATC	17818	SauCas9KKH	73	0
787	TTA	TAATGGAATCAGCCAAAATC	17819	SpyCas9-SpRY	73	0
788	CTT	GAGAACTCTCTTAAGACTAC	17820	SpyCas9-SpRY	73	0
789	CTTTC	actgAGAACTCTCTTAAGACTAC	17821	BlatCas9	73	0
790	TTAAGC	TTAATGGAATCAGCCAAAATC	17822	cCas9-v17	73	0
791	TTAAGC	TTAATGGAATCAGCCAAAATC	17823	cCas9-v42	73	0
792	CTTAA	GTTAATGGAATCAGCCAAAAT	17824	SauCas9KKH	74	0
793	CTT	TTAATGGAATCAGCCAAAAT	17825	SpyCas9-SpRY	74	0
794	CCT	TGAGAACTCTCTTAAGACTA	17826	SpyCas9-SpRY	74	0
795	TCT	GTTAATGGAATCAGCCAAAA	17827	SpyCas9-SpRY	75	0
796	ACC	CTGAGAACTCTCTTAAGACT	17828	SpyCas9-SpRY	75	0
797	TAC	ACTGAGAACTCTCTTAAGAC	17829	SpyCas9-SpRY	76	0
798	ATC	TGTTAATGGAATCAGCCAAA	17830	SpyCas9-SpRY	76	0
799	TACC	ACTGAGAACTCTCTTAAGAC	17831	SpyCas9-3var-NRCH	76	0

800	AAT	CTGTTAATGGAATCAGCCAA	17832	SpyCas9-SpRY	77	0
801	CTA	CACTGAGAACTCTCTTAAGA	17833	SpyCas9-SpRY	77	0
802	CTACCTTT	tgccACTGAGAACTCTCTTAAGA	17834	BlatCas9	77	0
803	CTACC	tgccACTGAGAACTCTCTTAAGA	17835	BlatCas9	77	0
804	CTACCTT	GCCACTGAGAACTCTCTTAAGA	17836	CdiCas9	77	0
805	AATC	CTGTTAATGGAATCAGCCAA	17837	SpyCas9-3var-NRTH	77	0
806	ACTACC	aaTGCCACTGAGAACTCTCTTAAG	17838	Nme2Cas9	78	0
807	AAA	ACTGTTAATGGAATCAGCCA	17839	SpyCas9-SpRY	78	0
808	ACT	CCACTGAGAACTCTCTTAAG	17840	SpyCas9-SpRY	78	0
809	AAATCTTA	cttaCTGTTAATGGAATCAGCCA	17841	BlatCas9	78	0
810	ACTACCTT	atgcCACTGAGAACTCTCTTAAG	17842	BlatCas9	78	0
811	AAATC	cttaCTGTTAATGGAATCAGCCA	17843	BlatCas9	78	0
812	ACTAC	atgcCACTGAGAACTCTCTTAAG	17844	BlatCas9	78	0
813	AAATCTT	TTACTGTTAATGGAATCAGCCA	17845	CdiCas9	78	0
814	AAAT	ACTGTTAATGGAATCAGCCA	17846	SpyCas9-3var-NRRH	78	0
815	AAAT	taCTGTTAATGGAATCAGCCA	17847	iSpyMacCas9	78	0
816	AAA	TACTGTTAATGGAATCAGCC	17848	SpyCas9-SpRY	79	0
817	GAC	GCCACTGAGAACTCTCTTAA	17849	SpyCas9-SpRY	79	0
818	AAAATCT	CTTACTGTTAATGGAATCAGCC	17850	CdiCas9	79	0
819	AAAA	TACTGTTAATGGAATCAGCC	17851	SpyCas9-3var-NRRH	79	0
820	AAAA	ttACTGTTAATGGAATCAGCC	17852	iSpyMacCas9	79	0
821	GACT	GCCACTGAGAACTCTCTTAA	17853	SpyCas9-3var-NRCH	79	0
822	CAAAA	CTTACTGTTAATGGAATCAGC	17854	SauCas9KKH	80	0
823	CAAAAT	CTTACTGTTAATGGAATCAGC	17855	SauCas9KKH	80	0
824	CAAAAT	CTTACTGTTAATGGAATCAGC	17856	cCas9-v17	80	0
825	CAAAAT	CTTACTGTTAATGGAATCAGC	17857	cCas9-v42	80	0
826	AG	TGCCACTGAGAACTCTCTTA	17858	SpyCas9-NG	80	0

827	AG	TGCCACTGAGAACTCTCTTA	17859	SpyCas9-xCas	80	0
828	AG	TGCCACTGAGAACTCTCTTA	17860	SpyCas9-xCas-NG	80	0
829	CAA	TTACTGTTAATGGAATCAGC	17861	SpyCas9-SpRY	80	0
830	AGA	TGCCACTGAGAACTCTCTTA	17862	SpyCas9-SpG	80	0
831	AGA	TGCCACTGAGAACTCTCTTA	17863	SpyCas9-SpRY	80	0
832	CAAAATC	ACTTACTGTTAATGGAATCAGC	17864	CdiCas9	80	0
833	AGACTAC	AATGCCACTGAGAACTCTCTTA	17865	CdiCas9	80	0
834	CAAA	TTACTGTTAATGGAATCAGC	17866	SpyCas9-3var-NRRH	80	0
835	CAAA	ctTACTGTTAATGGAATCAGC	17867	iSpyMacCas9	80	0
836	AGAC	TGCCACTGAGAACTCTCTTA	17868	SpyCas9-3var-NRRH	80	0
837	AGAC	TGCCACTGAGAACTCTCTTA	17869	SpyCas9-VQR	80	0
838	CCAAA	ACTTACTGTTAATGGAATCAG	17870	SauCas9KKH	81	0
839	AAG	ATGCCACTGAGAACTCTCTT	17871	ScaCas9	81	0
840	AAG	ATGCCACTGAGAACTCTCTT	17872	ScaCas9-HiFi-Sc++	81	0
841	AAG	ATGCCACTGAGAACTCTCTT	17873	ScaCas9-Sc++	81	0
842	AAG	ATGCCACTGAGAACTCTCTT	17874	SpyCas9-SpRY	81	0
843	CCA	CTTACTGTTAATGGAATCAG	17875	SpyCas9-SpRY	81	0
844	AAGAC	aaaaTGCCACTGAGAACTCTCTT	17876	BlatCas9	81	0
845	AAGACT	AATGCCACTGAGAACTCTCTT	17877	cCas9-v16	81	0
846	AAGACT	AATGCCACTGAGAACTCTCTT	17878	cCas9-v21	81	0
847	CCAAAA	CTTACTGTTAATGGAATCAG	17879	St1Cas9-MTH17CL396	81	0
848	CCAAAA	ACTTACTGTTAATGGAATCAG	17880	cCas9-v17	81	0
849	CCAAAA	ACTTACTGTTAATGGAATCAG	17881	cCas9-v42	81	0
850	CCAAAAT	TACTTACTGTTAATGGAATCAG	17882	CdiCas9	81	0
851	CCAAAAT	TACTTACTGTTAATGGAATCAG	17883	CdiCas9	81	0
852	AAGA	ATGCCACTGAGAACTCTCTT	17884	SpyCas9-3var-NRRH	81	0

853	GCCAA	TACTTACTGTTAATGGAATCA	17885	SauCas9KKH	82	0
854	TAAGA	AAATGCCACTGAGAACTCTCT	17886	SauCas9KKH	82	0
855	TAAG	AAATGCCACTGAGAACTCTCT	17887	SauriCas9-KKH	82	0
856	TAAG	AATGCCACTGAGAACTCTCT	17888	SpyCas9-QQR1	82	0
857	TAAG	aaATGCCACTGAGAACTCTCT	17889	iSpyMacCas9	82	0
858	TAA	AATGCCACTGAGAACTCTCT	17890	SpyCas9-SpRY	82	0
859	GCC	ACTTACTGTTAATGGAATCA	17891	SpyCas9-SpRY	82	0
860	GCCAAA	TACTTACTGTTAATGGAATCA	17892	cCas9-v17	82	0
861	GCCAAA	TACTTACTGTTAATGGAATCA	17893	cCas9-v42	82	0
862	TAAGAC	AAATGCCACTGAGAACTCTCT	17894	cCas9-v17	82	0
863	TAAGAC	AAATGCCACTGAGAACTCTCT	17895	cCas9-v42	82	0
864	TTAAG	AAAATGCCACTGAGAACTCTC	17896	SauCas9KKH	83	0
865	AG	TACTTACTGTTAATGGAATC	17897	SpyCas9-NG	83	0
866	AG	TACTTACTGTTAATGGAATC	17898	SpyCas9-xCas	83	0
867	AG	TACTTACTGTTAATGGAATC	17899	SpyCas9-xCas-NG	83	0
868	AGC	TACTTACTGTTAATGGAATC	17900	SpyCas9-SpG	83	0
869	AGC	TACTTACTGTTAATGGAATC	17901	SpyCas9-SpRY	83	0
870	TTA	AAATGCCACTGAGAACTCTC	17902	SpyCas9-SpRY	83	0
871	TTAAGA	AAAATGCCACTGAGAACTCTC	17903	cCas9-v17	83	0
872	TTAAGA	AAAATGCCACTGAGAACTCTC	17904	cCas9-v42	83	0
873	TTAAGACT	agtaAAATGCCACTGAGAACTCTC	17905	NmeCas9	83	0
874	AGCC	TACTTACTGTTAATGGAATC	17906	SpyCas9-3var-NRCH	83	0
875	CTTAA	TAAAATGCCACTGAGAACTCT	17907	SauCas9KKH	84	0
876	CAG	TTACTTACTGTTAATGGAAT	17908	ScaCas9	84	0
877	CAG	TTACTTACTGTTAATGGAAT	17909	ScaCas9-HiFi-Sc++	84	0
878	CAG	TTACTTACTGTTAATGGAAT	17910	ScaCas9-Sc++	84	0
879	CAG	TTACTTACTGTTAATGGAAT	17911	SpyCas9-SpRY	84	0

880	CTT	AAAATGCCACTGAGAACTCT	17912	SpyCas9-SpRY	84	0
881	CAGCCAAA	aaatTACTTACTGTTAATGGAAT	17913	BlatCas9	84	0
882	CAGCCAAA	aaatTACTTACTGTTAATGGAAT	17914	BlatCas9	84	0
883	CAGCCAAA	aaATTACTTACTGTTAATGGAAT	17915	GeoCas9	84	0
884	CAGCC	aaatTACTTACTGTTAATGGAAT	17916	BlatCas9	84	0
885	CAGC	TTACTTACTGTTAATGGAAT	17917	SpyCas9-3var-NRRH	84	0
886	TCAGCC	gtAAATTACTTACTGTTAATGGAA	17918	Nme2Cas9	85	0
887	TCAG	AATTACTTACTGTTAATGGAA	17919	SauriCas9-KKH	85	0
888	TCA	ATTACTTACTGTTAATGGAA	17920	SpyCas9-SpRY	85	0
889	TCT	TAAAATGCCACTGAGAACTC	17921	SpyCas9-SpRY	85	0
890	TCAGCCAA	taaaTTACTTACTGTTAATGGAA	17922	BlatCas9	85	0
891	TCAGCCAA	taaaTTACTTACTGTTAATGGAA	17923	BlatCas9	85	0
892	TCAGC	taaaTTACTTACTGTTAATGGAA	17924	BlatCas9	85	0
893	ATCAG	AAATTACTTACTGTTAATGGA	17925	SauCas9KKH	86	0
894	ATC	AATTACTTACTGTTAATGGA	17926	SpyCas9-SpRY	86	0
895	CTC	GTAAAATGCCACTGAGAACT	17927	SpyCas9-SpRY	86	0
896	ATCAGC	AAATTACTTACTGTTAATGGA	17928	cCas9-v17	86	0
897	ATCAGC	AAATTACTTACTGTTAATGGA	17929	cCas9-v42	86	0
898	AAT	AAATTACTTACTGTTAATGG	17930	SpyCas9-SpRY	87	0
899	TCT	AGTAAAATGCCACTGAGAAC	17931	SpyCas9-SpRY	87	0
900	AATC	AAATTACTTACTGTTAATGG	17932	SpyCas9-3var-NRTH	87	0
901	GAA	TAAATTACTTACTGTTAATG	17933	SpyCas9-SpRY	88	0
902	GAA	TAAATTACTTACTGTTAATG	17934	SpyCas9-xCas	88	0
903	CTC	AAGTAAAATGCCACTGAGAA	17935	SpyCas9-SpRY	88	0
904	CTCTCTTA	aagaAGTAAAATGCCACTGAGAA	17936	BlatCas9	88	0
905	GAATC	gtgtAAATTACTTACTGTTAATG	17937	BlatCas9	88	0
906	CTCTC	aagaAGTAAAATGCCACTGAGAA	17938	BlatCas9	88	0

907	GAAT	TAAATTACTTACTGTTAATG	17939	SpyCas9-3var-NRRH	88	0
908	GAAT	gtAAATTACTTACTGTTAATG	17940	iSpyMacCas9	88	0
909	GG	GTAAATTACTTACTGTTAAT	17941	SpyCas9-NG	89	0
910	GG	GTAAATTACTTACTGTTAAT	17942	SpyCas9-xCas	89	0
911	GG	GTAAATTACTTACTGTTAAT	17943	SpyCas9-xCas-NG	89	0
912	GGA	GTAAATTACTTACTGTTAAT	17944	SpyCas9-SpG	89	0
913	GGA	GTAAATTACTTACTGTTAAT	17945	SpyCas9-SpRY	89	0
914	ACT	GAAGTAAAATGCCACTGAGA	17946	SpyCas9-SpRY	89	0
915	GGAA	GTAAATTACTTACTGTTAAT	17947	SpyCas9-3var-NRRH	89	0
916	GGAA	GTAAATTACTTACTGTTAAT	17948	SpyCas9-VQR	89	0
917	TGGAA	agGTGTAAATTACTTACTGTTAA	17949	SauCas9	90	0
918	TGGAA	GTGTAAATTACTTACTGTTAA	17950	SauCas9KKH	90	0
919	TGGAAT	agGTGTAAATTACTTACTGTTAA	17951	SauCas9	90	0
920	TGGAAT	GTGTAAATTACTTACTGTTAA	17952	SauCas9KKH	90	0
921	TGGAAT	GTGTAAATTACTTACTGTTAA	17953	cCas9-v17	90	0
922	TGGAAT	GTGTAAATTACTTACTGTTAA	17954	cCas9-v42	90	0
923	TGG	TGTAAATTACTTACTGTTAA	17955	ScaCas9	90	0
924	TGG	TGTAAATTACTTACTGTTAA	17956	ScaCas9-HiFi-Sc++	90	0
925	TGG	TGTAAATTACTTACTGTTAA	17957	ScaCas9-Sc++	90	0
926	TGG	TGTAAATTACTTACTGTTAA	17958	SpyCas9	90	0
927	TGG	TGTAAATTACTTACTGTTAA	17959	SpyCas9-HF1	90	0
928	TGG	TGTAAATTACTTACTGTTAA	17960	SpyCas9-SpG	90	0
929	TGG	TGTAAATTACTTACTGTTAA	17961	SpyCas9-SpRY	90	0
930	TG	TGTAAATTACTTACTGTTAA	17962	SpyCas9-NG	90	0
931	TG	TGTAAATTACTTACTGTTAA	17963	SpyCas9-xCas	90	0
932	TG	TGTAAATTACTTACTGTTAA	17964	SpyCas9-xCas-NG	90	0
933	AAC	AGAAGTAAAATGCCACTGAG	17965	SpyCas9-SpRY	90	0

934	AACTC	aaaaGAAGTAAAATGCCACTGAG	17966	BlatCas9	90	0
935	TGGAATC	GGTGTAAATTACTTACTGTTAA	17967	CdiCas9	90	0
936	TGGA	TGTAAATTACTTACTGTTAA	17968	SpyCas9-3var-NRRH	90	0
937	AACT	AGAAGTAAAATGCCACTGAG	17969	SpyCas9-3var-NRCH	90	0
938	ATGGA	aaGGTGTAAATTACTTACTGTTA	17970	SauCas9	91	0
939	ATGGA	GGTGTAAATTACTTACTGTTA	17971	SauCas9KKH	91	0
940	ATGG	GGTGTAAATTACTTACTGTTA	17972	SauriCas9	91	0
941	ATGG	GGTGTAAATTACTTACTGTTA	17973	SauriCas9-KKH	91	0
942	ATG	GTGTAAATTACTTACTGTTA	17974	ScaCas9	91	0
943	ATG	GTGTAAATTACTTACTGTTA	17975	ScaCas9-HiFi-Sc++	91	0
944	ATG	GTGTAAATTACTTACTGTTA	17976	ScaCas9-Sc++	91	0
945	ATG	GTGTAAATTACTTACTGTTA	17977	SpyCas9-SpRY	91	0
946	GAA	AAGAAGTAAAATGCCACTGA	17978	SpyCas9-SpRY	91	0
947	GAA	AAGAAGTAAAATGCCACTGA	17979	SpyCas9-xCas	91	0
948	ATGGAAT	GTGTAAATTACTTACTGTTA	17980	St1Cas9	91	0
949	ATGGAA	GGTGTAAATTACTTACTGTTA	17981	cCas9-v17	91	0
950	ATGGAA	GGTGTAAATTACTTACTGTTA	17982	cCas9-v42	91	0
951	GAACTCT	AAAAGAAGTAAAATGCCACTGA	17983	CdiCas9	91	0
952	GAAC	AAGAAGTAAAATGCCACTGA	17984	SpyCas9-3var-NRRH	91	0
953	GAAC	aaAGAAGTAAAATGCCACTGA	17985	iSpyMacCas9	91	0
954	AATGG	AGGTGTAAATTACTTACTGTT	17986	SauCas9KKH	92	0
955	AG	AAAGAAGTAAAATGCCACTG	17987	SpyCas9-NG	92	0
956	AG	AAAGAAGTAAAATGCCACTG	17988	SpyCas9-xCas	92	0
957	AG	AAAGAAGTAAAATGCCACTG	17989	SpyCas9-xCas-NG	92	0
958	AAT	GGTGTAAATTACTTACTGTT	17990	SpyCas9-SpRY	92	0
959	AGA	AAAGAAGTAAAATGCCACTG	17991	SpyCas9-SpG	92	0
960	AGA	AAAGAAGTAAAATGCCACTG	17992	SpyCas9-SpRY	92	0

961	AGAAC	aaaaAAGAAGTAAAATGCCACTG	17993	BlatCas9	92	0
962	AGAACT	AAAAGAAGTAAAATGCCACTG	17994	cCas9-v16	92	0
963	AGAACT	AAAAGAAGTAAAATGCCACTG	17995	cCas9-v21	92	0
964	AGAACTC	AAAAAGAAGTAAAATGCCACTG	17996	CdiCas9	92	0
965	AGAA	AAAGAAGTAAAATGCCACTG	17997	SpyCas9-3var-NRRH	92	0
966	AGAA	AAAGAAGTAAAATGCCACTG	17998	SpyCas9-VQR	92	0
967	GAGAA	taAAAAAGAAGTAAAATGCCACT	17999	SauCas9	93	0
968	GAGAA	AAAAAGAAGTAAAATGCCACT	18000	SauCas9KKH	93	0
969	GAG	AAAAGAAGTAAAATGCCACT	18001	ScaCas9	93	0
970	GAG	AAAAGAAGTAAAATGCCACT	18002	ScaCas9-HiFi-Sc++	93	0
971	GAG	AAAAGAAGTAAAATGCCACT	18003	ScaCas9-Sc++	93	0
972	GAG	AAAAGAAGTAAAATGCCACT	18004	SpyCas9-SpRY	93	0
973	TAA	AGGTGTAAATTACTTACTGT	18005	SpyCas9-SpRY	93	0
974	GAGAAC	AAAAAGAAGTAAAATGCCACT	18006	cCas9-v17	93	0
975	GAGAAC	AAAAAGAAGTAAAATGCCACT	18007	cCas9-v42	93	0
976	GAGAACT	AAAAAAGAAGTAAAATGCCACT	18008	CdiCas9	93	0
977	TAAT	AGGTGTAAATTACTTACTGT	18009	SpyCas9-3var-NRRH	93	0
978	TAAT	aaGGTGTAAATTACTTACTGT	18010	iSpyMacCas9	93	0
979	GAGA	AAAAGAAGTAAAATGCCACT	18011	SpyCas9-3var-NRRH	93	0
980	TGAGA	AAAAAAGAAGTAAAATGCCAC	18012	SauCas9KKH	94	0
981	TGAG	AAAAAAGAAGTAAAATGCCAC	18013	SauriCas9-KKH	94	0
982	TGAG	AAAAAGAAGTAAAATGCCAC	18014	SpyCas9-VQR	94	0
983	TG	AAAAAGAAGTAAAATGCCAC	18015	SpyCas9-NG	94	0
984	TG	AAAAAGAAGTAAAATGCCAC	18016	SpyCas9-xCas	94	0
985	TG	AAAAAGAAGTAAAATGCCAC	18017	SpyCas9-xCas-NG	94	0
986	TGA	AAAAAGAAGTAAAATGCCAC	18018	SpyCas9-SpG	94	0
987	TGA	AAAAAGAAGTAAAATGCCAC	18019	SpyCas9-SpRY	94	0

988	TTA	AAGGTGTAAATTACTTACTG	18020	SpyCas9-SpRY	94	0
989	TGAGAA	AAAAAAGAAGTAAAATGCCAC	18021	cCas9-v17	94	0
990	TGAGAA	AAAAAAGAAGTAAAATGCCAC	18022	cCas9-v42	94	0
991	CTGAG	ccTAAAAAAGAAGTAAAATGCCA	18023	SauCas9	95	0
992	CTGAG	TAAAAAAGAAGTAAAATGCCA	18024	SauCas9KKH	95	0
993	GTTAA	GTAAGGTGTAAATTACTTACT	18025	SauCas9KKH	95	0
994	GTTAAT	GTAAGGTGTAAATTACTTACT	18026	SauCas9KKH	95	0
995	CTG	AAAAAAGAAGTAAAATGCCA	18027	ScaCas9	95	0
996	CTG	AAAAAAGAAGTAAAATGCCA	18028	ScaCas9-HiFi-Sc++	95	0
997	CTG	AAAAAAGAAGTAAAATGCCA	18029	ScaCas9-Sc++	95	0
998	CTG	AAAAAAGAAGTAAAATGCCA	18030	SpyCas9-SpRY	95	0
999	GTT	TAAGGTGTAAATTACTTACT	18031	SpyCas9-SpRY	95	0
1000	CTGAGA	TAAAAAAGAAGTAAAATGCCA	18032	cCas9-v17	95	0
1001	CTGAGA	TAAAAAAGAAGTAAAATGCCA	18033	cCas9-v42	95	0
1002	ACTGA	CTAAAAAAGAAGTAAAATGCC	18034	SauCas9KKH	96	0
1003	TG	GTAAGGTGTAAATTACTTAC	18035	SpyCas9-NG	96	0
1004	TG	GTAAGGTGTAAATTACTTAC	18036	SpyCas9-xCas	96	0
1005	TG	GTAAGGTGTAAATTACTTAC	18037	SpyCas9-xCas-NG	96	0
1006	TGT	GTAAGGTGTAAATTACTTAC	18038	SpyCas9-SpG	96	0
1007	TGT	GTAAGGTGTAAATTACTTAC	18039	SpyCas9-SpRY	96	0
1008	ACT	TAAAAAAGAAGTAAAATGCC	18040	SpyCas9-SpRY	96	0
1009	TGTT	GTAAGGTGTAAATTACTTAC	18041	SpyCas9-3var-NRTH	96	0
1010	CTG	CGTAAGGTGTAAATTACTTA	18042	ScaCas9	97	0
1011	CTG	CGTAAGGTGTAAATTACTTA	18043	ScaCas9-HiFi-Sc++	97	0
1012	CTG	CGTAAGGTGTAAATTACTTA	18044	ScaCas9-Sc++	97	0
1013	CTG	CGTAAGGTGTAAATTACTTA	18045	SpyCas9-SpRY	97	0
1014	CAC	CTAAAAAAGAAGTAAAATGC	18046	SpyCas9-SpRY	97	0

1015	CACT	CTAAAAAAGAAGTAAAATGC	18047	SpyCas9-3var-NRCH	97	0
1016	ACT	TCGTAAGGTGTAAATTACTT	18048	SpyCas9-SpRY	98	0
1017	CCA	CCTAAAAAAGAAGTAAAATG	18049	SpyCas9-SpRY	98	0
1018	TACTGTT	tggCCTCGTAAGGTGTAAATTACT	18050	PpnCas9	99	0
1019	TAC	CTCGTAAGGTGTAAATTACT	18051	SpyCas9-SpRY	99	0
1020	GCC	TCCTAAAAAAGAAGTAAAAT	18052	SpyCas9-SpRY	99	0
1021	GCCACTGA	tgttCCTAAAAAAGAAGTAAAAT	18053	BlatCas9	99	0
1022	GCCAC	tgttCCTAAAAAAGAAGTAAAAT	18054	BlatCas9	99	0
1023	GCCACT	TTCCTAAAAAAGAAGTAAAAT	18055	cCas9-v16	99	0
1024	GCCACT	TTCCTAAAAAAGAAGTAAAAT	18056	cCas9-v21	99	0
1025	TACT	CTCGTAAGGTGTAAATTACT	18057	SpyCas9-3var-NRCH	99	0
1026	TG	TTCCTAAAAAAGAAGTAAAA	18058	SpyCas9-NG	100	0
1027	TG	TTCCTAAAAAAGAAGTAAAA	18059	SpyCas9-xCas	100	0
1028	TG	TTCCTAAAAAAGAAGTAAAA	18060	SpyCas9-xCas-NG	100	0
1029	TGC	TTCCTAAAAAAGAAGTAAAA	18061	SpyCas9-SpG	100	0
1030	TGC	TTCCTAAAAAAGAAGTAAAA	18062	SpyCas9-SpRY	100	0
1031	TTA	CCTCGTAAGGTGTAAATTAC	18063	SpyCas9-SpRY	100	0
1032	TGCC	TTCCTAAAAAAGAAGTAAAA	18064	SpyCas9-3var-NRCH	100	0

Table 1B: Exemplary gRNA spacer Cas pairs for correcting the pathogenic R261Q mutation

Table 1B provides a gRNA database for correcting the pathogenic R261Q mutation in PAH. List of spacers, PAMs, and Cas variants for generating a nick at an appropriate position to enable installation of a desired genomic edit with a gene modifying system. The spacers in this table are designed to be used with a gene modifying polypeptide comprising a nickase variant of the Cas species indicated in the table. Tables 2B, 3B, and 4B detail the other components of the system and are organized such that the ID number shown here in Column 1 (“ID”) is meant to correspond to the same ID number in Tables 2B, 2B, and 4B.

ID	PAM sequence	gRNA spacer	SEQ ID NO	Cas species	distance	Overlaps mutation
1	TCTTCC	tcTTGGGTGGCCTGGCCTTCCAAG	19152	Nme2Cas9	0	0
2	TCT	GGGTGGCCTGGCCTTCCAAG	19153	SpyCas9-SpRY	0	0
3	TCTTC	cttgGGTGGCCTGGCCTTCCAAG	19154	BlatCas9	0	0
4	GAAGG	CTGTGTGCAGTGGAAGACTTG	19155	SauCas9KKH	1	0
5	GAAG	CTGTGTGCAGTGGAAGACTTG	19156	SauriCas9-KKH	1	0
6	GAAG	TGTGTGCAGTGGAAGACTTG	19157	SpyCas9-QQR1	1	0
7	GAAG	ctGTGTGCAGTGGAAGACTTG	19158	iSpyMacCas9	1	0
8	GAA	TGTGTGCAGTGGAAGACTTG	19159	SpyCas9-SpRY	1	0
9	GAA	TGTGTGCAGTGGAAGACTTG	19160	SpyCas9-xCas	1	0
10	GTC	TGGGTGGCCTGGCCTTCCAA	19161	SpyCas9-SpRY	1	0
11	GAAGGC	CTGTGTGCAGTGGAAGACTTG	19162	cCas9-v17	1	0
12	GAAGGC	CTGTGTGCAGTGGAAGACTTG	19163	cCas9-v42	1	0
13	GGAAG	ACTGTGTGCAGTGGAAGACTT	19164	SauCas9KKH	2	0
14	AG	TTGGGTGGCCTGGCCTTCCA	19165	SpyCas9-NG	2	0
15	AG	TTGGGTGGCCTGGCCTTCCA	19166	SpyCas9-xCas	2	0
16	AG	TTGGGTGGCCTGGCCTTCCA	19167	SpyCas9-xCas-NG	2	0
17	GG	CTGTGTGCAGTGGAAGACTT	19168	SpyCas9-NG	2	0
18	GG	CTGTGTGCAGTGGAAGACTT	19169	SpyCas9-xCas	2	0
19	GG	CTGTGTGCAGTGGAAGACTT	19170	SpyCas9-xCas-NG	2	0
20	AGT	TTGGGTGGCCTGGCCTTCCA	19171	SpyCas9-SpG	2	0
21	AGT	TTGGGTGGCCTGGCCTTCCA	19172	SpyCas9-SpRY	2	0
22	GGA	CTGTGTGCAGTGGAAGACTT	19173	SpyCas9-SpG	2	0
23	GGA	CTGTGTGCAGTGGAAGACTT	19174	SpyCas9-SpRY	2	0
24	GGAAGG	ACTGTGTGCAGTGGAAGACTT	19175	cCas9-v17	2	0
25	GGAAGG	ACTGTGTGCAGTGGAAGACTT	19176	cCas9-v42	2	0
26	GGAA	CTGTGTGCAGTGGAAGACTT	19177	SpyCas9-3var-NRRH	2	0
27	GGAA	CTGTGTGCAGTGGAAGACTT	19178	SpyCas9-VQR	2	0
28	AGTC	TTGGGTGGCCTGGCCTTCCA	19179	SpyCas9-3var-NRTH	2	0
29	tGGAA	tgTACTGTGTGCAGTGGAAGACT	19180	SauCas9	3	1
30	tGGAA	TACTGTGTGCAGTGGAAGACT	19181	SauCas9KKH	3	1
31	aAG	CTTGGGTGGCCTGGCCTTCC	19182	ScaCas9	3	1
32	aAG	CTTGGGTGGCCTGGCCTTCC	19183	ScaCas9-HiFi-Sc++	3	1
33	aAG	CTTGGGTGGCCTGGCCTTCC	19184	ScaCas9-Sc++	3	1
34	aAG	CTTGGGTGGCCTGGCCTTCC	19185	SpyCas9-SpRY	3	1

35	tGG	ACTGTGTGCAGTGGAAGACT	19186	ScaCas9	3	1
36	tGG	ACTGTGTGCAGTGGAAGACT	19187	ScaCas9-HiFi-Sc++	3	1
37	tGG	ACTGTGTGCAGTGGAAGACT	19188	ScaCas9-Sc++	3	1
38	tGG	ACTGTGTGCAGTGGAAGACT	19189	SpyCas9	3	1
39	tGG	ACTGTGTGCAGTGGAAGACT	19190	SpyCas9-HF1	3	1
40	tGG	ACTGTGTGCAGTGGAAGACT	19191	SpyCas9-SpG	3	1
41	tGG	ACTGTGTGCAGTGGAAGACT	19192	SpyCas9-SpRY	3	1
42	tG	ACTGTGTGCAGTGGAAGACT	19193	SpyCas9-NG	3	1
43	tG	ACTGTGTGCAGTGGAAGACT	19194	SpyCas9-xCas	3	1
44	tG	ACTGTGTGCAGTGGAAGACT	19195	SpyCas9-xCas-NG	3	1
45	aAGTC	tttcTTGGGTGGCCTGGCCTTCC	19196	BlatCas9	3	1
46	tGGAAG	TACTGTGTGCAGTGGAAGACT	19197	cCas9-v17	3	1
47	tGGAAG	TACTGTGTGCAGTGGAAGACT	19198	cCas9-v42	3	1
48	aAGTCTT	TTCTTGGGTGGCCTGGCCTTCC	19199	CdiCas9	3	1
49	aAGT	CTTGGGTGGCCTGGCCTTCC	19200	SpyCas9-3var-NRRH	3	1
50	tGGA	ACTGTGTGCAGTGGAAGACT	19201	SpyCas9-3var-NRRH	3	1
51	TtGGA	atGTACTGTGTGCAGTGGAAGAC	19202	SauCas9	4	1
52	TtGGA	GTACTGTGTGCAGTGGAAGAC	19203	SauCas9KKH	4	1
53	TtGG	GTACTGTGTGCAGTGGAAGAC	19204	SauriCas9	4	1
54	TtGG	GTACTGTGTGCAGTGGAAGAC	19205	SauriCas9-KKH	4	1
55	CaAG	TTCTTGGGTGGCCTGGCCTTC	19206	SauriCas9-KKH	4	1
56	CaAG	TCTTGGGTGGCCTGGCCTTC	19207	SpyCas9-QQR1	4	1
57	CaAG	ttCTTGGGTGGCCTGGCCTTC	19208	iSpyMacCas9	4	1
58	TtG	TACTGTGTGCAGTGGAAGAC	19209	ScaCas9	4	1
59	TtG	TACTGTGTGCAGTGGAAGAC	19210	ScaCas9-HiFi-Sc++	4	1
60	TtG	TACTGTGTGCAGTGGAAGAC	19211	ScaCas9-Sc++	4	1
61	TtG	TACTGTGTGCAGTGGAAGAC	19212	SpyCas9-SpRY	4	1
62	CaA	TCTTGGGTGGCCTGGCCTTC	19213	SpyCas9-SpRY	4	1
63	TtGGAA	GTACTGTGTGCAGTGGAAGAC	19214	cCas9-v17	4	1
64	TtGGAA	GTACTGTGTGCAGTGGAAGAC	19215	cCas9-v42	4	1
65	CCaAG	TTTCTTGGGTGGCCTGGCCTT	19216	SauCas9KKH	5	1
66	CTtGG	TGTACTGTGTGCAGTGGAAGA	19217	SauCas9KKH	5	1
67	CCaAGT	TTTCTTGGGTGGCCTGGCCTT	19218	SauCas9KKH	5	1
68	CCaAGT	TTTCTTGGGTGGCCTGGCCTT	19219	cCas9-v17	5	1
69	CCaAGT	TTTCTTGGGTGGCCTGGCCTT	19220	cCas9-v42	5	1
70	CTt	GTACTGTGTGCAGTGGAAGA	19221	SpyCas9-SpRY	5	1
71	CCa	TTCTTGGGTGGCCTGGCCTT	19222	SpyCas9-SpRY	5	1

72	CCaAGTCT	ggatTTCTTGGGTGGCCTGGCCTT	19223	NmeCas9	5	1
73	TCCaA	ATTTCTTGGGTGGCCTGGCCT	19224	SauCas9KKH	6	1
74	ACT	TGTACTGTGTGCAGTGGAAG	19225	SpyCas9-SpRY	6	0
75	TCC	TTTCTTGGGTGGCCTGGCCT	19226	SpyCas9-SpRY	6	0
76	TCCaAG	ATTTCTTGGGTGGCCTGGCCT	19227	cCas9-v17	6	1
77	TCCaAG	ATTTCTTGGGTGGCCTGGCCT	19228	cCas9-v42	6	1
78	GAC	ATGTACTGTGTGCAGTGGAA	19229	SpyCas9-SpRY	7	0
79	TTC	ATTTCTTGGGTGGCCTGGCC	19230	SpyCas9-SpRY	7	0
80	GACT	ATGTACTGTGTGCAGTGGAA	19231	SpyCas9-3var-NRCH	7	0
81	AG	GATGTACTGTGTGCAGTGGA	19232	SpyCas9-NG	8	0
82	AG	GATGTACTGTGTGCAGTGGA	19233	SpyCas9-xCas	8	0
83	AG	GATGTACTGTGTGCAGTGGA	19234	SpyCas9-xCas-NG	8	0
84	AGA	GATGTACTGTGTGCAGTGGA	19235	SpyCas9-SpG	8	0
85	AGA	GATGTACTGTGTGCAGTGGA	19236	SpyCas9-SpRY	8	0
86	CTT	GATTTCTTGGGTGGCCTGGC	19237	SpyCas9-SpRY	8	0
87	CTTCCaAG	cgggATTTCTTGGGTGGCCTGGC	19238	BlatCas9	8	1
88	CTTCC	cgggATTTCTTGGGTGGCCTGGC	19239	BlatCas9	8	0
89	AGAC	GATGTACTGTGTGCAGTGGA	19240	SpyCas9-3var-NRRH	8	0
90	AGAC	GATGTACTGTGTGCAGTGGA	19241	SpyCas9-VQR	8	0
91	CCTTCC	ctCGGGATTTCTTGGGTGGCCTGG	19242	Nme2Cas9	9	0
92	AAG	TGATGTACTGTGTGCAGTGG	19243	ScaCas9	9	0
93	AAG	TGATGTACTGTGTGCAGTGG	19244	ScaCas9-HiFi-Sc++	9	0
94	AAG	TGATGTACTGTGTGCAGTGG	19245	ScaCas9-Sc++	9	0
95	AAG	TGATGTACTGTGTGCAGTGG	19246	SpyCas9-SpRY	9	0
96	CCT	GGATTTCTTGGGTGGCCTGG	19247	SpyCas9-SpRY	9	0
97	AAGACTtG	gtctGATGTACTGTGTGCAGTGG	19248	BlatCas9	9	1
98	CCTTCCaA	tcggGATTTCTTGGGTGGCCTGG	19249	BlatCas9	9	1
99	CCTTCCaA	tcggGATTTCTTGGGTGGCCTGG	19250	BlatCas9	9	1
100	AAGAC	gtctGATGTACTGTGTGCAGTGG	19251	BlatCas9	9	0
101	CCTTC	tcggGATTTCTTGGGTGGCCTGG	19252	BlatCas9	9	0
102	AAGACT	CTGATGTACTGTGTGCAGTGG	19253	cCas9-v16	9	0
103	AAGACT	CTGATGTACTGTGTGCAGTGG	19254	cCas9-v21	9	0
104	AAGACTt	TCTGATGTACTGTGTGCAGTGG	19255	CdiCas9	9	1
105	AAGA	TGATGTACTGTGTGCAGTGG	19256	SpyCas9-3var-NRRH	9	0
106	GAAGA	TCTGATGTACTGTGTGCAGTG	19257	SauCas9KKH	10	0
107	GAAG	TCTGATGTACTGTGTGCAGTG	19258	SauriCas9-KKH	10	0
108	GAAG	CTGATGTACTGTGTGCAGTG	19259	SpyCas9-QQR1	10	0

109	GAAG	tcTGATGTACTGTGTGCAGTG	19260	iSpyMacCas9	10	0
110	GAA	CTGATGTACTGTGTGCAGTG	19261	SpyCas9-SpRY	10	0
111	GAA	CTGATGTACTGTGTGCAGTG	19262	SpyCas9-xCas	10	0
112	GCC	GGGATTTCTTGGGTGGCCTG	19263	SpyCas9-SpRY	10	0
113	GAAGAC	TCTGATGTACTGTGTGCAGTG	19264	cCas9-v17	10	0
114	GAAGAC	TCTGATGTACTGTGTGCAGTG	19265	cCas9-v42	10	0
115	GGAAG	GTCTGATGTACTGTGTGCAGT	19266	SauCas9KKH	11	0
116	GG	TCTGATGTACTGTGTGCAGT	19267	SpyCas9-NG	11	0
117	GG	TCTGATGTACTGTGTGCAGT	19268	SpyCas9-xCas	11	0
118	GG	TCTGATGTACTGTGTGCAGT	19269	SpyCas9-xCas-NG	11	0
119	GG	CGGGATTTCTTGGGTGGCCT	19270	SpyCas9-NG	11	0
120	GG	CGGGATTTCTTGGGTGGCCT	19271	SpyCas9-xCas	11	0
121	GG	CGGGATTTCTTGGGTGGCCT	19272	SpyCas9-xCas-NG	11	0
122	GGA	TCTGATGTACTGTGTGCAGT	19273	SpyCas9-SpG	11	0
123	GGA	TCTGATGTACTGTGTGCAGT	19274	SpyCas9-SpRY	11	0
124	GGC	CGGGATTTCTTGGGTGGCCT	19275	SpyCas9-SpG	11	0
125	GGC	CGGGATTTCTTGGGTGGCCT	19276	SpyCas9-SpRY	11	0
126	GGAAGA	GTCTGATGTACTGTGTGCAGT	19277	cCas9-v17	11	0
127	GGAAGA	GTCTGATGTACTGTGTGCAGT	19278	cCas9-v42	11	0
128	GGAAGACT	catgTCTGATGTACTGTGTGCAGT	19279	NmeCas9	11	0
129	GGAA	TCTGATGTACTGTGTGCAGT	19280	SpyCas9-3var-NRRH	11	0
130	GGAA	TCTGATGTACTGTGTGCAGT	19281	SpyCas9-VQR	11	0
131	GGCC	CGGGATTTCTTGGGTGGCCT	19282	SpyCas9-3var-NRCH	11	0
132	TGGAA	caTGTCTGATGTACTGTGTGCAG	19283	SauCas9	12	0
133	TGGAA	TGTCTGATGTACTGTGTGCAG	19284	SauCas9KKH	12	0
134	TGG	GTCTGATGTACTGTGTGCAG	19285	ScaCas9	12	0
135	TGG	GTCTGATGTACTGTGTGCAG	19286	ScaCas9-HiFi-Sc++	12	0
136	TGG	GTCTGATGTACTGTGTGCAG	19287	ScaCas9-Sc++	12	0
137	TGG	GTCTGATGTACTGTGTGCAG	19288	SpyCas9	12	0
138	TGG	GTCTGATGTACTGTGTGCAG	19289	SpyCas9-HF1	12	0
139	TGG	GTCTGATGTACTGTGTGCAG	19290	SpyCas9-SpG	12	0
140	TGG	GTCTGATGTACTGTGTGCAG	19291	SpyCas9-SpRY	12	0
141	TGG	TCGGGATTTCTTGGGTGGCC	19292	ScaCas9	12	0
142	TGG	TCGGGATTTCTTGGGTGGCC	19293	ScaCas9-HiFi-Sc++	12	0
143	TGG	TCGGGATTTCTTGGGTGGCC	19294	ScaCas9-Sc++	12	0
144	TGG	TCGGGATTTCTTGGGTGGCC	19295	SpyCas9	12	0
145	TGG	TCGGGATTTCTTGGGTGGCC	19296	SpyCas9-HF1	12	0

146	TGG	TCGGGATTTCTTGGGTGGCC	19297	SpyCas9-SpG	12	0
147	TGG	TCGGGATTTCTTGGGTGGCC	19298	SpyCas9-SpRY	12	0
148	TG	GTCTGATGTACTGTGTGCAG	19299	SpyCas9-NG	12	0
149	TG	GTCTGATGTACTGTGTGCAG	19300	SpyCas9-xCas	12	0
150	TG	GTCTGATGTACTGTGTGCAG	19301	SpyCas9-xCas-NG	12	0
151	TG	TCGGGATTTCTTGGGTGGCC	19302	SpyCas9-NG	12	0
152	TG	TCGGGATTTCTTGGGTGGCC	19303	SpyCas9-xCas	12	0
153	TG	TCGGGATTTCTTGGGTGGCC	19304	SpyCas9-xCas-NG	12	0
154	TGGCC	ctctCGGGATTTCTTGGGTGGCC	19305	BlatCas9	12	0
155	TGGAAG	TGTCTGATGTACTGTGTGCAG	19306	cCas9-v17	12	0
156	TGGAAG	TGTCTGATGTACTGTGTGCAG	19307	cCas9-v42	12	0
157	TGGCCTT	TCTCGGGATTTCTTGGGTGGCC	19308	CdiCas9	12	0
158	TGGA	GTCTGATGTACTGTGTGCAG	19309	SpyCas9-3var-NRRH	12	0
159	TGGC	TCGGGATTTCTTGGGTGGCC	19310	SpyCas9-3var-NRRH	12	0
160	CTGGCC	tcCTCTCGGGATTTCTTGGGTGGC	19311	Nme2Cas9	13	0
161	GTGGA	ccATGTCTGATGTACTGTGTGCA	19312	SauCas9	13	0
162	GTGGA	ATGTCTGATGTACTGTGTGCA	19313	SauCas9KKH	13	0
163	GTGG	ATGTCTGATGTACTGTGTGCA	19314	SauriCas9	13	0
164	GTGG	ATGTCTGATGTACTGTGTGCA	19315	SauriCas9-KKH	13	0
165	CTGG	TCTCGGGATTTCTTGGGTGGC	19316	SauriCas9	13	0
166	CTGG	TCTCGGGATTTCTTGGGTGGC	19317	SauriCas9-KKH	13	0
167	GTG	TGTCTGATGTACTGTGTGCA	19318	ScaCas9	13	0
168	GTG	TGTCTGATGTACTGTGTGCA	19319	ScaCas9-HiFi-Sc++	13	0
169	GTG	TGTCTGATGTACTGTGTGCA	19320	ScaCas9-Sc++	13	0
170	GTG	TGTCTGATGTACTGTGTGCA	19321	SpyCas9-SpRY	13	0
171	CTG	CTCGGGATTTCTTGGGTGGC	19322	ScaCas9	13	0
172	CTG	CTCGGGATTTCTTGGGTGGC	19323	ScaCas9-HiFi-Sc++	13	0
173	CTG	CTCGGGATTTCTTGGGTGGC	19324	ScaCas9-Sc++	13	0
174	CTG	CTCGGGATTTCTTGGGTGGC	19325	SpyCas9-SpRY	13	0
175	CTGGCCTT	cctcTCGGGATTTCTTGGGTGGC	19326	BlatCas9	13	0
176	CTGGC	cctcTCGGGATTTCTTGGGTGGC	19327	BlatCas9	13	0
177	GTGGAA	ATGTCTGATGTACTGTGTGCA	19328	cCas9-v17	13	0
178	GTGGAA	ATGTCTGATGTACTGTGTGCA	19329	cCas9-v42	13	0
179	AGTGG	CATGTCTGATGTACTGTGTGC	19330	SauCas9KKH	14	0
180	CCTGG	CTCTCGGGATTTCTTGGGTGG	19331	SauCas9KKH	14	0
181	AG	ATGTCTGATGTACTGTGTGC	19332	SpyCas9-NG	14	0
182	AG	ATGTCTGATGTACTGTGTGC	19333	SpyCas9-xCas	14	0

183	AG	ATGTCTGATGTACTGTGTGC	19334	SpyCas9-xCas-NG	14	0
184	AGT	ATGTCTGATGTACTGTGTGC	19335	SpyCas9-SpG	14	0
185	AGT	ATGTCTGATGTACTGTGTGC	19336	SpyCas9-SpRY	14	0
186	CCT	TCTCGGGATTTCTTGGGTGG	19337	SpyCas9-SpRY	14	0
187	CAG	CATGTCTGATGTACTGTGTG	19338	ScaCas9	15	0
188	CAG	CATGTCTGATGTACTGTGTG	19339	ScaCas9-HiFi-Sc++	15	0
189	CAG	CATGTCTGATGTACTGTGTG	19340	ScaCas9-Sc++	15	0
190	CAG	CATGTCTGATGTACTGTGTG	19341	SpyCas9-SpRY	15	0
191	GCC	CTCTCGGGATTTCTTGGGTG	19342	SpyCas9-SpRY	15	0
192	CAGT	CATGTCTGATGTACTGTGTG	19343	SpyCas9-3var-NRRH	15	0
193	GCAG	TCCATGTCTGATGTACTGTGT	19344	SauriCas9-KKH	16	0
194	GG	CCTCTCGGGATTTCTTGGGT	19345	SpyCas9-NG	16	0
195	GG	CCTCTCGGGATTTCTTGGGT	19346	SpyCas9-xCas	16	0
196	GG	CCTCTCGGGATTTCTTGGGT	19347	SpyCas9-xCas-NG	16	0
197	GGC	CCTCTCGGGATTTCTTGGGT	19348	SpyCas9-SpG	16	0
198	GGC	CCTCTCGGGATTTCTTGGGT	19349	SpyCas9-SpRY	16	0
199	GCA	CCATGTCTGATGTACTGTGT	19350	SpyCas9-SpRY	16	0
200	GCAGTG	TCCATGTCTGATGTACTGTGT	19351	cCas9-v16	16	0
201	GCAGTG	TCCATGTCTGATGTACTGTGT	19352	cCas9-v21	16	0
202	GGCC	CCTCTCGGGATTTCTTGGGT	19353	SpyCas9-3var-NRCH	16	0
203	TGCAG	ATCCATGTCTGATGTACTGTG	19354	SauCas9KKH	17	0
204	TGCAGT	ATCCATGTCTGATGTACTGTG	19355	SauCas9KKH	17	0
205	TGCAGT	ATCCATGTCTGATGTACTGTG	19356	cCas9-v17	17	0
206	TGCAGT	ATCCATGTCTGATGTACTGTG	19357	cCas9-v42	17	0
207	TGG	TCCTCTCGGGATTTCTTGGG	19358	ScaCas9	17	0
208	TGG	TCCTCTCGGGATTTCTTGGG	19359	ScaCas9-HiFi-Sc++	17	0
209	TGG	TCCTCTCGGGATTTCTTGGG	19360	ScaCas9-Sc++	17	0
210	TGG	TCCTCTCGGGATTTCTTGGG	19361	SpyCas9	17	0
211	TGG	TCCTCTCGGGATTTCTTGGG	19362	SpyCas9-HF1	17	0
212	TGG	TCCTCTCGGGATTTCTTGGG	19363	SpyCas9-SpG	17	0
213	TGG	TCCTCTCGGGATTTCTTGGG	19364	SpyCas9-SpRY	17	0
214	TG	TCCATGTCTGATGTACTGTG	19365	SpyCas9-NG	17	0
215	TG	TCCATGTCTGATGTACTGTG	19366	SpyCas9-xCas	17	0
216	TG	TCCATGTCTGATGTACTGTG	19367	SpyCas9-xCas-NG	17	0
217	TG	TCCTCTCGGGATTTCTTGGG	19368	SpyCas9-NG	17	0
218	TG	TCCTCTCGGGATTTCTTGGG	19369	SpyCas9-xCas	17	0

219	TG	TCCTCTCGGGATTTCTTGGG	19370	SpyCas9-xCas-NG	17	0
220	TGC	TCCATGTCTGATGTACTGTG	19371	SpyCas9-SpG	17	0
221	TGC	TCCATGTCTGATGTACTGTG	19372	SpyCas9-SpRY	17	0
222	TGGCCTGG	ctttCCTCTCGGGATTTCTTGGG	19373	BlatCas9	17	0
223	TGGCC	ctttCCTCTCGGGATTTCTTGGG	19374	BlatCas9	17	0
224	TGGC	TCCTCTCGGGATTTCTTGGG	19375	SpyCas9-3var-NRRH	17	0
225	TGCA	TCCATGTCTGATGTACTGTG	19376	SpyCas9-3var-NRCH	17	0
226	GTGGCC	tgCTTTCCTCTCGGGATTTCTTGG	19377	Nme2Cas9	18	0
227	GTGG	TTTCCTCTCGGGATTTCTTGG	19378	SauriCas9	18	0
228	GTGG	TTTCCTCTCGGGATTTCTTGG	19379	SauriCas9-KKH	18	0
229	GTG	ATCCATGTCTGATGTACTGT	19380	ScaCas9	18	0
230	GTG	ATCCATGTCTGATGTACTGT	19381	ScaCas9-HiFi-Sc++	18	0
231	GTG	ATCCATGTCTGATGTACTGT	19382	ScaCas9-Sc++	18	0
232	GTG	ATCCATGTCTGATGTACTGT	19383	SpyCas9-SpRY	18	0
233	GTG	TTCCTCTCGGGATTTCTTGG	19384	ScaCas9	18	0
234	GTG	TTCCTCTCGGGATTTCTTGG	19385	ScaCas9-HiFi-Sc++	18	0
235	GTG	TTCCTCTCGGGATTTCTTGG	19386	ScaCas9-Sc++	18	0
236	GTG	TTCCTCTCGGGATTTCTTGG	19387	SpyCas9-SpRY	18	0
237	GTGGCCTG	gcttTCCTCTCGGGATTTCTTGG	19388	BlatCas9	18	0
238	GTGGC	gcttTCCTCTCGGGATTTCTTGG	19389	BlatCas9	18	0
239	GGTGG	CTTTCCTCTCGGGATTTCTTG	19390	SauCas9KKH	19	0
240	TG	GATCCATGTCTGATGTACTG	19391	SpyCas9-NG	19	0
241	TG	GATCCATGTCTGATGTACTG	19392	SpyCas9-xCas	19	0
242	TG	GATCCATGTCTGATGTACTG	19393	SpyCas9-xCas-NG	19	0
243	GG	TTTCCTCTCGGGATTTCTTG	19394	SpyCas9-NG	19	0
244	GG	TTTCCTCTCGGGATTTCTTG	19395	SpyCas9-xCas	19	0
245	GG	TTTCCTCTCGGGATTTCTTG	19396	SpyCas9-xCas-NG	19	0
246	TGT	GATCCATGTCTGATGTACTG	19397	SpyCas9-SpG	19	0
247	TGT	GATCCATGTCTGATGTACTG	19398	SpyCas9-SpRY	19	0
248	GGT	TTTCCTCTCGGGATTTCTTG	19399	SpyCas9-SpG	19	0
249	GGT	TTTCCTCTCGGGATTTCTTG	19400	SpyCas9-SpRY	19	0
250	TGTGCAGT	ttggATCCATGTCTGATGTACTG	19401	BlatCas9	19	0
251	TGTGC	ttggATCCATGTCTGATGTACTG	19402	BlatCas9	19	0
252	GTG	GGATCCATGTCTGATGTACT	19403	ScaCas9	20	0

253	GTG	GGATCCATGTCTGATGTACT	19404	ScaCas9-HiFi-Sc++	20	0
254	GTG	GGATCCATGTCTGATGTACT	19405	ScaCas9-Sc++	20	0
255	GTG	GGATCCATGTCTGATGTACT	19406	SpyCas9-SpRY	20	0
256	GGG	CTTTCCTCTCGGGATTTCTT	19407	ScaCas9	20	0
257	GGG	CTTTCCTCTCGGGATTTCTT	19408	ScaCas9-HiFi-Sc++	20	0
258	GGG	CTTTCCTCTCGGGATTTCTT	19409	ScaCas9-Sc++	20	0
259	GGG	CTTTCCTCTCGGGATTTCTT	19410	SpyCas9	20	0
260	GGG	CTTTCCTCTCGGGATTTCTT	19411	SpyCas9-HF1	20	0
261	GGG	CTTTCCTCTCGGGATTTCTT	19412	SpyCas9-SpG	20	0
262	GGG	CTTTCCTCTCGGGATTTCTT	19413	SpyCas9-SpRY	20	0
263	GG	CTTTCCTCTCGGGATTTCTT	19414	SpyCas9-NG	20	0
264	GG	CTTTCCTCTCGGGATTTCTT	19415	SpyCas9-xCas	20	0
265	GG	CTTTCCTCTCGGGATTTCTT	19416	SpyCas9-xCas-NG	20	0
266	GGGT	CTTTCCTCTCGGGATTTCTT	19417	SpyCas9-3var-NRRH	20	0
267	TGGG	TGCTTTCCTCTCGGGATTTCT	19418	SauriCas9	21	0
268	TGGG	TGCTTTCCTCTCGGGATTTCT	19419	SauriCas9-KKH	21	0
269	TGG	GCTTTCCTCTCGGGATTTCT	19420	ScaCas9	21	0
270	TGG	GCTTTCCTCTCGGGATTTCT	19421	ScaCas9-HiFi-Sc++	21	0
271	TGG	GCTTTCCTCTCGGGATTTCT	19422	ScaCas9-Sc++	21	0
272	TGG	GCTTTCCTCTCGGGATTTCT	19423	SpyCas9	21	0
273	TGG	GCTTTCCTCTCGGGATTTCT	19424	SpyCas9-HF1	21	0
274	TGG	GCTTTCCTCTCGGGATTTCT	19425	SpyCas9-SpG	21	0
275	TGG	GCTTTCCTCTCGGGATTTCT	19426	SpyCas9-SpRY	21	0
276	TG	TGGATCCATGTCTGATGTAC	19427	SpyCas9-NG	21	0
277	TG	TGGATCCATGTCTGATGTAC	19428	SpyCas9-xCas	21	0
278	TG	TGGATCCATGTCTGATGTAC	19429	SpyCas9-xCas-NG	21	0
279	TG	GCTTTCCTCTCGGGATTTCT	19430	SpyCas9-NG	21	0
280	TG	GCTTTCCTCTCGGGATTTCT	19431	SpyCas9-xCas	21	0
281	TG	GCTTTCCTCTCGGGATTTCT	19432	SpyCas9-xCas-NG	21	0
282	TGT	TGGATCCATGTCTGATGTAC	19433	SpyCas9-SpG	21	0
283	TGT	TGGATCCATGTCTGATGTAC	19434	SpyCas9-SpRY	21	0
284	TGGGTG	TGCTTTCCTCTCGGGATTTCT	19435	cCas9-v16	21	0
285	TGGGTG	TGCTTTCCTCTCGGGATTTCT	19436	cCas9-v21	21	0
286	TTGGG	gcCTGCTTTCCTCTCGGGATTTC	19437	SauCas9	22	0
287	TTGGG	CTGCTTTCCTCTCGGGATTTC	19438	SauCas9KKH	22	0
288	TTGGGT	gcCTGCTTTCCTCTCGGGATTTC	19439	SauCas9	22	0
289	TTGGGT	CTGCTTTCCTCTCGGGATTTC	19440	SauCas9KKH	22	0

290	TTGGGT	CTGCTTTCCTCTCGGGATTTC	19441	cCas9-v17	22	0
291	TTGGGT	CTGCTTTCCTCTCGGGATTTC	19442	cCas9-v42	22	0
292	TTGG	CTGCTTTCCTCTCGGGATTTC	19443	SauriCas9	22	0
293	TTGG	CTGCTTTCCTCTCGGGATTTC	19444	SauriCas9-KKH	22	0
294	CTG	TTGGATCCATGTCTGATGTA	19445	ScaCas9	22	0
295	CTG	TTGGATCCATGTCTGATGTA	19446	ScaCas9-HiFi-Sc++	22	0
296	CTG	TTGGATCCATGTCTGATGTA	19447	ScaCas9-Sc++	22	0
297	CTG	TTGGATCCATGTCTGATGTA	19448	SpyCas9-SpRY	22	0
298	TTG	TGCTTTCCTCTCGGGATTTC	19449	ScaCas9	22	0
299	TTG	TGCTTTCCTCTCGGGATTTC	19450	ScaCas9-HiFi-Sc++	22	0
300	TTG	TGCTTTCCTCTCGGGATTTC	19451	ScaCas9-Sc++	22	0
301	TTG	TGCTTTCCTCTCGGGATTTC	19452	SpyCas9-SpRY	22	0
302	CTTGG	CCTGCTTTCCTCTCGGGATTT	19453	SauCas9KKH	23	0
303	ACT	CTTGGATCCATGTCTGATGT	19454	SpyCas9-SpRY	23	0
304	CTT	CTGCTTTCCTCTCGGGATTT	19455	SpyCas9-SpRY	23	0
305	TAC	GCTTGGATCCATGTCTGATG	19456	SpyCas9-SpRY	24	0
306	TCT	CCTGCTTTCCTCTCGGGATT	19457	SpyCas9-SpRY	24	0
307	TACT	GCTTGGATCCATGTCTGATG	19458	SpyCas9-3var-NRCH	24	0
308	GTA	GGCTTGGATCCATGTCTGAT	19459	SpyCas9-SpRY	25	0
309	TTC	GCCTGCTTTCCTCTCGGGAT	19460	SpyCas9-SpRY	25	0
310	TG	GGGCTTGGATCCATGTCTGA	19461	SpyCas9-NG	26	0
311	TG	GGGCTTGGATCCATGTCTGA	19462	SpyCas9-xCas	26	0
312	TG	GGGCTTGGATCCATGTCTGA	19463	SpyCas9-xCas-NG	26	0
313	TGT	GGGCTTGGATCCATGTCTGA	19464	SpyCas9-SpG	26	0
314	TGT	GGGCTTGGATCCATGTCTGA	19465	SpyCas9-SpRY	26	0
315	TTT	GGCCTGCTTTCCTCTCGGGA	19466	SpyCas9-SpRY	26	0
316	TGTACTGT	catgGGCTTGGATCCATGTCTGA	19467	BlatCas9	26	0
317	TGTAC	catgGGCTTGGATCCATGTCTGA	19468	BlatCas9	26	0
318	TGTA	GGGCTTGGATCCATGTCTGA	19469	SpyCas9-3var-NRTH	26	0
319	ATG	TGGGCTTGGATCCATGTCTG	19470	ScaCas9	27	0
320	ATG	TGGGCTTGGATCCATGTCTG	19471	ScaCas9-HiFi-Sc++	27	0
321	ATG	TGGGCTTGGATCCATGTCTG	19472	ScaCas9-Sc++	27	0
322	ATG	TGGGCTTGGATCCATGTCTG	19473	SpyCas9-SpRY	27	0
323	ATT	TGGCCTGCTTTCCTCTCGGG	19474	SpyCas9-SpRY	27	0
324	ATTTCTTG	ggctGGCCTGCTTTCCTCTCGGG	19475	BlatCas9	27	0
325	ATTTC	ggctGGCCTGCTTTCCTCTCGGG	19476	BlatCas9	27	0
326	ATGTACT	CATGGGCTTGGATCCATGTCTG	19477	CdiCas9	27	0

327	GAT	ATGGGCTTGGATCCATGTCT	19478	SpyCas9-SpRY	28	0
328	GAT	ATGGGCTTGGATCCATGTCT	19479	SpyCas9-xCas	28	0
329	GAT	CTGGCCTGCTTTCCTCTCGG	19480	SpyCas9-SpRY	28	0
330	GAT	CTGGCCTGCTTTCCTCTCGG	19481	SpyCas9-xCas	28	0
331	GATT	CTGGCCTGCTTTCCTCTCGG	19482	SpyCas9-3var-NRTH	28	0
332	TG	CATGGGCTTGGATCCATGTC	19483	SpyCas9-NG	29	0
333	TG	CATGGGCTTGGATCCATGTC	19484	SpyCas9-xCas	29	0
334	TG	CATGGGCTTGGATCCATGTC	19485	SpyCas9-xCas-NG	29	0
335	GG	GCTGGCCTGCTTTCCTCTCG	19486	SpyCas9-NG	29	0
336	GG	GCTGGCCTGCTTTCCTCTCG	19487	SpyCas9-xCas	29	0
337	GG	GCTGGCCTGCTTTCCTCTCG	19488	SpyCas9-xCas-NG	29	0
338	TGA	CATGGGCTTGGATCCATGTC	19489	SpyCas9-SpG	29	0
339	TGA	CATGGGCTTGGATCCATGTC	19490	SpyCas9-SpRY	29	0
340	GGA	GCTGGCCTGCTTTCCTCTCG	19491	SpyCas9-SpG	29	0
341	GGA	GCTGGCCTGCTTTCCTCTCG	19492	SpyCas9-SpRY	29	0
342	GGATTTC	TGGCTGGCCTGCTTTCCTCTCG	19493	CdiCas9	29	0
343	TGATGTAC	atACATGGGCTTGGATCCATGTC	19494	CjeCas9	29	0
344	TGAT	CATGGGCTTGGATCCATGTC	19495	SpyCas9-3var-NRRH	29	0
345	TGAT	CATGGGCTTGGATCCATGTC	19496	SpyCas9-VQR	29	0
346	GGAT	GCTGGCCTGCTTTCCTCTCG	19497	SpyCas9-3var-NRRH	29	0
347	GGAT	GCTGGCCTGCTTTCCTCTCG	19498	SpyCas9-VQR	29	0
348	CTG	ACATGGGCTTGGATCCATGT	19499	ScaCas9	30	0
349	CTG	ACATGGGCTTGGATCCATGT	19500	ScaCas9-HiFi-Sc++	30	0
350	CTG	ACATGGGCTTGGATCCATGT	19501	ScaCas9-Sc++	30	0
351	CTG	ACATGGGCTTGGATCCATGT	19502	SpyCas9-SpRY	30	0
352	GGG	GGCTGGCCTGCTTTCCTCTC	19503	ScaCas9	30	0
353	GGG	GGCTGGCCTGCTTTCCTCTC	19504	ScaCas9-HiFi-Sc++	30	0
354	GGG	GGCTGGCCTGCTTTCCTCTC	19505	ScaCas9-Sc++	30	0
355	GGG	GGCTGGCCTGCTTTCCTCTC	19506	SpyCas9	30	0
356	GGG	GGCTGGCCTGCTTTCCTCTC	19507	SpyCas9-HF1	30	0
357	GGG	GGCTGGCCTGCTTTCCTCTC	19508	SpyCas9-SpG	30	0
358	GGG	GGCTGGCCTGCTTTCCTCTC	19509	SpyCas9-SpRY	30	0
359	GG	GGCTGGCCTGCTTTCCTCTC	19510	SpyCas9-NG	30	0
360	GG	GGCTGGCCTGCTTTCCTCTC	19511	SpyCas9-xCas	30	0
361	GG	GGCTGGCCTGCTTTCCTCTC	19512	SpyCas9-xCas-NG	30	0
362	GGGATT	TGGCTGGCCTGCTTTCCTCTC	19513	cCas9-v16	30	0

363	GGGATT	TGGCTGGCCTGCTTTCCTCTC	19514	cCas9-v21	30	0
364	GGGATTT	GTGGCTGGCCTGCTTTCCTCTC	19515	CdiCas9	30	0
365	GGGA	GGCTGGCCTGCTTTCCTCTC	19516	SpyCas9-3var-NRRH	30	0
366	CGGGATT	cctGTGGCTGGCCTGCTTTCCTCT	19517	PpnCas9	31	0
367	CGGGA	ctGTGGCTGGCCTGCTTTCCTCT	19518	SauCas9	31	0
368	CGGGA	GTGGCTGGCCTGCTTTCCTCT	19519	SauCas9KKH	31	0
369	CGGGAT	ctGTGGCTGGCCTGCTTTCCTCT	19520	SauCas9	31	0
370	CGGGAT	GTGGCTGGCCTGCTTTCCTCT	19521	SauCas9KKH	31	0
371	CGGGAT	GTGGCTGGCCTGCTTTCCTCT	19522	cCas9-v17	31	0
372	CGGGAT	GTGGCTGGCCTGCTTTCCTCT	19523	cCas9-v42	31	0
373	TCTGA	ATACATGGGCTTGGATCCATG	19524	SauCas9KKH	31	0
374	TCTGAT	ATACATGGGCTTGGATCCATG	19525	SauCas9KKH	31	0
375	CGGG	GTGGCTGGCCTGCTTTCCTCT	19526	SauriCas9	31	0
376	CGGG	GTGGCTGGCCTGCTTTCCTCT	19527	SauriCas9-KKH	31	0
377	CGG	TGGCTGGCCTGCTTTCCTCT	19528	ScaCas9	31	0
378	CGG	TGGCTGGCCTGCTTTCCTCT	19529	ScaCas9-HiFi-Sc++	31	0
379	CGG	TGGCTGGCCTGCTTTCCTCT	19530	ScaCas9-Sc++	31	0
380	CGG	TGGCTGGCCTGCTTTCCTCT	19531	SpyCas9	31	0
381	CGG	TGGCTGGCCTGCTTTCCTCT	19532	SpyCas9-HF1	31	0
382	CGG	TGGCTGGCCTGCTTTCCTCT	19533	SpyCas9-SpG	31	0
383	CGG	TGGCTGGCCTGCTTTCCTCT	19534	SpyCas9-SpRY	31	0
384	CG	TGGCTGGCCTGCTTTCCTCT	19535	SpyCas9-NG	31	0
385	CG	TGGCTGGCCTGCTTTCCTCT	19536	SpyCas9-xCas	31	0
386	CG	TGGCTGGCCTGCTTTCCTCT	19537	SpyCas9-xCas-NG	31	0
387	TCT	TACATGGGCTTGGATCCATG	19538	SpyCas9-SpRY	31	0
388	TCGGG	ccTGTGGCTGGCCTGCTTTCCTC	19539	SauCas9	32	0
389	TCGGG	TGTGGCTGGCCTGCTTTCCTC	19540	SauCas9KKH	32	0
390	TCGG	TGTGGCTGGCCTGCTTTCCTC	19541	SauriCas9	32	0
391	TCGG	TGTGGCTGGCCTGCTTTCCTC	19542	SauriCas9-KKH	32	0
392	TCG	GTGGCTGGCCTGCTTTCCTC	19543	ScaCas9	32	0
393	TCG	GTGGCTGGCCTGCTTTCCTC	19544	ScaCas9-HiFi-Sc++	32	0
394	TCG	GTGGCTGGCCTGCTTTCCTC	19545	ScaCas9-Sc++	32	0
395	TCG	GTGGCTGGCCTGCTTTCCTC	19546	SpyCas9-SpRY	32	0
396	GTC	ATACATGGGCTTGGATCCAT	19547	SpyCas9-SpRY	32	0
397	TCGGGA	TGTGGCTGGCCTGCTTTCCTC	19548	cCas9-v17	32	0
398	TCGGGA	TGTGGCTGGCCTGCTTTCCTC	19549	cCas9-v42	32	0
399	TCGGGATT	acctGTGGCTGGCCTGCTTTCCTC	19550	NmeCas9	32	0

400	CTCGG	CTGTGGCTGGCCTGCTTTCCT	19551	SauCas9KKH	33	0
401	TG	TATACATGGGCTTGGATCCA	19552	SpyCas9-NG	33	0
402	TG	TATACATGGGCTTGGATCCA	19553	SpyCas9-xCas	33	0
403	TG	TATACATGGGCTTGGATCCA	19554	SpyCas9-xCas-NG	33	0
404	TGT	TATACATGGGCTTGGATCCA	19555	SpyCas9-SpG	33	0
405	TGT	TATACATGGGCTTGGATCCA	19556	SpyCas9-SpRY	33	0
406	CTC	TGTGGCTGGCCTGCTTTCCT	19557	SpyCas9-SpRY	33	0
407	CTCGGG	CTGTGGCTGGCCTGCTTTCCT	19558	cCas9-v17	33	0
408	CTCGGG	CTGTGGCTGGCCTGCTTTCCT	19559	cCas9-v42	33	0
409	TGTC	TATACATGGGCTTGGATCCA	19560	SpyCas9-3var-NRTH	33	0
410	ATG	GTATACATGGGCTTGGATCC	19561	ScaCas9	34	0
411	ATG	GTATACATGGGCTTGGATCC	19562	ScaCas9-HiFi-Sc++	34	0
412	ATG	GTATACATGGGCTTGGATCC	19563	ScaCas9-Sc++	34	0
413	ATG	GTATACATGGGCTTGGATCC	19564	SpyCas9-SpRY	34	0
414	TCT	CTGTGGCTGGCCTGCTTTCC	19565	SpyCas9-SpRY	34	0
415	ATGTCTGA	ggggTATACATGGGCTTGGATCC	19566	BlatCas9	34	0
416	ATGTC	ggggTATACATGGGCTTGGATCC	19567	BlatCas9	34	0
417	CAT	GGTATACATGGGCTTGGATC	19568	SpyCas9-SpRY	35	0
418	CTC	CCTGTGGCTGGCCTGCTTTC	19569	SpyCas9-SpRY	35	0
419	CTCTCGGG	cgacCTGTGGCTGGCCTGCTTTC	19570	BlatCas9	35	0
420	CTCTC	cgacCTGTGGCTGGCCTGCTTTC	19571	BlatCas9	35	0
421	CCA	GGGTATACATGGGCTTGGAT	19572	SpyCas9-SpRY	36	0
422	CCT	ACCTGTGGCTGGCCTGCTTT	19573	SpyCas9-SpRY	36	0
423	CCATGTCT	tcggGGGTATACATGGGCTTGGAT	19574	NmeCas9	36	0
424	TCC	GGGGTATACATGGGCTTGGA	19575	SpyCas9-SpRY	37	0
425	TCC	GACCTGTGGCTGGCCTGCTT	19576	SpyCas9-SpRY	37	0
426	TCCTC	tccgACCTGTGGCTGGCCTGCTT	19577	BlatCas9	37	0
427	ATC	GGGGGTATACATGGGCTTGG	19578	SpyCas9-SpRY	38	0
428	TTC	CGACCTGTGGCTGGCCTGCT	19579	SpyCas9-SpRY	38	0
429	GAT	CGGGGGTATACATGGGCTTG	19580	SpyCas9-SpRY	39	0
430	GAT	CGGGGGTATACATGGGCTTG	19581	SpyCas9-xCas	39	0
431	TTT	CCGACCTGTGGCTGGCCTGC	19582	SpyCas9-SpRY	39	0
432	GATCCATG	gttcGGGGGTATACATGGGCTTG	19583	BlatCas9	39	0
433	GATCC	gttcGGGGGTATACATGGGCTTG	19584	BlatCas9	39	0
434	TTTCC	cctcCGACCTGTGGCTGGCCTGC	19585	BlatCas9	39	0
435	GATC	CGGGGGTATACATGGGCTTG	19586	SpyCas9-3var-NRTH	39	0

436	GGATCC	cgGTTCGGGGGTATACATGGGCTT	19587	Nme2Cas9	40	0
437	CTTTCC	cgCCTCCGACCTGTGGCTGGCCTG	19588	Nme2Cas9	40	0
438	GG	TCGGGGGTATACATGGGCTT	19589	SpyCas9-NG	40	0
439	GG	TCGGGGGTATACATGGGCTT	19590	SpyCas9-xCas	40	0
440	GG	TCGGGGGTATACATGGGCTT	19591	SpyCas9-xCas-NG	40	0
441	GGA	TCGGGGGTATACATGGGCTT	19592	SpyCas9-SpG	40	0
442	GGA	TCGGGGGTATACATGGGCTT	19593	SpyCas9-SpRY	40	0
443	CTT	TCCGACCTGTGGCTGGCCTG	19594	SpyCas9-SpRY	40	0
444	GGATCCAT	ggttCGGGGGTATACATGGGCTT	19595	BlatCas9	40	0
445	GGATC	ggttCGGGGGTATACATGGGCTT	19596	BlatCas9	40	0
446	CTTTC	gcctCCGACCTGTGGCTGGCCTG	19597	BlatCas9	40	0
447	GGAT	TCGGGGGTATACATGGGCTT	19598	SpyCas9-3var-NRRH	40	0
448	GGAT	TCGGGGGTATACATGGGCTT	19599	SpyCas9-VQR	40	0
449	TGG	TTCGGGGGTATACATGGGCT	19600	ScaCas9	41	0
450	TGG	TTCGGGGGTATACATGGGCT	19601	ScaCas9-HiFi-Sc++	41	0
451	TGG	TTCGGGGGTATACATGGGCT	19602	ScaCas9-Sc++	41	0
452	TGG	TTCGGGGGTATACATGGGCT	19603	SpyCas9	41	0
453	TGG	TTCGGGGGTATACATGGGCT	19604	SpyCas9-HF1	41	0
454	TGG	TTCGGGGGTATACATGGGCT	19605	SpyCas9-SpG	41	0
455	TGG	TTCGGGGGTATACATGGGCT	19606	SpyCas9-SpRY	41	0
456	TG	TTCGGGGGTATACATGGGCT	19607	SpyCas9-NG	41	0
457	TG	TTCGGGGGTATACATGGGCT	19608	SpyCas9-xCas	41	0
458	TG	TTCGGGGGTATACATGGGCT	19609	SpyCas9-xCas-NG	41	0
459	GCT	CTCCGACCTGTGGCTGGCCT	19610	SpyCas9-SpRY	41	0
460	TGGATCC	GGTTCGGGGGTATACATGGGCT	19611	CdiCas9	41	0
461	TGGA	TTCGGGGGTATACATGGGCT	19612	SpyCas9-3var-NRRH	41	0
462	TTGGA	acGGTTCGGGGGTATACATGGGC	19613	SauCas9	42	0
463	TTGGA	GGTTCGGGGGTATACATGGGC	19614	SauCas9KKH	42	0
464	TTGGAT	acGGTTCGGGGGTATACATGGGC	19615	SauCas9	42	0
465	TTGGAT	GGTTCGGGGGTATACATGGGC	19616	SauCas9KKH	42	0
466	TTGGAT	GGTTCGGGGGTATACATGGGC	19617	cCas9-v17	42	0
467	TTGGAT	GGTTCGGGGGTATACATGGGC	19618	cCas9-v42	42	0
468	TTGG	GGTTCGGGGGTATACATGGGC	19619	SauriCas9	42	0
469	TTGG	GGTTCGGGGGTATACATGGGC	19620	SauriCas9-KKH	42	0
470	TTG	GTTCGGGGGTATACATGGGC	19621	ScaCas9	42	0

471	TTG	GTTCGGGGGTATACATGGGC	19622	ScaCas9-HiFi-Sc++	42	0
472	TTG	GTTCGGGGGTATACATGGGC	19623	ScaCas9-Sc++	42	0
473	TTG	GTTCGGGGGTATACATGGGC	19624	SpyCas9-SpRY	42	0
474	TG	CCTCCGACCTGTGGCTGGCC	19625	SpyCas9-NG	42	0
475	TG	CCTCCGACCTGTGGCTGGCC	19626	SpyCas9-xCas	42	0
476	TG	CCTCCGACCTGTGGCTGGCC	19627	SpyCas9-xCas-NG	42	0
477	TGC	CCTCCGACCTGTGGCTGGCC	19628	SpyCas9-SpG	42	0
478	TGC	CCTCCGACCTGTGGCTGGCC	19629	SpyCas9-SpRY	42	0
479	TGCT	CCTCCGACCTGTGGCTGGCC	19630	SpyCas9-3var-NRCH	42	0
480	CTTGG	CGGTTCGGGGGTATACATGGG	19631	SauCas9KKH	43	0
481	CTG	GCCTCCGACCTGTGGCTGGC	19632	ScaCas9	43	0
482	CTG	GCCTCCGACCTGTGGCTGGC	19633	ScaCas9-HiFi-Sc++	43	0
483	CTG	GCCTCCGACCTGTGGCTGGC	19634	ScaCas9-Sc++	43	0
484	CTG	GCCTCCGACCTGTGGCTGGC	19635	SpyCas9-SpRY	43	0
485	CTT	GGTTCGGGGGTATACATGGG	19636	SpyCas9-SpRY	43	0
486	CTGCTTT	CCGCCTCCGACCTGTGGCTGGC	19637	CdiCas9	43	0
487	GCT	CGGTTCGGGGGTATACATGG	19638	SpyCas9-SpRY	44	0
488	CCT	CGCCTCCGACCTGTGGCTGG	19639	SpyCas9-SpRY	44	0
489	CCTGCTTT	ttccGCCTCCGACCTGTGGCTGG	19640	BlatCas9	44	0
490	CCTGC	ttccGCCTCCGACCTGTGGCTGG	19641	BlatCas9	44	0
491	GG	ACGGTTCGGGGGTATACATG	19642	SpyCas9-NG	45	0
492	GG	ACGGTTCGGGGGTATACATG	19643	SpyCas9-xCas	45	0
493	GG	ACGGTTCGGGGGTATACATG	19644	SpyCas9-xCas-NG	45	0
494	GGC	ACGGTTCGGGGGTATACATG	19645	SpyCas9-SpG	45	0
495	GGC	ACGGTTCGGGGGTATACATG	19646	SpyCas9-SpRY	45	0
496	GCC	CCGCCTCCGACCTGTGGCTG	19647	SpyCas9-SpRY	45	0
497	GCCTGCTT	gtttCCGCCTCCGACCTGTGGCTG	19648	NmeCas9	45	0
498	GGCT	ACGGTTCGGGGGTATACATG	19649	SpyCas9-3var-NRCH	45	0
499	GGG	CACGGTTCGGGGGTATACAT	19650	ScaCas9	46	0
500	GGG	CACGGTTCGGGGGTATACAT	19651	ScaCas9-HiFi-Sc++	46	0
501	GGG	CACGGTTCGGGGGTATACAT	19652	ScaCas9-Sc++	46	0
502	GGG	CACGGTTCGGGGGTATACAT	19653	SpyCas9	46	0
503	GGG	CACGGTTCGGGGGTATACAT	19654	SpyCas9-HF1	46	0
504	GGG	CACGGTTCGGGGGTATACAT	19655	SpyCas9-SpG	46	0
505	GGG	CACGGTTCGGGGGTATACAT	19656	SpyCas9-SpRY	46	0
506	GG	CACGGTTCGGGGGTATACAT	19657	SpyCas9-NG	46	0
507	GG	CACGGTTCGGGGGTATACAT	19658	SpyCas9-xCas	46	0

508	GG	CACGGTTCGGGGGTATACAT	19659	SpyCas9-xCas-NG	46	0
509	GG	TCCGCCTCCGACCTGTGGCT	19660	SpyCas9-NG	46	0
510	GG	TCCGCCTCCGACCTGTGGCT	19661	SpyCas9-xCas	46	0
511	GG	TCCGCCTCCGACCTGTGGCT	19662	SpyCas9-xCas-NG	46	0
512	GGC	TCCGCCTCCGACCTGTGGCT	19663	SpyCas9-SpG	46	0
513	GGC	TCCGCCTCCGACCTGTGGCT	19664	SpyCas9-SpRY	46	0
514	GGGC	CACGGTTCGGGGGTATACAT	19665	SpyCas9-3var-NRRH	46	0
515	GGCC	TCCGCCTCCGACCTGTGGCT	19666	SpyCas9-3var-NRCH	46	0
516	TGGG	CTCACGGTTCGGGGGTATACA	19667	SauriCas9	47	0
517	TGGG	CTCACGGTTCGGGGGTATACA	19668	SauriCas9-KKH	47	0
518	TGG	TCACGGTTCGGGGGTATACA	19669	ScaCas9	47	0
519	TGG	TCACGGTTCGGGGGTATACA	19670	ScaCas9-HiFi-Sc++	47	0
520	TGG	TCACGGTTCGGGGGTATACA	19671	ScaCas9-Sc++	47	0
521	TGG	TCACGGTTCGGGGGTATACA	19672	SpyCas9	47	0
522	TGG	TCACGGTTCGGGGGTATACA	19673	SpyCas9-HF1	47	0
523	TGG	TCACGGTTCGGGGGTATACA	19674	SpyCas9-SpG	47	0
524	TGG	TCACGGTTCGGGGGTATACA	19675	SpyCas9-SpRY	47	0
525	TGG	TTCCGCCTCCGACCTGTGGC	19676	ScaCas9	47	0
526	TGG	TTCCGCCTCCGACCTGTGGC	19677	ScaCas9-HiFi-Sc++	47	0
527	TGG	TTCCGCCTCCGACCTGTGGC	19678	ScaCas9-Sc++	47	0
528	TGG	TTCCGCCTCCGACCTGTGGC	19679	SpyCas9	47	0
529	TGG	TTCCGCCTCCGACCTGTGGC	19680	SpyCas9-HF1	47	0
530	TGG	TTCCGCCTCCGACCTGTGGC	19681	SpyCas9-SpG	47	0
531	TGG	TTCCGCCTCCGACCTGTGGC	19682	SpyCas9-SpRY	47	0
532	TG	TCACGGTTCGGGGGTATACA	19683	SpyCas9-NG	47	0
533	TG	TCACGGTTCGGGGGTATACA	19684	SpyCas9-xCas	47	0
534	TG	TCACGGTTCGGGGGTATACA	19685	SpyCas9-xCas-NG	47	0
535	TG	TTCCGCCTCCGACCTGTGGC	19686	SpyCas9-NG	47	0
536	TG	TTCCGCCTCCGACCTGTGGC	19687	SpyCas9-xCas	47	0
537	TG	TTCCGCCTCCGACCTGTGGC	19688	SpyCas9-xCas-NG	47	0
538	TGGGCTTG	tactCACGGTTCGGGGGTATACA	19689	BlatCas9	47	0
539	TGGGC	tactCACGGTTCGGGGGTATACA	19690	BlatCas9	47	0
540	TGGCC	ggttTCCGCCTCCGACCTGTGGC	19691	BlatCas9	47	0
541	TGGGCT	CTCACGGTTCGGGGGTATACA	19692	cCas9-v16	47	0
542	TGGGCT	CTCACGGTTCGGGGGTATACA	19693	cCas9-v21	47	0

543	TGGC	TTCCGCCTCCGACCTGTGGC	19694	SpyCas9-3var-NRRH	47	0
544	CTGGCC	ctGGTTTCCGCCTCCGACCTGTGG	19695	Nme2Cas9	48	0
545	ATGGG	gtACTCACGGTTCGGGGGTATAC	19696	SauCas9	48	0
546	ATGGG	ACTCACGGTTCGGGGGTATAC	19697	SauCas9KKH	48	0
547	ATGG	ACTCACGGTTCGGGGGTATAC	19698	SauriCas9	48	0
548	ATGG	ACTCACGGTTCGGGGGTATAC	19699	SauriCas9-KKH	48	0
549	CTGG	GTTTCCGCCTCCGACCTGTGG	19700	SauriCas9	48	0
550	CTGG	GTTTCCGCCTCCGACCTGTGG	19701	SauriCas9-KKH	48	0
551	ATG	CTCACGGTTCGGGGGTATAC	19702	ScaCas9	48	0
552	ATG	CTCACGGTTCGGGGGTATAC	19703	ScaCas9-HiFi-Sc++	48	0
553	ATG	CTCACGGTTCGGGGGTATAC	19704	ScaCas9-Sc++	48	0
554	ATG	CTCACGGTTCGGGGGTATAC	19705	SpyCas9-SpRY	48	0
555	CTG	TTTCCGCCTCCGACCTGTGG	19706	ScaCas9	48	0
556	CTG	TTTCCGCCTCCGACCTGTGG	19707	ScaCas9-HiFi-Sc++	48	0
557	CTG	TTTCCGCCTCCGACCTGTGG	19708	ScaCas9-Sc++	48	0
558	CTG	TTTCCGCCTCCGACCTGTGG	19709	SpyCas9-SpRY	48	0
559	CTGGCCTG	tggtTTCCGCCTCCGACCTGTGG	19710	BlatCas9	48	0
560	CTGGC	tggtTTCCGCCTCCGACCTGTGG	19711	BlatCas9	48	0
561	ATGGGC	ACTCACGGTTCGGGGGTATAC	19712	cCas9-v17	48	0
562	ATGGGC	ACTCACGGTTCGGGGGTATAC	19713	cCas9-v42	48	0
563	ATGGGCTT	agtaCTCACGGTTCGGGGGTATAC	19714	NmeCas9	48	0
564	CATGG	TACTCACGGTTCGGGGGTATA	19715	SauCas9KKH	49	0
565	GCTGG	GGTTTCCGCCTCCGACCTGTG	19716	SauCas9KKH	49	0
566	CAT	ACTCACGGTTCGGGGGTATA	19717	SpyCas9-SpRY	49	0
567	GCT	GTTTCCGCCTCCGACCTGTG	19718	SpyCas9-SpRY	49	0
568	GG	GGTTTCCGCCTCCGACCTGT	19719	SpyCas9-NG	50	0
569	GG	GGTTTCCGCCTCCGACCTGT	19720	SpyCas9-xCas	50	0
570	GG	GGTTTCCGCCTCCGACCTGT	19721	SpyCas9-xCas-NG	50	0
571	GGC	GGTTTCCGCCTCCGACCTGT	19722	SpyCas9-SpG	50	0
572	GGC	GGTTTCCGCCTCCGACCTGT	19723	SpyCas9-SpRY	50	0
573	ACA	TACTCACGGTTCGGGGGTAT	19724	SpyCas9-SpRY	50	0
574	GGCT	GGTTTCCGCCTCCGACCTGT	19725	SpyCas9-3var-NRCH	50	0
575	TGG	TGGTTTCCGCCTCCGACCTG	19726	ScaCas9	51	0
576	TGG	TGGTTTCCGCCTCCGACCTG	19727	ScaCas9-HiFi-Sc++	51	0
577	TGG	TGGTTTCCGCCTCCGACCTG	19728	ScaCas9-Sc++	51	0

578	TGG	TGGTTTCCGCCTCCGACCTG	19729	SpyCas9	51	0
579	TGG	TGGTTTCCGCCTCCGACCTG	19730	SpyCas9-HF1	51	0
580	TGG	TGGTTTCCGCCTCCGACCTG	19731	SpyCas9-SpG	51	0
581	TGG	TGGTTTCCGCCTCCGACCTG	19732	SpyCas9-SpRY	51	0
582	TG	TGGTTTCCGCCTCCGACCTG	19733	SpyCas9-NG	51	0
583	TG	TGGTTTCCGCCTCCGACCTG	19734	SpyCas9-xCas	51	0
584	TG	TGGTTTCCGCCTCCGACCTG	19735	SpyCas9-xCas-NG	51	0
585	TAC	GTACTCACGGTTCGGGGGTA	19736	SpyCas9-SpRY	51	0
586	TGGC	TGGTTTCCGCCTCCGACCTG	19737	SpyCas9-3var-NRRH	51	0
587	TACA	GTACTCACGGTTCGGGGGTA	19738	SpyCas9-3var-NRCH	51	0
588	GTGG	ACTGGTTTCCGCCTCCGACCT	19739	SauriCas9	52	0
589	GTGG	ACTGGTTTCCGCCTCCGACCT	19740	SauriCas9-KKH	52	0
590	GTG	CTGGTTTCCGCCTCCGACCT	19741	ScaCas9	52	0
591	GTG	CTGGTTTCCGCCTCCGACCT	19742	ScaCas9-HiFi-Sc++	52	0
592	GTG	CTGGTTTCCGCCTCCGACCT	19743	ScaCas9-Sc++	52	0
593	GTG	CTGGTTTCCGCCTCCGACCT	19744	SpyCas9-SpRY	52	0
594	ATA	AGTACTCACGGTTCGGGGGT	19745	SpyCas9-SpRY	52	0
595	GTGGCTGG	gcacTGGTTTCCGCCTCCGACCT	19746	BlatCas9	52	0
596	GTGGC	gcacTGGTTTCCGCCTCCGACCT	19747	BlatCas9	52	0
597	GTGGCT	ACTGGTTTCCGCCTCCGACCT	19748	cCas9-v16	52	0
598	GTGGCT	ACTGGTTTCCGCCTCCGACCT	19749	cCas9-v21	52	0
599	TGTGG	CACTGGTTTCCGCCTCCGACC	19750	SauCas9KKH	53	0
600	TG	ACTGGTTTCCGCCTCCGACC	19751	SpyCas9-NG	53	0
601	TG	ACTGGTTTCCGCCTCCGACC	19752	SpyCas9-xCas	53	0
602	TG	ACTGGTTTCCGCCTCCGACC	19753	SpyCas9-xCas-NG	53	0
603	TAT	CAGTACTCACGGTTCGGGGG	19754	SpyCas9-SpRY	53	0
604	TGT	ACTGGTTTCCGCCTCCGACC	19755	SpyCas9-SpG	53	0
605	TGT	ACTGGTTTCCGCCTCCGACC	19756	SpyCas9-SpRY	53	0
606	TATACATG	ggacAGTACTCACGGTTCGGGGG	19757	BlatCas9	53	0
607	TATAC	ggacAGTACTCACGGTTCGGGGG	19758	BlatCas9	53	0
608	TATA	CAGTACTCACGGTTCGGGGG	19759	SpyCas9-3var-NRTH	53	0
609	CTG	CACTGGTTTCCGCCTCCGAC	19760	ScaCas9	54	0
610	CTG	CACTGGTTTCCGCCTCCGAC	19761	ScaCas9-HiFi-Sc++	54	0
611	CTG	CACTGGTTTCCGCCTCCGAC	19762	ScaCas9-Sc++	54	0
612	CTG	CACTGGTTTCCGCCTCCGAC	19763	SpyCas9-SpRY	54	0
613	GTA	ACAGTACTCACGGTTCGGGG	19764	SpyCas9-SpRY	54	0

614	GG	GACAGTACTCACGGTTCGGG	19765	SpyCas9-NG	55	0
615	GG	GACAGTACTCACGGTTCGGG	19766	SpyCas9-xCas	55	0
616	GG	GACAGTACTCACGGTTCGGG	19767	SpyCas9-xCas-NG	55	0
617	GGT	GACAGTACTCACGGTTCGGG	19768	SpyCas9-SpG	55	0
618	GGT	GACAGTACTCACGGTTCGGG	19769	SpyCas9-SpRY	55	0
619	CCT	GCACTGGTTTCCGCCTCCGA	19770	SpyCas9-SpRY	55	0
620	GGTA	GACAGTACTCACGGTTCGGG	19771	SpyCas9-3var-NRTH	55	0
621	GGG	GGACAGTACTCACGGTTCGG	19772	ScaCas9	56	0
622	GGG	GGACAGTACTCACGGTTCGG	19773	ScaCas9-HiFi-Sc++	56	0
623	GGG	GGACAGTACTCACGGTTCGG	19774	ScaCas9-Sc++	56	0
624	GGG	GGACAGTACTCACGGTTCGG	19775	SpyCas9	56	0
625	GGG	GGACAGTACTCACGGTTCGG	19776	SpyCas9-HF1	56	0
626	GGG	GGACAGTACTCACGGTTCGG	19777	SpyCas9-SpG	56	0
627	GGG	GGACAGTACTCACGGTTCGG	19778	SpyCas9-SpRY	56	0
628	GG	GGACAGTACTCACGGTTCGG	19779	SpyCas9-NG	56	0
629	GG	GGACAGTACTCACGGTTCGG	19780	SpyCas9-xCas	56	0
630	GG	GGACAGTACTCACGGTTCGG	19781	SpyCas9-xCas-NG	56	0
631	ACC	TGCACTGGTTTCCGCCTCCG	19782	SpyCas9-SpRY	56	0
632	GGGTATAC	ggAGGACAGTACTCACGGTTCGG	19783	CjeCas9	56	0
633	GGGT	GGACAGTACTCACGGTTCGG	19784	SpyCas9-3var-NRRH	56	0
634	GGGG	GAGGACAGTACTCACGGTTCG	19785	SauriCas9	57	0
635	GGGG	GAGGACAGTACTCACGGTTCG	19786	SauriCas9-KKH	57	0
636	GGG	AGGACAGTACTCACGGTTCG	19787	ScaCas9	57	0
637	GGG	AGGACAGTACTCACGGTTCG	19788	ScaCas9-HiFi-Sc++	57	0
638	GGG	AGGACAGTACTCACGGTTCG	19789	ScaCas9-Sc++	57	0
639	GGG	AGGACAGTACTCACGGTTCG	19790	SpyCas9	57	0
640	GGG	AGGACAGTACTCACGGTTCG	19791	SpyCas9-HF1	57	0
641	GGG	AGGACAGTACTCACGGTTCG	19792	SpyCas9-SpG	57	0
642	GGG	AGGACAGTACTCACGGTTCG	19793	SpyCas9-SpRY	57	0
643	GG	AGGACAGTACTCACGGTTCG	19794	SpyCas9-NG	57	0
644	GG	AGGACAGTACTCACGGTTCG	19795	SpyCas9-xCas	57	0
645	GG	AGGACAGTACTCACGGTTCG	19796	SpyCas9-xCas-NG	57	0
646	GAC	TTGCACTGGTTTCCGCCTCC	19797	SpyCas9-SpRY	57	0
647	GACC	TTGCACTGGTTTCCGCCTCC	19798	SpyCas9-3var-NRCH	57	0
648	GGGGG	ctGGAGGACAGTACTCACGGTTC	19799	SauCas9	58	0

649	GGGGG	GGAGGACAGTACTCACGGTTC	19800	SauCas9KKH	58	0
650	GGGGGT	ctGGAGGACAGTACTCACGGTTC	19801	SauCas9	58	0
651	GGGGGT	GGAGGACAGTACTCACGGTTC	19802	SauCas9KKH	58	0
652	GGGGGT	GGAGGACAGTACTCACGGTTC	19803	cCas9-v17	58	0
653	GGGGGT	GGAGGACAGTACTCACGGTTC	19804	cCas9-v42	58	0
654	GGGG	GGAGGACAGTACTCACGGTTC	19805	SauriCas9	58	0
655	GGGG	GGAGGACAGTACTCACGGTTC	19806	SauriCas9-KKH	58	0
656	GGG	GAGGACAGTACTCACGGTTC	19807	ScaCas9	58	0
657	GGG	GAGGACAGTACTCACGGTTC	19808	ScaCas9-HiFi-Sc++	58	0
658	GGG	GAGGACAGTACTCACGGTTC	19809	ScaCas9-Sc++	58	0
659	GGG	GAGGACAGTACTCACGGTTC	19810	SpyCas9	58	0
660	GGG	GAGGACAGTACTCACGGTTC	19811	SpyCas9-HF1	58	0
661	GGG	GAGGACAGTACTCACGGTTC	19812	SpyCas9-SpG	58	0
662	GGG	GAGGACAGTACTCACGGTTC	19813	SpyCas9-SpRY	58	0
663	GG	GAGGACAGTACTCACGGTTC	19814	SpyCas9-NG	58	0
664	GG	GAGGACAGTACTCACGGTTC	19815	SpyCas9-xCas	58	0
665	GG	GAGGACAGTACTCACGGTTC	19816	SpyCas9-xCas-NG	58	0
666	CG	CTTGCACTGGTTTCCGCCTC	19817	SpyCas9-NG	58	0
667	CG	CTTGCACTGGTTTCCGCCTC	19818	SpyCas9-xCas	58	0
668	CG	CTTGCACTGGTTTCCGCCTC	19819	SpyCas9-xCas-NG	58	0
669	CGA	CTTGCACTGGTTTCCGCCTC	19820	SpyCas9-SpG	58	0
670	CGA	CTTGCACTGGTTTCCGCCTC	19821	SpyCas9-SpRY	58	0
671	CGACCTGT	cagcTTGCACTGGTTTCCGCCTC	19822	BlatCas9	58	0
672	CGACC	cagcTTGCACTGGTTTCCGCCTC	19823	BlatCas9	58	0
673	CGAC	CTTGCACTGGTTTCCGCCTC	19824	SpyCas9-3var-NRRH	58	0
674	CGAC	CTTGCACTGGTTTCCGCCTC	19825	SpyCas9-VQR	58	0
675	CCGACC	ccCAGCTTGCACTGGTTTCCGCCT	19826	Nme2Cas9	59	0
676	CGGGG	gcTGGAGGACAGTACTCACGGTT	19827	SauCas9	59	0
677	CGGGG	TGGAGGACAGTACTCACGGTT	19828	SauCas9KKH	59	0
678	CGGG	TGGAGGACAGTACTCACGGTT	19829	SauriCas9	59	0
679	CGGG	TGGAGGACAGTACTCACGGTT	19830	SauriCas9-KKH	59	0
680	CGG	GGAGGACAGTACTCACGGTT	19831	ScaCas9	59	0
681	CGG	GGAGGACAGTACTCACGGTT	19832	ScaCas9-HiFi-Sc++	59	0
682	CGG	GGAGGACAGTACTCACGGTT	19833	ScaCas9-Sc++	59	0
683	CGG	GGAGGACAGTACTCACGGTT	19834	SpyCas9	59	0
684	CGG	GGAGGACAGTACTCACGGTT	19835	SpyCas9-HF1	59	0

685	CGG	GGAGGACAGTACTCACGGTT	19836	SpyCas9-SpG	59	0
686	CGG	GGAGGACAGTACTCACGGTT	19837	SpyCas9-SpRY	59	0
687	CCG	GCTTGCACTGGTTTCCGCCT	19838	ScaCas9	59	0
688	CCG	GCTTGCACTGGTTTCCGCCT	19839	ScaCas9-HiFi-Sc++	59	0
689	CCG	GCTTGCACTGGTTTCCGCCT	19840	ScaCas9-Sc++	59	0
690	CCG	GCTTGCACTGGTTTCCGCCT	19841	SpyCas9-SpRY	59	0
691	CG	GGAGGACAGTACTCACGGTT	19842	SpyCas9-NG	59	0
692	CG	GGAGGACAGTACTCACGGTT	19843	SpyCas9-xCas	59	0
693	CG	GGAGGACAGTACTCACGGTT	19844	SpyCas9-xCas-NG	59	0
694	CCGACCTG	ccagCTTGCACTGGTTTCCGCCT	19845	BlatCas9	59	0
695	CCGAC	ccagCTTGCACTGGTTTCCGCCT	19846	BlatCas9	59	0
696	CGGGGG	TGGAGGACAGTACTCACGGTT	19847	cCas9-v17	59	0
697	CGGGGG	TGGAGGACAGTACTCACGGTT	19848	cCas9-v42	59	0
698	CCGACCT	CAGCTTGCACTGGTTTCCGCCT	19849	CdiCas9	59	0
699	TCGGG	agCTGGAGGACAGTACTCACGGT	19850	SauCas9	60	0
700	TCGGG	CTGGAGGACAGTACTCACGGT	19851	SauCas9KKH	60	0
701	TCCGA	CAGCTTGCACTGGTTTCCGCC	19852	SauCas9KKH	60	0
702	TCGG	CTGGAGGACAGTACTCACGGT	19853	SauriCas9	60	0
703	TCGG	CTGGAGGACAGTACTCACGGT	19854	SauriCas9-KKH	60	0
704	TCG	TGGAGGACAGTACTCACGGT	19855	ScaCas9	60	0
705	TCG	TGGAGGACAGTACTCACGGT	19856	ScaCas9-HiFi-Sc++	60	0
706	TCG	TGGAGGACAGTACTCACGGT	19857	ScaCas9-Sc++	60	0
707	TCG	TGGAGGACAGTACTCACGGT	19858	SpyCas9-SpRY	60	0
708	TCC	AGCTTGCACTGGTTTCCGCC	19859	SpyCas9-SpRY	60	0
709	TCGGGG	CTGGAGGACAGTACTCACGGT	19860	cCas9-v17	60	0
710	TCGGGG	CTGGAGGACAGTACTCACGGT	19861	cCas9-v42	60	0
711	TCCGAC	CAGCTTGCACTGGTTTCCGCC	19862	cCas9-v17	60	0
712	TCCGAC	CAGCTTGCACTGGTTTCCGCC	19863	cCas9-v42	60	0
713	TTCGG	GCTGGAGGACAGTACTCACGG	19864	SauCas9KKH	61	0
714	TTC	CTGGAGGACAGTACTCACGG	19865	SpyCas9-SpRY	61	0
715	CTC	CAGCTTGCACTGGTTTCCGC	19866	SpyCas9-SpRY	61	0
716	TTCGGG	GCTGGAGGACAGTACTCACGG	19867	cCas9-v17	61	0
717	TTCGGG	GCTGGAGGACAGTACTCACGG	19868	cCas9-v42	61	0
718	GTT	GCTGGAGGACAGTACTCACG	19869	SpyCas9-SpRY	62	0
719	CCT	CCAGCTTGCACTGGTTTCCG	19870	SpyCas9-SpRY	62	0
720	CCTCC	atccCAGCTTGCACTGGTTTCCG	19871	BlatCas9	62	0
721	GCCTCC	tcATCCCAGCTTGCACTGGTTTCC	19872	Nme2Cas9	63	0

722	GG	AGCTGGAGGACAGTACTCAC	19873	SpyCas9-NG	63	0
723	GG	AGCTGGAGGACAGTACTCAC	19874	SpyCas9-xCas	63	0
724	GG	AGCTGGAGGACAGTACTCAC	19875	SpyCas9-xCas-NG	63	0
725	GGT	AGCTGGAGGACAGTACTCAC	19876	SpyCas9-SpG	63	0
726	GGT	AGCTGGAGGACAGTACTCAC	19877	SpyCas9-SpRY	63	0
727	GCC	CCCAGCTTGCACTGGTTTCC	19878	SpyCas9-SpRY	63	0
728	GGTTCGGG	ggtaGCTGGAGGACAGTACTCAC	19879	BlatCas9	63	0
729	GCCTCCGA	catcCCAGCTTGCACTGGTTTCC	19880	BlatCas9	63	0
730	GGTTC	ggtaGCTGGAGGACAGTACTCAC	19881	BlatCas9	63	0
731	GCCTC	catcCCAGCTTGCACTGGTTTCC	19882	BlatCas9	63	0
732	GGTT	AGCTGGAGGACAGTACTCAC	19883	SpyCas9-3var-NRTH	63	0
733	CGG	TAGCTGGAGGACAGTACTCA	19884	ScaCas9	64	0
734	CGG	TAGCTGGAGGACAGTACTCA	19885	ScaCas9-HiFi-Sc++	64	0
735	CGG	TAGCTGGAGGACAGTACTCA	19886	ScaCas9-Sc++	64	0
736	CGG	TAGCTGGAGGACAGTACTCA	19887	SpyCas9	64	0
737	CGG	TAGCTGGAGGACAGTACTCA	19888	SpyCas9-HF1	64	0
738	CGG	TAGCTGGAGGACAGTACTCA	19889	SpyCas9-SpG	64	0
739	CGG	TAGCTGGAGGACAGTACTCA	19890	SpyCas9-SpRY	64	0
740	CG	TAGCTGGAGGACAGTACTCA	19891	SpyCas9-NG	64	0
741	CG	TAGCTGGAGGACAGTACTCA	19892	SpyCas9-xCas	64	0
742	CG	TAGCTGGAGGACAGTACTCA	19893	SpyCas9-xCas-NG	64	0
743	CG	TCCCAGCTTGCACTGGTTTC	19894	SpyCas9-NG	64	0
744	CG	TCCCAGCTTGCACTGGTTTC	19895	SpyCas9-xCas	64	0
745	CG	TCCCAGCTTGCACTGGTTTC	19896	SpyCas9-xCas-NG	64	0
746	CGC	TCCCAGCTTGCACTGGTTTC	19897	SpyCas9-SpG	64	0
747	CGC	TCCCAGCTTGCACTGGTTTC	19898	SpyCas9-SpRY	64	0
748	CGGT	TAGCTGGAGGACAGTACTCA	19899	SpyCas9-3var-NRRH	64	0
749	CGCC	TCCCAGCTTGCACTGGTTTC	19900	SpyCas9-3var-NRCH	64	0
750	ACGG	GGTAGCTGGAGGACAGTACTC	19901	SauriCas9	65	0
751	ACGG	GGTAGCTGGAGGACAGTACTC	19902	SauriCas9-KKH	65	0
752	ACG	GTAGCTGGAGGACAGTACTC	19903	ScaCas9	65	0
753	ACG	GTAGCTGGAGGACAGTACTC	19904	ScaCas9-HiFi-Sc++	65	0
754	ACG	GTAGCTGGAGGACAGTACTC	19905	ScaCas9-Sc++	65	0
755	ACG	GTAGCTGGAGGACAGTACTC	19906	SpyCas9-SpRY	65	0
756	CCG	ATCCCAGCTTGCACTGGTTT	19907	ScaCas9	65	0

757	CCG	ATCCCAGCTTGCACTGGTTT	19908	ScaCas9-HiFi-Sc++	65	0
758	CCG	ATCCCAGCTTGCACTGGTTT	19909	ScaCas9-Sc++	65	0
759	CCG	ATCCCAGCTTGCACTGGTTT	19910	SpyCas9-SpRY	65	0
760	CCGCC	ttcaTCCCAGCTTGCACTGGTTT	19911	BlatCas9	65	0
761	ACGGTT	GGTAGCTGGAGGACAGTACTC	19912	cCas9-v16	65	0
762	ACGGTT	GGTAGCTGGAGGACAGTACTC	19913	cCas9-v21	65	0
763	CCGCCTC	TCATCCCAGCTTGCACTGGTTT	19914	CdiCas9	65	0
764	TCCGCC	ttTTCATCCCAGCTTGCACTGGTT	19915	Nme2Cas9	66	0
765	CACGGTT	aacTGGTAGCTGGAGGACAGTACT	19916	PpnCas9	66	0
766	CACGG	TGGTAGCTGGAGGACAGTACT	19917	SauCas9KKH	66	0
767	CACGGT	TGGTAGCTGGAGGACAGTACT	19918	SauCas9KKH	66	0
768	CACGGT	TGGTAGCTGGAGGACAGTACT	19919	cCas9-v17	66	0
769	CACGGT	TGGTAGCTGGAGGACAGTACT	19920	cCas9-v42	66	0
770	CAC	GGTAGCTGGAGGACAGTACT	19921	SpyCas9-SpRY	66	0
771	TCC	CATCCCAGCTTGCACTGGTT	19922	SpyCas9-SpRY	66	0
772	TCCGC	tttcATCCCAGCTTGCACTGGTT	19923	BlatCas9	66	0
773	TCA	TGGTAGCTGGAGGACAGTAC	19924	SpyCas9-SpRY	67	0
774	TTC	TCATCCCAGCTTGCACTGGT	19925	SpyCas9-SpRY	67	0
775	CTC	CTGGTAGCTGGAGGACAGTA	19926	SpyCas9-SpRY	68	0
776	TTT	TTCATCCCAGCTTGCACTGG	19927	SpyCas9-SpRY	68	0
777	CTCACGGT	caacTGGTAGCTGGAGGACAGTA	19928	BlatCas9	68	0
778	CTCAC	caacTGGTAGCTGGAGGACAGTA	19929	BlatCas9	68	0
779	TTTCC	ctttTCATCCCAGCTTGCACTGG	19930	BlatCas9	68	0
780	GTTTCC	ttCTTTTCATCCCAGCTTGCACTG	19931	Nme2Cas9	69	0
781	ACT	ACTGGTAGCTGGAGGACAGT	19932	SpyCas9-SpRY	69	0
782	GTT	TTTCATCCCAGCTTGCACTG	19933	SpyCas9-SpRY	69	0
783	GTTTC	tcttTTCATCCCAGCTTGCACTG	19934	BlatCas9	69	0
784	GG	TTTTCATCCCAGCTTGCACT	19935	SpyCas9-NG	70	0
785	GG	TTTTCATCCCAGCTTGCACT	19936	SpyCas9-xCas	70	0
786	GG	TTTTCATCCCAGCTTGCACT	19937	SpyCas9-xCas-NG	70	0
787	TAC	AACTGGTAGCTGGAGGACAG	19938	SpyCas9-SpRY	70	0
788	GGT	TTTTCATCCCAGCTTGCACT	19939	SpyCas9-SpG	70	0
789	GGT	TTTTCATCCCAGCTTGCACT	19940	SpyCas9-SpRY	70	0
790	TACTC	ggcaACTGGTAGCTGGAGGACAG	19941	BlatCas9	70	0
791	GGTT	TTTTCATCCCAGCTTGCACT	19942	SpyCas9-3var-NRTH	70	0
792	TACT	AACTGGTAGCTGGAGGACAG	19943	SpyCas9-3var-NRCH	70	0

793	TGG	CTTTTCATCCCAGCTTGCAC	19944	ScaCas9	71	0
794	TGG	CTTTTCATCCCAGCTTGCAC	19945	ScaCas9-HiFi-Sc++	71	0
795	TGG	CTTTTCATCCCAGCTTGCAC	19946	ScaCas9-Sc++	71	0
796	TGG	CTTTTCATCCCAGCTTGCAC	19947	SpyCas9	71	0
797	TGG	CTTTTCATCCCAGCTTGCAC	19948	SpyCas9-HF1	71	0
798	TGG	CTTTTCATCCCAGCTTGCAC	19949	SpyCas9-SpG	71	0
799	TGG	CTTTTCATCCCAGCTTGCAC	19950	SpyCas9-SpRY	71	0
800	TG	CTTTTCATCCCAGCTTGCAC	19951	SpyCas9-NG	71	0
801	TG	CTTTTCATCCCAGCTTGCAC	19952	SpyCas9-xCas	71	0
802	TG	CTTTTCATCCCAGCTTGCAC	19953	SpyCas9-xCas-NG	71	0
803	GTA	CAACTGGTAGCTGGAGGACA	19954	SpyCas9-SpRY	71	0
804	TGGTTTC	TTCTTTTCATCCCAGCTTGCAC	19955	CdiCas9	71	0
805	TGGT	CTTTTCATCCCAGCTTGCAC	19956	SpyCas9-3var-NRRH	71	0
806	CTGG	TTCTTTTCATCCCAGCTTGCA	19957	SauriCas9	72	0
807	CTGG	TTCTTTTCATCCCAGCTTGCA	19958	SauriCas9-KKH	72	0
808	CTG	TCTTTTCATCCCAGCTTGCA	19959	ScaCas9	72	0
809	CTG	TCTTTTCATCCCAGCTTGCA	19960	ScaCas9-HiFi-Sc++	72	0
810	CTG	TCTTTTCATCCCAGCTTGCA	19961	ScaCas9-Sc++	72	0
811	CTG	TCTTTTCATCCCAGCTTGCA	19962	SpyCas9-SpRY	72	0
812	AG	GCAACTGGTAGCTGGAGGAC	19963	SpyCas9-NG	72	0
813	AG	GCAACTGGTAGCTGGAGGAC	19964	SpyCas9-xCas	72	0
814	AG	GCAACTGGTAGCTGGAGGAC	19965	SpyCas9-xCas-NG	72	0
815	AGT	GCAACTGGTAGCTGGAGGAC	19966	SpyCas9-SpG	72	0
816	AGT	GCAACTGGTAGCTGGAGGAC	19967	SpyCas9-SpRY	72	0
817	AGTAC	ctggCAACTGGTAGCTGGAGGAC	19968	BlatCas9	72	0
818	CTGGTT	TTCTTTTCATCCCAGCTTGCA	19969	cCas9-v16	72	0
819	CTGGTT	TTCTTTTCATCCCAGCTTGCA	19970	cCas9-v21	72	0
820	AGTA	GCAACTGGTAGCTGGAGGAC	19971	SpyCas9-3var-NRTH	72	0
821	ACTGGTT	tttCTTCTTTTCATCCCAGCTTGC	19972	PpnCas9	73	0
822	ACTGG	CTTCTTTTCATCCCAGCTTGC	19973	SauCas9KKH	73	0
823	ACTGGT	CTTCTTTTCATCCCAGCTTGC	19974	SauCas9KKH	73	0
824	CAG	GGCAACTGGTAGCTGGAGGA	19975	ScaCas9	73	0
825	CAG	GGCAACTGGTAGCTGGAGGA	19976	ScaCas9-HiFi-Sc++	73	0
826	CAG	GGCAACTGGTAGCTGGAGGA	19977	ScaCas9-Sc++	73	0
827	CAG	GGCAACTGGTAGCTGGAGGA	19978	SpyCas9-SpRY	73	0
828	ACT	TTCTTTTCATCCCAGCTTGC	19979	SpyCas9-SpRY	73	0

829	CAGTACT	CTGGCAACTGGTAGCTGGAGGA	19980	CdiCas9	73	0
830	ACTGGTTT	tttcTTCTTTTCATCCCAGCTTGC	19981	NmeCas9	73	0
831	CAGT	GGCAACTGGTAGCTGGAGGA	19982	SpyCas9-3var-NRRH	73	0
832	ACAG	CTGGCAACTGGTAGCTGGAGG	19983	SauriCas9-KKH	74	0
833	CAC	CTTCTTTTCATCCCAGCTTG	19984	SpyCas9-SpRY	74	0
834	ACA	TGGCAACTGGTAGCTGGAGG	19985	SpyCas9-SpRY	74	0
835	CACT	CTTCTTTTCATCCCAGCTTG	19986	SpyCas9-3var-NRCH	74	0
836	GACAG	CCTGGCAACTGGTAGCTGGAG	19987	SauCas9KKH	75	0
837	GACAGT	CCTGGCAACTGGTAGCTGGAG	19988	SauCas9KKH	75	0
838	GACAGT	CCTGGCAACTGGTAGCTGGAG	19989	cCas9-v17	75	0
839	GACAGT	CCTGGCAACTGGTAGCTGGAG	19990	cCas9-v42	75	0
840	GAC	CTGGCAACTGGTAGCTGGAG	19991	SpyCas9-SpRY	75	0
841	GCA	TCTTCTTTTCATCCCAGCTT	19992	SpyCas9-SpRY	75	0
842	GACAGTAC	tgCCTGGCAACTGGTAGCTGGAG	19993	CjeCas9	75	0
843	GACA	CTGGCAACTGGTAGCTGGAG	19994	SpyCas9-3var-NRCH	75	0
844	GG	CCTGGCAACTGGTAGCTGGA	19995	SpyCas9-NG	76	0
845	GG	CCTGGCAACTGGTAGCTGGA	19996	SpyCas9-xCas	76	0
846	GG	CCTGGCAACTGGTAGCTGGA	19997	SpyCas9-xCas-NG	76	0
847	TG	TTCTTCTTTTCATCCCAGCT	19998	SpyCas9-NG	76	0
848	TG	TTCTTCTTTTCATCCCAGCT	19999	SpyCas9-xCas	76	0
849	TG	TTCTTCTTTTCATCCCAGCT	20000	SpyCas9-xCas-NG	76	0
850	GGA	CCTGGCAACTGGTAGCTGGA	20001	SpyCas9-SpG	76	0
851	GGA	CCTGGCAACTGGTAGCTGGA	20002	SpyCas9-SpRY	76	0
852	TGC	TTCTTCTTTTCATCCCAGCT	20003	SpyCas9-SpG	76	0
853	TGC	TTCTTCTTTTCATCCCAGCT	20004	SpyCas9-SpRY	76	0
854	TGCACTGG	tcttTCTTCTTTTCATCCCAGCT	20005	BlatCas9	76	0
855	TGCAC	tcttTCTTCTTTTCATCCCAGCT	20006	BlatCas9	76	0
856	TGCACT	TTTCTTCTTTTCATCCCAGCT	20007	cCas9-v16	76	0
857	TGCACT	TTTCTTCTTTTCATCCCAGCT	20008	cCas9-v21	76	0
858	GGAC	CCTGGCAACTGGTAGCTGGA	20009	SpyCas9-3var-NRRH	76	0
859	GGAC	CCTGGCAACTGGTAGCTGGA	20010	SpyCas9-VQR	76	0
860	TGCA	TTCTTCTTTTCATCCCAGCT	20011	SpyCas9-3var-NRCH	76	0
861	AGG	GCCTGGCAACTGGTAGCTGG	20012	ScaCas9	77	0
862	AGG	GCCTGGCAACTGGTAGCTGG	20013	ScaCas9-HiFi-Sc++	77	0
863	AGG	GCCTGGCAACTGGTAGCTGG	20014	ScaCas9-Sc++	77	0

864	AGG	GCCTGGCAACTGGTAGCTGG	20015	SpyCas9	77	0
865	AGG	GCCTGGCAACTGGTAGCTGG	20016	SpyCas9-HF1	77	0
866	AGG	GCCTGGCAACTGGTAGCTGG	20017	SpyCas9-SpG	77	0
867	AGG	GCCTGGCAACTGGTAGCTGG	20018	SpyCas9-SpRY	77	0
868	TTG	TTTCTTCTTTTCATCCCAGC	20019	ScaCas9	77	0
869	TTG	TTTCTTCTTTTCATCCCAGC	20020	ScaCas9-HiFi-Sc++	77	0
870	TTG	TTTCTTCTTTTCATCCCAGC	20021	ScaCas9-Sc++	77	0
871	TTG	TTTCTTCTTTTCATCCCAGC	20022	SpyCas9-SpRY	77	0
872	AG	GCCTGGCAACTGGTAGCTGG	20023	SpyCas9-NG	77	0
873	AG	GCCTGGCAACTGGTAGCTGG	20024	SpyCas9-xCas	77	0
874	AG	GCCTGGCAACTGGTAGCTGG	20025	SpyCas9-xCas-NG	77	0
875	AGGACAGT	tgtgCCTGGCAACTGGTAGCTGG	20026	BlatCas9	77	0
876	AGGAC	tgtgCCTGGCAACTGGTAGCTGG	20027	BlatCas9	77	0
877	TTGCACT	TCTTTCTTCTTTTCATCCCAGC	20028	CdiCas9	77	0
878	AGGA	GCCTGGCAACTGGTAGCTGG	20029	SpyCas9-3var-NRRH	77	0
879	GAGGA	ttGTGCCTGGCAACTGGTAGCTG	20030	SauCas9	78	0
880	GAGGA	GTGCCTGGCAACTGGTAGCTG	20031	SauCas9KKH	78	0
881	GAGG	GTGCCTGGCAACTGGTAGCTG	20032	SauriCas9	78	0
882	GAGG	GTGCCTGGCAACTGGTAGCTG	20033	SauriCas9-KKH	78	0
883	GAG	TGCCTGGCAACTGGTAGCTG	20034	ScaCas9	78	0
884	GAG	TGCCTGGCAACTGGTAGCTG	20035	ScaCas9-HiFi-Sc++	78	0
885	GAG	TGCCTGGCAACTGGTAGCTG	20036	ScaCas9-Sc++	78	0
886	GAG	TGCCTGGCAACTGGTAGCTG	20037	SpyCas9-SpRY	78	0
887	CTT	CTTTCTTCTTTTCATCCCAG	20038	SpyCas9-SpRY	78	0
888	CTTGC	tttcTTTCTTCTTTTCATCCCAG	20039	BlatCas9	78	0
889	GAGGAC	GTGCCTGGCAACTGGTAGCTG	20040	cCas9-v17	78	0
890	GAGGAC	GTGCCTGGCAACTGGTAGCTG	20041	cCas9-v42	78	0
891	GGAGG	TGTGCCTGGCAACTGGTAGCT	20042	SauCas9KKH	79	0
892	GGAG	TGTGCCTGGCAACTGGTAGCT	20043	SauriCas9-KKH	79	0
893	GGAG	GTGCCTGGCAACTGGTAGCT	20044	SpyCas9-VQR	79	0
894	GG	GTGCCTGGCAACTGGTAGCT	20045	SpyCas9-NG	79	0
895	GG	GTGCCTGGCAACTGGTAGCT	20046	SpyCas9-xCas	79	0
896	GG	GTGCCTGGCAACTGGTAGCT	20047	SpyCas9-xCas-NG	79	0
897	GGA	GTGCCTGGCAACTGGTAGCT	20048	SpyCas9-SpG	79	0
898	GGA	GTGCCTGGCAACTGGTAGCT	20049	SpyCas9-SpRY	79	0
899	GCT	TCTTTCTTCTTTTCATCCCA	20050	SpyCas9-SpRY	79	0
900	GGAGGA	TGTGCCTGGCAACTGGTAGCT	20051	cCas9-v17	79	0

901	GGAGGA	TGTGCCTGGCAACTGGTAGCT	20052	cCas9-v42	79	0
902	GCTTGCAC	ttTTCTTTCTTCTTTTCATCCCA	20053	CjeCas9	79	0
903	GGAGGACA	cattGTGCCTGGCAACTGGTAGCT	20054	NmeCas9	79	0
904	TGGAG	caTTGTGCCTGGCAACTGGTAGC	20055	SauCas9	80	0
905	TGGAG	TTGTGCCTGGCAACTGGTAGC	20056	SauCas9KKH	80	0
906	TGG	TGTGCCTGGCAACTGGTAGC	20057	ScaCas9	80	0
907	TGG	TGTGCCTGGCAACTGGTAGC	20058	ScaCas9-HiFi-Sc++	80	0
908	TGG	TGTGCCTGGCAACTGGTAGC	20059	ScaCas9-Sc++	80	0
909	TGG	TGTGCCTGGCAACTGGTAGC	20060	SpyCas9	80	0
910	TGG	TGTGCCTGGCAACTGGTAGC	20061	SpyCas9-HF1	80	0
911	TGG	TGTGCCTGGCAACTGGTAGC	20062	SpyCas9-SpG	80	0
912	TGG	TGTGCCTGGCAACTGGTAGC	20063	SpyCas9-SpRY	80	0
913	TG	TGTGCCTGGCAACTGGTAGC	20064	SpyCas9-NG	80	0
914	TG	TGTGCCTGGCAACTGGTAGC	20065	SpyCas9-xCas	80	0
915	TG	TGTGCCTGGCAACTGGTAGC	20066	SpyCas9-xCas-NG	80	0
916	AG	TTCTTTCTTCTTTTCATCCC	20067	SpyCas9-NG	80	0
917	AG	TTCTTTCTTCTTTTCATCCC	20068	SpyCas9-xCas	80	0
918	AG	TTCTTTCTTCTTTTCATCCC	20069	SpyCas9-xCas-NG	80	0
919	AGC	TTCTTTCTTCTTTTCATCCC	20070	SpyCas9-SpG	80	0
920	AGC	TTCTTTCTTCTTTTCATCCC	20071	SpyCas9-SpRY	80	0
921	TGGAGG	TTGTGCCTGGCAACTGGTAGC	20072	cCas9-v17	80	0
922	TGGAGG	TTGTGCCTGGCAACTGGTAGC	20073	cCas9-v42	80	0
923	TGGA	TGTGCCTGGCAACTGGTAGC	20074	SpyCas9-3var-NRRH	80	0
924	AGCT	TTCTTTCTTCTTTTCATCCC	20075	SpyCas9-3var-NRCH	80	0
925	CTGGA	tcATTGTGCCTGGCAACTGGTAG	20076	SauCas9	81	0
926	CTGGA	ATTGTGCCTGGCAACTGGTAG	20077	SauCas9KKH	81	0
927	CTGG	ATTGTGCCTGGCAACTGGTAG	20078	SauriCas9	81	0
928	CTGG	ATTGTGCCTGGCAACTGGTAG	20079	SauriCas9-KKH	81	0
929	CTG	TTGTGCCTGGCAACTGGTAG	20080	ScaCas9	81	0
930	CTG	TTGTGCCTGGCAACTGGTAG	20081	ScaCas9-HiFi-Sc++	81	0
931	CTG	TTGTGCCTGGCAACTGGTAG	20082	ScaCas9-Sc++	81	0
932	CTG	TTGTGCCTGGCAACTGGTAG	20083	SpyCas9-SpRY	81	0
933	CAG	TTTCTTTCTTCTTTTCATCC	20084	ScaCas9	81	0
934	CAG	TTTCTTTCTTCTTTTCATCC	20085	ScaCas9-HiFi-Sc++	81	0
935	CAG	TTTCTTTCTTCTTTTCATCC	20086	ScaCas9-Sc++	81	0

936	CAG	TTTCTTTCTTCTTTTCATCC	20087	SpyCas9-SpRY	81	0
937	CTGGAG	ATTGTGCCTGGCAACTGGTAG	20088	cCas9-v17	81	0
938	CTGGAG	ATTGTGCCTGGCAACTGGTAG	20089	cCas9-v42	81	0
939	CAGC	TTTCTTTCTTCTTTTCATCC	20090	SpyCas9-3var-NRRH	81	0
940	GCTGG	CATTGTGCCTGGCAACTGGTA	20091	SauCas9KKH	82	0
941	CCAG	GTTTTCTTTCTTCTTTTCATC	20092	SauriCas9-KKH	82	0
942	GCT	ATTGTGCCTGGCAACTGGTA	20093	SpyCas9-SpRY	82	0
943	CCA	TTTTCTTTCTTCTTTTCATC	20094	SpyCas9-SpRY	82	0
944	CCAGCTTG	gagtTTTCTTTCTTCTTTTCATC	20095	BlatCas9	82	0
945	CCAGC	gagtTTTCTTTCTTCTTTTCATC	20096	BlatCas9	82	0
946	CCAGCT	GTTTTCTTTCTTCTTTTCATC	20097	cCas9-v16	82	0
947	CCAGCT	GTTTTCTTTCTTCTTTTCATC	20098	cCas9-v21	82	0
948	CCCAG	AGTTTTCTTTCTTCTTTTCAT	20099	SauCas9KKH	83	0
949	AG	CATTGTGCCTGGCAACTGGT	20100	SpyCas9-NG	83	0
950	AG	CATTGTGCCTGGCAACTGGT	20101	SpyCas9-xCas	83	0
951	AG	CATTGTGCCTGGCAACTGGT	20102	SpyCas9-xCas-NG	83	0
952	AGC	CATTGTGCCTGGCAACTGGT	20103	SpyCas9-SpG	83	0
953	AGC	CATTGTGCCTGGCAACTGGT	20104	SpyCas9-SpRY	83	0
954	CCC	GTTTTCTTTCTTCTTTTCAT	20105	SpyCas9-SpRY	83	0
955	CCCAGC	AGTTTTCTTTCTTCTTTTCAT	20106	cCas9-v17	83	0
956	CCCAGC	AGTTTTCTTTCTTCTTTTCAT	20107	cCas9-v42	83	0
957	CCCAGCTT	ttgaGTTTTCTTTCTTCTTTTCAT	20108	NmeCas9	83	0
958	AGCT	CATTGTGCCTGGCAACTGGT	20109	SpyCas9-3var-NRCH	83	0
959	TAG	TCATTGTGCCTGGCAACTGG	20110	ScaCas9	84	0
960	TAG	TCATTGTGCCTGGCAACTGG	20111	ScaCas9-HiFi-Sc++	84	0
961	TAG	TCATTGTGCCTGGCAACTGG	20112	ScaCas9-Sc++	84	0
962	TAG	TCATTGTGCCTGGCAACTGG	20113	SpyCas9-SpRY	84	0
963	TCC	AGTTTTCTTTCTTCTTTTCA	20114	SpyCas9-SpRY	84	0
964	TAGC	TCATTGTGCCTGGCAACTGG	20115	SpyCas9-3var-NRRH	84	0
965	GTAG	GCTCATTGTGCCTGGCAACTG	20116	SauriCas9-KKH	85	0
966	GTA	CTCATTGTGCCTGGCAACTG	20117	SpyCas9-SpRY	85	0
967	ATC	GAGTTTTCTTTCTTCTTTTC	20118	SpyCas9-SpRY	85	0
968	GTAGCTGG	gcgcTCATTGTGCCTGGCAACTG	20119	BlatCas9	85	0
969	GTAGC	gcgcTCATTGTGCCTGGCAACTG	20120	BlatCas9	85	0
970	ATCCC	tttgAGTTTTCTTTCTTCTTTTC	20121	BlatCas9	85	0
971	GTAGCT	GCTCATTGTGCCTGGCAACTG	20122	cCas9-v16	85	0

972	GTAGCT	GCTCATTGTGCCTGGCAACTG	20123	cCas9-v21	85	0
973	CATCCC	gcTTTGAGTTTTCTTTCTTCTTTT	20124	Nme2Cas9	86	0
974	GGTAG	CGCTCATTGTGCCTGGCAACT	20125	SauCas9KKH	86	0
975	GG	GCTCATTGTGCCTGGCAACT	20126	SpyCas9-NG	86	0
976	GG	GCTCATTGTGCCTGGCAACT	20127	SpyCas9-xCas	86	0
977	GG	GCTCATTGTGCCTGGCAACT	20128	SpyCas9-xCas-NG	86	0
978	GGT	GCTCATTGTGCCTGGCAACT	20129	SpyCas9-SpG	86	0
979	GGT	GCTCATTGTGCCTGGCAACT	20130	SpyCas9-SpRY	86	0
980	CAT	TGAGTTTTCTTTCTTCTTTT	20131	SpyCas9-SpRY	86	0
981	CATCCCAG	ctttGAGTTTTCTTTCTTCTTTT	20132	BlatCas9	86	0
982	CATCC	ctttGAGTTTTCTTTCTTCTTTT	20133	BlatCas9	86	0
983	GGTA	GCTCATTGTGCCTGGCAACT	20134	SpyCas9-3var-NRTH	86	0
984	CATC	TGAGTTTTCTTTCTTCTTTT	20135	SpyCas9-3var-NRTH	86	0
985	TCATCC	agCTTTGAGTTTTCTTTCTTCTTT	20136	Nme2Cas9	87	0
986	TGG	CGCTCATTGTGCCTGGCAAC	20137	ScaCas9	87	0
987	TGG	CGCTCATTGTGCCTGGCAAC	20138	ScaCas9-HiFi-Sc++	87	0
988	TGG	CGCTCATTGTGCCTGGCAAC	20139	ScaCas9-Sc++	87	0
989	TGG	CGCTCATTGTGCCTGGCAAC	20140	SpyCas9	87	0
990	TGG	CGCTCATTGTGCCTGGCAAC	20141	SpyCas9-HF1	87	0
991	TGG	CGCTCATTGTGCCTGGCAAC	20142	SpyCas9-SpG	87	0
992	TGG	CGCTCATTGTGCCTGGCAAC	20143	SpyCas9-SpRY	87	0
993	TG	CGCTCATTGTGCCTGGCAAC	20144	SpyCas9-NG	87	0
994	TG	CGCTCATTGTGCCTGGCAAC	20145	SpyCas9-xCas	87	0
995	TG	CGCTCATTGTGCCTGGCAAC	20146	SpyCas9-xCas-NG	87	0
996	TCA	TTGAGTTTTCTTTCTTCTTT	20147	SpyCas9-SpRY	87	0
997	TCATC	gcttTGAGTTTTCTTTCTTCTTT	20148	BlatCas9	87	0
998	TCATCCC	CTTTGAGTTTTCTTTCTTCTTT	20149	CdiCas9	87	0
999	TGGT	CGCTCATTGTGCCTGGCAAC	20150	SpyCas9-3var-NRRH	87	0
1000	CTGG	GGCGCTCATTGTGCCTGGCAA	20151	SauriCas9	88	0
1001	CTGG	GGCGCTCATTGTGCCTGGCAA	20152	SauriCas9-KKH	88	0
1002	CTG	GCGCTCATTGTGCCTGGCAA	20153	ScaCas9	88	0
1003	CTG	GCGCTCATTGTGCCTGGCAA	20154	ScaCas9-HiFi-Sc++	88	0
1004	CTG	GCGCTCATTGTGCCTGGCAA	20155	ScaCas9-Sc++	88	0
1005	CTG	GCGCTCATTGTGCCTGGCAA	20156	SpyCas9-SpRY	88	0
1006	TTC	TTTGAGTTTTCTTTCTTCTT	20157	SpyCas9-SpRY	88	0
1007	ACTGG	TGGCGCTCATTGTGCCTGGCA	20158	SauCas9KKH	89	0

1008	ACTGGT	TGGCGCTCATTGTGCCTGGCA	20159	SauCas9KKH	89	0
1009	ACT	GGCGCTCATTGTGCCTGGCA	20160	SpyCas9-SpRY	89	0
1010	TTT	CTTTGAGTTTTCTTTCTTCT	20161	SpyCas9-SpRY	89	0
1011	AAC	TGGCGCTCATTGTGCCTGGC	20162	SpyCas9-SpRY	90	0
1012	TTT	GCTTTGAGTTTTCTTTCTTC	20163	SpyCas9-SpRY	90	0
1013	TTTTC	tgagCTTTGAGTTTTCTTTCTTC	20164	BlatCas9	90	0
1014	AACT	TGGCGCTCATTGTGCCTGGC	20165	SpyCas9-3var-NRCH	90	0
1015	CAA	ATGGCGCTCATTGTGCCTGG	20166	SpyCas9-SpRY	91	0
1016	CTT	AGCTTTGAGTTTTCTTTCTT	20167	SpyCas9-SpRY	91	0
1017	CAAC	ATGGCGCTCATTGTGCCTGG	20168	SpyCas9-3var-NRRH	91	0
1018	CAAC	gaTGGCGCTCATTGTGCCTGG	20169	iSpyMacCas9	91	0
1019	GCA	GATGGCGCTCATTGTGCCTG	20170	SpyCas9-SpRY	92	0
1020	TCT	GAGCTTTGAGTTTTCTTTCT	20171	SpyCas9-SpRY	92	0
1021	GCAACTGG	aaagATGGCGCTCATTGTGCCTG	20172	BlatCas9	92	0
1022	GCAAC	aaagATGGCGCTCATTGTGCCTG	20173	BlatCas9	92	0
1023	GCAACT	AGATGGCGCTCATTGTGCCTG	20174	cCas9-v16	92	0
1024	GCAACT	AGATGGCGCTCATTGTGCCTG	20175	cCas9-v21	92	0
1025	GGCAA	AAGATGGCGCTCATTGTGCCT	20176	SauCas9KKH	93	0
1026	GG	AGATGGCGCTCATTGTGCCT	20177	SpyCas9-NG	93	0
1027	GG	AGATGGCGCTCATTGTGCCT	20178	SpyCas9-xCas	93	0
1028	GG	AGATGGCGCTCATTGTGCCT	20179	SpyCas9-xCas-NG	93	0
1029	GGC	AGATGGCGCTCATTGTGCCT	20180	SpyCas9-SpG	93	0
1030	GGC	AGATGGCGCTCATTGTGCCT	20181	SpyCas9-SpRY	93	0
1031	TTC	TGAGCTTTGAGTTTTCTTTC	20182	SpyCas9-SpRY	93	0
1032	GGCAAC	AAGATGGCGCTCATTGTGCCT	20183	cCas9-v17	93	0
1033	GGCAAC	AAGATGGCGCTCATTGTGCCT	20184	cCas9-v42	93	0
1034	GGCA	AGATGGCGCTCATTGTGCCT	20185	SpyCas9-3var-NRCH	93	0
1035	TGG	AAGATGGCGCTCATTGTGCC	20186	ScaCas9	94	0
1036	TGG	AAGATGGCGCTCATTGTGCC	20187	ScaCas9-HiFi-Sc++	94	0
1037	TGG	AAGATGGCGCTCATTGTGCC	20188	ScaCas9-Sc++	94	0
1038	TGG	AAGATGGCGCTCATTGTGCC	20189	SpyCas9	94	0
1039	TGG	AAGATGGCGCTCATTGTGCC	20190	SpyCas9-HF1	94	0
1040	TGG	AAGATGGCGCTCATTGTGCC	20191	SpyCas9-SpG	94	0
1041	TGG	AAGATGGCGCTCATTGTGCC	20192	SpyCas9-SpRY	94	0
1042	TG	AAGATGGCGCTCATTGTGCC	20193	SpyCas9-NG	94	0
1043	TG	AAGATGGCGCTCATTGTGCC	20194	SpyCas9-xCas	94	0
1044	TG	AAGATGGCGCTCATTGTGCC	20195	SpyCas9-xCas-NG	94	0

1045	CTT	ATGAGCTTTGAGTTTTCTTT	20196	SpyCas9-SpRY	94	0
1046	TGGCAAC	AAAAGATGGCGCTCATTGTGCC	20197	CdiCas9	94	0
1047	TGGC	AAGATGGCGCTCATTGTGCC	20198	SpyCas9-3var-NRRH	94	0
1048	TGGCAA	AAGATGGCGCTCATTGTGCC	20199	St1Cas9-LMG1831	94	0
1049	CTGG	AAAAGATGGCGCTCATTGTGC	20200	SauriCas9	95	0
1050	CTGG	AAAAGATGGCGCTCATTGTGC	20201	SauriCas9-KKH	95	0
1051	CTG	AAAGATGGCGCTCATTGTGC	20202	ScaCas9	95	0
1052	CTG	AAAGATGGCGCTCATTGTGC	20203	ScaCas9-HiFi-Sc++	95	0
1053	CTG	AAAGATGGCGCTCATTGTGC	20204	ScaCas9-Sc++	95	0
1054	CTG	AAAGATGGCGCTCATTGTGC	20205	SpyCas9-SpRY	95	0
1055	TCT	GATGAGCTTTGAGTTTTCTT	20206	SpyCas9-SpRY	95	0
1056	TCTTCTTT	ggtgATGAGCTTTGAGTTTTCTT	20207	BlatCas9	95	0
1057	CTGGC	ggaaAAGATGGCGCTCATTGTGC	20208	BlatCas9	95	0
1058	TCTTC	ggtgATGAGCTTTGAGTTTTCTT	20209	BlatCas9	95	0
1059	CCTGG	GAAAAGATGGCGCTCATTGTG	20210	SauCas9KKH	96	0
1060	CCT	AAAAGATGGCGCTCATTGTG	20211	SpyCas9-SpRY	96	0
1061	TTC	TGATGAGCTTTGAGTTTTCT	20212	SpyCas9-SpRY	96	0
1062	GCC	GAAAAGATGGCGCTCATTGT	20213	SpyCas9-SpRY	97	0
1063	TTT	GTGATGAGCTTTGAGTTTTC	20214	SpyCas9-SpRY	97	0
1064	TG	GGAAAAGATGGCGCTCATTG	20215	SpyCas9-NG	98	0
1065	TG	GGAAAAGATGGCGCTCATTG	20216	SpyCas9-xCas	98	0
1066	TG	GGAAAAGATGGCGCTCATTG	20217	SpyCas9-xCas-NG	98	0
1067	TGC	GGAAAAGATGGCGCTCATTG	20218	SpyCas9-SpG	98	0
1068	TGC	GGAAAAGATGGCGCTCATTG	20219	SpyCas9-SpRY	98	0
1069	CTT	GGTGATGAGCTTTGAGTTTT	20220	SpyCas9-SpRY	98	0
1070	CTTTC	agtgGTGATGAGCTTTGAGTTTT	20221	BlatCas9	98	0
1071	TGCC	GGAAAAGATGGCGCTCATTG	20222	SpyCas9-3var-NRCH	98	0
1072	GTG	AGGAAAAGATGGCGCTCATT	20223	ScaCas9	99	0
1073	GTG	AGGAAAAGATGGCGCTCATT	20224	ScaCas9-HiFi-Sc++	99	0
1074	GTG	AGGAAAAGATGGCGCTCATT	20225	ScaCas9-Sc++	99	0
1075	GTG	AGGAAAAGATGGCGCTCATT	20226	SpyCas9-SpRY	99	0
1076	TCT	TGGTGATGAGCTTTGAGTTT	20227	SpyCas9-SpRY	99	0
1077	GTGCCTGG	agcaGGAAAAGATGGCGCTCATT	20228	BlatCas9	99	0
1078	GTGCC	agcaGGAAAAGATGGCGCTCATT	20229	BlatCas9	99	0
1079	TGTGCC	gcAGCAGGAAAAGATGGCGCTCAT	20230	Nme2Cas9	100	0
1080	TG	CAGGAAAAGATGGCGCTCAT	20231	SpyCas9-NG	100	0

1081	TG	CAGGAAAAGATGGCGCTCAT	20232	SpyCas9-xCas	100	0
1082	TG	CAGGAAAAGATGGCGCTCAT	20233	SpyCas9-xCas-NG	100	0
1083	TGT	CAGGAAAAGATGGCGCTCAT	20234	SpyCas9-SpG	100	0
1084	TGT	CAGGAAAAGATGGCGCTCAT	20235	SpyCas9-SpRY	100	0
1085	TTC	GTGGTGATGAGCTTTGAGTT	20236	SpyCas9-SpRY	100	0
1086	TGTGCCTG	cagcAGGAAAAGATGGCGCTCAT	20237	BlatCas9	100	0
1087	TGTGC	cagcAGGAAAAGATGGCGCTCAT	20238	BlatCas9	100	0

Table 1C: Exemplary gRNA spacer Cas pairs for correcting the pathogenic R243Q mutation

Table 1C provides a gRNA database for correcting the pathogenic R243Q mutation in PAH. List of spacers, PAMs, and Cas variants for generating a nick at an appropriate position to enable installation of a desired genomic edit with a gene modifying system. The spacers in this table are designed to be used with a gene modifying polypeptide comprising a nickase variant of the Cas species indicated in the table. Tables 2C, 3C, and 4C detail the other components of the system and are organized such that the ID number shown here in Column 1 ("ID") is meant to correspond to the same ID number in Tables 2C, 2C, and 4C.

ID	PAM sequence	gRNA spacer	SEQ ID NO	Cas species	distance	Overlaps mutation
1	CTG	CACTGGTTTCCGCCTCCAAC	21312	ScaCas9	0	0
2	CTG	CACTGGTTTCCGCCTCCAAC	21313	ScaCas9-HiFi-Sc++	0	0
3	CTG	CACTGGTTTCCGCCTCCAAC	21314	ScaCas9-Sc++	0	0
4	CTG	CACTGGTTTCCGCCTCCAAC	21315	SpyCas9-SpRY	0	0
5	GAGG	AAGCAGGCCAGCCACAGGTTG	21316	SauriCas9	1	0
6	GAGG	AAGCAGGCCAGCCACAGGTTG	21317	SauriCas9-KKH	1	0
7	GAG	AGCAGGCCAGCCACAGGTTG	21318	ScaCas9	1	0
8	GAG	AGCAGGCCAGCCACAGGTTG	21319	ScaCas9-HiFi-Sc++	1	0
9	GAG	AGCAGGCCAGCCACAGGTTG	21320	ScaCas9-Sc++	1	0
10	GAG	AGCAGGCCAGCCACAGGTTG	21321	SpyCas9-SpRY	1	0

11	CCT	GCACTGGTTTCCGCCTCCAA	21322	SpyCas9-SpRY	1	0
12	GAGGCGGA	gaaaGCAGGCCAGCCACAGGTTG	21323	BlatCas9	1	0
13	GAGGC	gaaaGCAGGCCAGCCACAGGTTG	21324	BlatCas9	1	0
14	GGAGG	AAAGCAGGCCAGCCACAGGTT	21325	SauCas9KKH	2	0
15	GGAG	AAAGCAGGCCAGCCACAGGTT	21326	SauriCas9-KKH	2	0
16	GGAG	AAGCAGGCCAGCCACAGGTT	21327	SpyCas9-VQR	2	0
17	GG	AAGCAGGCCAGCCACAGGTT	21328	SpyCas9-NG	2	0
18	GG	AAGCAGGCCAGCCACAGGTT	21329	SpyCas9-xCas	2	0
19	GG	AAGCAGGCCAGCCACAGGTT	21330	SpyCas9-xCas-NG	2	0
20	GGA	AAGCAGGCCAGCCACAGGTT	21331	SpyCas9-SpG	2	0
21	GGA	AAGCAGGCCAGCCACAGGTT	21332	SpyCas9-SpRY	2	0
22	ACC	TGCACTGGTTTCCGCCTCCA	21333	SpyCas9-SpRY	2	0
23	GGAGGC	AAAGCAGGCCAGCCACAGGTT	21334	cCas9-v17	2	0
24	GGAGGC	AAAGCAGGCCAGCCACAGGTT	21335	cCas9-v42	2	0
25	tGGAG	agGAAAGCAGGCCAGCCACAGGT	21336	SauCas9	3	1
26	tGGAG	GAAAGCAGGCCAGCCACAGGT	21337	SauCas9KKH	3	1
27	tGG	AAAGCAGGCCAGCCACAGGT	21338	ScaCas9	3	1
28	tGG	AAAGCAGGCCAGCCACAGGT	21339	ScaCas9-HiFi-Sc++	3	1
29	tGG	AAAGCAGGCCAGCCACAGGT	21340	ScaCas9-Sc++	3	1
30	tGG	AAAGCAGGCCAGCCACAGGT	21341	SpyCas9	3	1
31	tGG	AAAGCAGGCCAGCCACAGGT	21342	SpyCas9-HF1	3	1
32	tGG	AAAGCAGGCCAGCCACAGGT	21343	SpyCas9-SpG	3	1
33	tGG	AAAGCAGGCCAGCCACAGGT	21344	SpyCas9-SpRY	3	1
34	tG	AAAGCAGGCCAGCCACAGGT	21345	SpyCas9-NG	3	1
35	tG	AAAGCAGGCCAGCCACAGGT	21346	SpyCas9-xCas	3	1
36	tG	AAAGCAGGCCAGCCACAGGT	21347	SpyCas9-xCas-NG	3	1
37	aAC	TTGCACTGGTTTCCGCCTCC	21348	SpyCas9-SpRY	3	1

38	tGGAGG	GAAAGCAGGCCAGCCACAGGT	21349	cCas9-v17	3	1
39	tGGAGG	GAAAGCAGGCCAGCCACAGGT	21350	cCas9-v42	3	1
40	tGGA	AAAGCAGGCCAGCCACAGGT	21351	SpyCas9-3var-NRRH	3	1
41	aACC	TTGCACTGGTTTCCGCCTCC	21352	SpyCas9-3var-NRCH	3	1
42	TtGGA	gaGGAAAGCAGGCCAGCCACAGG	21353	SauCas9	4	1
43	TtGGA	GGAAAGCAGGCCAGCCACAGG	21354	SauCas9KKH	4	1
44	TtGG	GGAAAGCAGGCCAGCCACAGG	21355	SauriCas9	4	1
45	TtGG	GGAAAGCAGGCCAGCCACAGG	21356	SauriCas9-KKH	4	1
46	TtG	GAAAGCAGGCCAGCCACAGG	21357	ScaCas9	4	1
47	TtG	GAAAGCAGGCCAGCCACAGG	21358	ScaCas9-HiFi-Sc++	4	1
48	TtG	GAAAGCAGGCCAGCCACAGG	21359	ScaCas9-Sc++	4	1
49	TtG	GAAAGCAGGCCAGCCACAGG	21360	SpyCas9-SpRY	4	1
50	CaA	CTTGCACTGGTTTCCGCCTC	21361	SpyCas9-SpRY	4	1
51	CaACCTGT	cagcTTGCACTGGTTTCCGCCTC	21362	BlatCas9	4	1
52	CaACC	cagcTTGCACTGGTTTCCGCCTC	21363	BlatCas9	4	1
53	TtGGAG	GGAAAGCAGGCCAGCCACAGG	21364	cCas9-v17	4	1
54	TtGGAG	GGAAAGCAGGCCAGCCACAGG	21365	cCas9-v42	4	1
55	CaAC	CTTGCACTGGTTTCCGCCTC	21366	SpyCas9-3var-NRRH	4	1
56	CaAC	gcTTGCACTGGTTTCCGCCTC	21367	iSpyMacCas9	4	1
57	CCaACC	ccCAGCTTGCACTGGTTTCCGCCT	21368	Nme2Cas9	5	1
58	GTtGG	AGGAAAGCAGGCCAGCCACAG	21369	SauCas9KKH	5	1
59	GTt	GGAAAGCAGGCCAGCCACAG	21370	SpyCas9-SpRY	5	1
60	CCa	GCTTGCACTGGTTTCCGCCT	21371	SpyCas9-SpRY	5	1
61	CCaACCTG	ccagCTTGCACTGGTTTCCGCCT	21372	BlatCas9	5	1
62	CCaAC	ccagCTTGCACTGGTTTCCGCCT	21373	BlatCas9	5	1
63	CCaACCT	CAGCTTGCACTGGTTTCCGCCT	21374	CdiCas9	5	1
64	TCCaA	CAGCTTGCACTGGTTTCCGCC	21375	SauCas9KKH	6	1

65	GG	AGGAAAGCAGGCCAGCCACA	21376	SpyCas9-NG	6	0
66	GG	AGGAAAGCAGGCCAGCCACA	21377	SpyCas9-xCas	6	0
67	GG	AGGAAAGCAGGCCAGCCACA	21378	SpyCas9-xCas-NG	6	0
68	GGT	AGGAAAGCAGGCCAGCCACA	21379	SpyCas9-SpG	6	0
69	GGT	AGGAAAGCAGGCCAGCCACA	21380	SpyCas9-SpRY	6	0
70	TCC	AGCTTGCACTGGTTTCCGCC	21381	SpyCas9-SpRY	6	0
71	TCCaAC	CAGCTTGCACTGGTTTCCGCC	21382	cCas9-v17	6	1
72	TCCaAC	CAGCTTGCACTGGTTTCCGCC	21383	cCas9-v42	6	1
73	GGTt	AGGAAAGCAGGCCAGCCACA	21384	SpyCas9-3var-NRTH	6	1
74	AGG	GAGGAAAGCAGGCCAGCCAC	21385	ScaCas9	7	0
75	AGG	GAGGAAAGCAGGCCAGCCAC	21386	ScaCas9-HiFi-Sc++	7	0
76	AGG	GAGGAAAGCAGGCCAGCCAC	21387	ScaCas9-Sc++	7	0
77	AGG	GAGGAAAGCAGGCCAGCCAC	21388	SpyCas9	7	0
78	AGG	GAGGAAAGCAGGCCAGCCAC	21389	SpyCas9-HF1	7	0
79	AGG	GAGGAAAGCAGGCCAGCCAC	21390	SpyCas9-SpG	7	0
80	AGG	GAGGAAAGCAGGCCAGCCAC	21391	SpyCas9-SpRY	7	0
81	AG	GAGGAAAGCAGGCCAGCCAC	21392	SpyCas9-NG	7	0
82	AG	GAGGAAAGCAGGCCAGCCAC	21393	SpyCas9-xCas	7	0
83	AG	GAGGAAAGCAGGCCAGCCAC	21394	SpyCas9-xCas-NG	7	0
84	CTC	CAGCTTGCACTGGTTTCCGC	21395	SpyCas9-SpRY	7	0
85	AGGT	GAGGAAAGCAGGCCAGCCAC	21396	SpyCas9-3var-NRRH	7	0
86	CAGG	GAGAGGAAAGCAGGCCAGCCA	21397	SauriCas9	8	0
87	CAGG	GAGAGGAAAGCAGGCCAGCCA	21398	SauriCas9-KKH	8	0
88	CAG	AGAGGAAAGCAGGCCAGCCA	21399	ScaCas9	8	0
89	CAG	AGAGGAAAGCAGGCCAGCCA	21400	ScaCas9-HiFi-Sc++	8	0
90	CAG	AGAGGAAAGCAGGCCAGCCA	21401	ScaCas9-Sc++	8	0
91	CAG	AGAGGAAAGCAGGCCAGCCA	21402	SpyCas9-SpRY	8	0

92	CCT	CCAGCTTGCACTGGTTTCCG	21403	SpyCas9-SpRY	8	0
93	CCTCC	atccCAGCTTGCACTGGTTTCCG	21404	BlatCas9	8	0
94	CAGGTt	GAGAGGAAAGCAGGCCAGCCA	21405	cCas9-v16	8	1
95	CAGGTt	GAGAGGAAAGCAGGCCAGCCA	21406	cCas9-v21	8	1
96	GCCTCC	tcATCCCAGCTTGCACTGGTTTCC	21407	Nme2Cas9	9	0
97	ACAGGTt	tccCGAGAGGAAAGCAGGCCAGCC	21408	PpnCas9	9	1
98	ACAGG	CGAGAGGAAAGCAGGCCAGCC	21409	SauCas9KKH	9	0
99	ACAGGT	CGAGAGGAAAGCAGGCCAGCC	21410	SauCas9KKH	9	0
100	ACAGGT	CGAGAGGAAAGCAGGCCAGCC	21411	cCas9-v17	9	0
101	ACAGGT	CGAGAGGAAAGCAGGCCAGCC	21412	cCas9-v42	9	0
102	ACAG	CGAGAGGAAAGCAGGCCAGCC	21413	SauriCas9-KKH	9	0
103	ACA	GAGAGGAAAGCAGGCCAGCC	21414	SpyCas9-SpRY	9	0
104	GCC	CCCAGCTTGCACTGGTTTCC	21415	SpyCas9-SpRY	9	0
105	GCCTCCaA	catcCCAGCTTGCACTGGTTTCC	21416	BlatCas9	9	1
106	GCCTCCaA	catcCCAGCTTGCACTGGTTTCC	21417	BlatCas9	9	1
107	GCCTC	catcCCAGCTTGCACTGGTTTCC	21418	BlatCas9	9	0
108	CACAG	CCGAGAGGAAAGCAGGCCAGC	21419	SauCas9KKH	10	0
109	CG	TCCCAGCTTGCACTGGTTTC	21420	SpyCas9-NG	10	0
110	CG	TCCCAGCTTGCACTGGTTTC	21421	SpyCas9-xCas	10	0
111	CG	TCCCAGCTTGCACTGGTTTC	21422	SpyCas9-xCas-NG	10	0
112	CAC	CGAGAGGAAAGCAGGCCAGC	21423	SpyCas9-SpRY	10	0
113	CGC	TCCCAGCTTGCACTGGTTTC	21424	SpyCas9-SpG	10	0
114	CGC	TCCCAGCTTGCACTGGTTTC	21425	SpyCas9-SpRY	10	0
115	CACAGG	CCGAGAGGAAAGCAGGCCAGC	21426	cCas9-v17	10	0
116	CACAGG	CCGAGAGGAAAGCAGGCCAGC	21427	cCas9-v42	10	0
117	CACA	CGAGAGGAAAGCAGGCCAGC	21428	SpyCas9-3var-NRCH	10	0
118	CGCC	TCCCAGCTTGCACTGGTTTC	21429	SpyCas9-3var-NRCH	10	0

119	CCG	ATCCCAGCTTGCACTGGTTT	21430	ScaCas9	11	0
120	CCG	ATCCCAGCTTGCACTGGTTT	21431	ScaCas9-HiFi-Sc++	11	0
121	CCG	ATCCCAGCTTGCACTGGTTT	21432	ScaCas9-Sc++	11	0
122	CCG	ATCCCAGCTTGCACTGGTTT	21433	SpyCas9-SpRY	11	0
123	CCA	CCGAGAGGAAAGCAGGCCAG	21434	SpyCas9-SpRY	11	0
124	CCGCC	ttcaTCCCAGCTTGCACTGGTTT	21435	BlatCas9	11	0
125	CCGCCTC	TCATCCCAGCTTGCACTGGTTT	21436	CdiCas9	11	0
126	TCCGCC	ttTTCATCCCAGCTTGCACTGGTT	21437	Nme2Cas9	12	0
127	GCC	CCCGAGAGGAAAGCAGGCCA	21438	SpyCas9-SpRY	12	0
128	TCC	CATCCCAGCTTGCACTGGTT	21439	SpyCas9-SpRY	12	0
129	GCCACAGG	aatcCCGAGAGGAAAGCAGGCCA	21440	BlatCas9	12	0
130	GCCAC	aatcCCGAGAGGAAAGCAGGCCA	21441	BlatCas9	12	0
131	TCCGC	tttcATCCCAGCTTGCACTGGTT	21442	BlatCas9	12	0
132	AG	TCCCGAGAGGAAAGCAGGCC	21443	SpyCas9-NG	13	0
133	AG	TCCCGAGAGGAAAGCAGGCC	21444	SpyCas9-xCas	13	0
134	AG	TCCCGAGAGGAAAGCAGGCC	21445	SpyCas9-xCas-NG	13	0
135	AGC	TCCCGAGAGGAAAGCAGGCC	21446	SpyCas9-SpG	13	0
136	AGC	TCCCGAGAGGAAAGCAGGCC	21447	SpyCas9-SpRY	13	0
137	TTC	TCATCCCAGCTTGCACTGGT	21448	SpyCas9-SpRY	13	0
138	AGCC	TCCCGAGAGGAAAGCAGGCC	21449	SpyCas9-3var-NRCH	13	0
139	CAG	ATCCCGAGAGGAAAGCAGGC	21450	ScaCas9	14	0
140	CAG	ATCCCGAGAGGAAAGCAGGC	21451	ScaCas9-HiFi-Sc++	14	0
141	CAG	ATCCCGAGAGGAAAGCAGGC	21452	ScaCas9-Sc++	14	0
142	CAG	ATCCCGAGAGGAAAGCAGGC	21453	SpyCas9-SpRY	14	0
143	TTT	TTCATCCCAGCTTGCACTGG	21454	SpyCas9-SpRY	14	0
144	CAGCC	gaaaTCCCGAGAGGAAAGCAGGC	21455	BlatCas9	14	0
145	TTTCC	ctttTCATCCCAGCTTGCACTGG	21456	BlatCas9	14	0

146	CAGCCAC	AAATCCCGAGAGGAAAGCAGGC	21457	CdiCas9	14	0
147	CAGC	ATCCCGAGAGGAAAGCAGGC	21458	SpyCas9-3var-NRRH	14	0
148	CCAGCC	aaGAAATCCCGAGAGGAAAGCAGG	21459	Nme2Cas9	15	0
149	GTTTCC	ttCTTTTCATCCCAGCTTGCACTG	21460	Nme2Cas9	15	0
150	CCAG	AAATCCCGAGAGGAAAGCAGG	21461	SauriCas9-KKH	15	0
151	CCA	AATCCCGAGAGGAAAGCAGG	21462	SpyCas9-SpRY	15	0
152	GTT	TTTCATCCCAGCTTGCACTG	21463	SpyCas9-SpRY	15	0
153	CCAGC	agaaATCCCGAGAGGAAAGCAGG	21464	BlatCas9	15	0
154	GTTTC	tcttTTCATCCCAGCTTGCACTG	21465	BlatCas9	15	0
155	GCCAG	GAAATCCCGAGAGGAAAGCAG	21466	SauCas9KKH	16	0
156	GG	TTTTCATCCCAGCTTGCACT	21467	SpyCas9-NG	16	0
157	GG	TTTTCATCCCAGCTTGCACT	21468	SpyCas9-xCas	16	0
158	GG	TTTTCATCCCAGCTTGCACT	21469	SpyCas9-xCas-NG	16	0
159	GGT	TTTTCATCCCAGCTTGCACT	21470	SpyCas9-SpG	16	0
160	GGT	TTTTCATCCCAGCTTGCACT	21471	SpyCas9-SpRY	16	0
161	GCC	AAATCCCGAGAGGAAAGCAG	21472	SpyCas9-SpRY	16	0
162	GCCAGC	GAAATCCCGAGAGGAAAGCAG	21473	cCas9-v17	16	0
163	GCCAGC	GAAATCCCGAGAGGAAAGCAG	21474	cCas9-v42	16	0
164	GGTT	TTTTCATCCCAGCTTGCACT	21475	SpyCas9-3var-NRTH	16	0
165	TGG	CTTTTCATCCCAGCTTGCAC	21476	ScaCas9	17	0
166	TGG	CTTTTCATCCCAGCTTGCAC	21477	ScaCas9-HiFi-Sc++	17	0
167	TGG	CTTTTCATCCCAGCTTGCAC	21478	ScaCas9-Sc++	17	0
168	TGG	CTTTTCATCCCAGCTTGCAC	21479	SpyCas9	17	0
169	TGG	CTTTTCATCCCAGCTTGCAC	21480	SpyCas9-HF1	17	0
170	TGG	CTTTTCATCCCAGCTTGCAC	21481	SpyCas9-SpG	17	0
171	TGG	CTTTTCATCCCAGCTTGCAC	21482	SpyCas9-SpRY	17	0
172	GG	GAAATCCCGAGAGGAAAGCA	21483	SpyCas9-NG	17	0

173	GG	GAAATCCCGAGAGGAAAGCA	2148 4	SpyCas9-xCas	17	0
174	GG	GAAATCCCGAGAGGAAAGCA	2148 5	SpyCas9-xCas-NG	17	0
175	TG	CTTTTCATCCCAGCTTGCAC	2148 6	SpyCas9-NG	17	0
176	TG	CTTTTCATCCCAGCTTGCAC	2148 7	SpyCas9-xCas	17	0
177	TG	CTTTTCATCCCAGCTTGCAC	2148 8	SpyCas9-xCas-NG	17	0
178	GGC	GAAATCCCGAGAGGAAAGCA	2148 9	SpyCas9-SpG	17	0
179	GGC	GAAATCCCGAGAGGAAAGCA	2149 0	SpyCas9-SpRY	17	0
180	TGGTTTC	TTCTTTTCATCCCAGCTTGCAC	2149 1	CdiCas9	17	0
181	TGGT	CTTTTCATCCCAGCTTGCAC	2149 2	SpyCas9-3var-NRRH	17	0
182	GGCC	GAAATCCCGAGAGGAAAGCA	2149 3	SpyCas9-3var-NRCH	17	0
183	CTGG	TTCTTTTCATCCCAGCTTGCA	2149 4	SauriCas9	18	0
184	CTGG	TTCTTTTCATCCCAGCTTGCA	2149 5	SauriCas9-KKH	18	0
185	AGG	AGAAATCCCGAGAGGAAAGC	2149 6	ScaCas9	18	0
186	AGG	AGAAATCCCGAGAGGAAAGC	2149 7	ScaCas9-HiFi-Sc++	18	0
187	AGG	AGAAATCCCGAGAGGAAAGC	2149 8	ScaCas9-Sc++	18	0
188	AGG	AGAAATCCCGAGAGGAAAGC	2149 9	SpyCas9	18	0
189	AGG	AGAAATCCCGAGAGGAAAGC	2150 0	SpyCas9-HF1	18	0
190	AGG	AGAAATCCCGAGAGGAAAGC	2150 1	SpyCas9-SpG	18	0
191	AGG	AGAAATCCCGAGAGGAAAGC	2150 2	SpyCas9-SpRY	18	0
192	CTG	TCTTTTCATCCCAGCTTGCA	2150 3	ScaCas9	18	0
193	CTG	TCTTTTCATCCCAGCTTGCA	2150 4	ScaCas9-HiFi-Sc++	18	0
194	CTG	TCTTTTCATCCCAGCTTGCA	2150 5	ScaCas9-Sc++	18	0
195	CTG	TCTTTTCATCCCAGCTTGCA	2150 6	SpyCas9-SpRY	18	0
196	AG	AGAAATCCCGAGAGGAAAGC	2150 7	SpyCas9-NG	18	0
197	AG	AGAAATCCCGAGAGGAAAGC	2150 8	SpyCas9-xCas	18	0
198	AG	AGAAATCCCGAGAGGAAAGC	2150 9	SpyCas9-xCas-NG	18	0
199	AGGCC	ccaaGAAATCCCGAGAGGAAAGC	2151 0	BlatCas9	18	0

200	CTGGTT	TTCTTTTCATCCCAGCTTGCA	21511	cCas9-v16	18	0
201	CTGGTT	TTCTTTTCATCCCAGCTTGCA	21512	cCas9-v21	18	0
202	AGGC	AGAAATCCCGAGAGGAAAGC	21513	SpyCas9-3var-NRRH	18	0
203	CAGGCC	acCCAAGAAATCCCGAGAGGAAAG	21514	Nme2Cas9	19	0
204	ACTGGTT	tttCTTCTTTTCATCCCAGCTTGC	21515	PpnCas9	19	0
205	ACTGG	CTTCTTTTCATCCCAGCTTGC	21516	SauCas9KKH	19	0
206	ACTGGT	CTTCTTTTCATCCCAGCTTGC	21517	SauCas9KKH	19	0
207	CAGG	CAAGAAATCCCGAGAGGAAAG	21518	SauriCas9	19	0
208	CAGG	CAAGAAATCCCGAGAGGAAAG	21519	SauriCas9-KKH	19	0
209	CAG	AAGAAATCCCGAGAGGAAAG	21520	ScaCas9	19	0
210	CAG	AAGAAATCCCGAGAGGAAAG	21521	ScaCas9-HiFi-Sc++	19	0
211	CAG	AAGAAATCCCGAGAGGAAAG	21522	ScaCas9-Sc++	19	0
212	CAG	AAGAAATCCCGAGAGGAAAG	21523	SpyCas9-SpRY	19	0
213	ACT	TTCTTTTCATCCCAGCTTGC	21524	SpyCas9-SpRY	19	0
214	CAGGCCAG	cccaAGAAATCCCGAGAGGAAAG	21525	BlatCas9	19	0
215	CAGGC	cccaAGAAATCCCGAGAGGAAAG	21526	BlatCas9	19	0
216	ACTGGTTT	tttcTTCTTTTCATCCCAGCTTGC	21527	NmeCas9	19	0
217	GCAGG	CCAAGAAATCCCGAGAGGAAA	21528	SauCas9KKH	20	0
218	GCAG	CCAAGAAATCCCGAGAGGAAA	21529	SauriCas9-KKH	20	0
219	CAC	CTTCTTTTCATCCCAGCTTG	21530	SpyCas9-SpRY	20	0
220	GCA	CAAGAAATCCCGAGAGGAAA	21531	SpyCas9-SpRY	20	0
221	GCAGGC	CCAAGAAATCCCGAGAGGAAA	21532	cCas9-v17	20	0
222	GCAGGC	CCAAGAAATCCCGAGAGGAAA	21533	cCas9-v42	20	0
223	CACT	CTTCTTTTCATCCCAGCTTG	21534	SpyCas9-3var-NRCH	20	0
224	AGCAG	CCCAAGAAATCCCGAGAGGAA	21535	SauCas9KKH	21	0
225	AG	CCAAGAAATCCCGAGAGGAA	21536	SpyCas9-NG	21	0
226	AG	CCAAGAAATCCCGAGAGGAA	21537	SpyCas9-xCas	21	0

227	AG	CCAAGAAATCCCGAGAGGAA	21538	SpyCas9-xCas-NG	21	0
228	AGC	CCAAGAAATCCCGAGAGGAA	21539	SpyCas9-SpG	21	0
229	AGC	CCAAGAAATCCCGAGAGGAA	21540	SpyCas9-SpRY	21	0
230	GCA	TCTTCTTTTCATCCCAGCTT	21541	SpyCas9-SpRY	21	0
231	AGCAGG	CCCAAGAAATCCCGAGAGGAA	21542	cCas9-v17	21	0
232	AGCAGG	CCCAAGAAATCCCGAGAGGAA	21543	cCas9-v42	21	0
233	AGCA	CCAAGAAATCCCGAGAGGAA	21544	SpyCas9-3var-NRCH	21	0
234	AAG	CCCAAGAAATCCCGAGAGGA	21545	ScaCas9	22	0
235	AAG	CCCAAGAAATCCCGAGAGGA	21546	ScaCas9-HiFi-Sc++	22	0
236	AAG	CCCAAGAAATCCCGAGAGGA	21547	ScaCas9-Sc++	22	0
237	AAG	CCCAAGAAATCCCGAGAGGA	21548	SpyCas9-SpRY	22	0
238	TG	TTCTTCTTTTCATCCCAGCT	21549	SpyCas9-NG	22	0
239	TG	TTCTTCTTTTCATCCCAGCT	21550	SpyCas9-xCas	22	0
240	TG	TTCTTCTTTTCATCCCAGCT	21551	SpyCas9-xCas-NG	22	0
241	TGC	TTCTTCTTTTCATCCCAGCT	21552	SpyCas9-SpG	22	0
242	TGC	TTCTTCTTTTCATCCCAGCT	21553	SpyCas9-SpRY	22	0
243	TGCACTGG	tcttTCTTCTTTTCATCCCAGCT	21554	BlatCas9	22	0
244	TGCAC	tcttTCTTCTTTTCATCCCAGCT	21555	BlatCas9	22	0
245	TGCACT	TTTCTTCTTTTCATCCCAGCT	21556	cCas9-v16	22	0
246	TGCACT	TTTCTTCTTTTCATCCCAGCT	21557	cCas9-v21	22	0
247	AAGC	CCCAAGAAATCCCGAGAGGA	21558	SpyCas9-3var-NRRH	22	0
248	TGCA	TTCTTCTTTTCATCCCAGCT	21559	SpyCas9-3var-NRCH	22	0
249	AAAG	CACCCAAGAAATCCCGAGAGG	21560	SauriCas9-KKH	23	0
250	AAAG	ACCCAAGAAATCCCGAGAGG	21561	SpyCas9-QQR1	23	0
251	AAAG	caCCCAAGAAATCCCGAGAGG	21562	iSpyMacCas9	23	0
252	TTG	TTTCTTCTTTTCATCCCAGC	21563	ScaCas9	23	0
253	TTG	TTTCTTCTTTTCATCCCAGC	21564	ScaCas9-HiFi-Sc++	23	0

254	TTG	TTTCTTCTTTTCATCCCAGC	21565	ScaCas9-Sc++	23	0
255	TTG	TTTCTTCTTTTCATCCCAGC	21566	SpyCas9-SpRY	23	0
256	AAA	ACCCAAGAAATCCCGAGAGG	21567	SpyCas9-SpRY	23	0
257	AAAGCAGG	gccaCCCAAGAAATCCCGAGAGG	21568	BlatCas9	23	0
258	AAAGC	gccaCCCAAGAAATCCCGAGAGG	21569	BlatCas9	23	0
259	TTGCACT	TCTTTCTTCTTTTCATCCCAGC	21570	CdiCas9	23	0
260	GAAAG	CCACCCAAGAAATCCCGAGAG	21571	SauCas9KKH	24	0
261	GAA	CACCCAAGAAATCCCGAGAG	21572	SpyCas9-SpRY	24	0
262	GAA	CACCCAAGAAATCCCGAGAG	21573	SpyCas9-xCas	24	0
263	CTT	CTTTCTTCTTTTCATCCCAG	21574	SpyCas9-SpRY	24	0
264	CTTGC	tttcTTTCTTCTTTTCATCCCAG	21575	BlatCas9	24	0
265	GAAAGC	CCACCCAAGAAATCCCGAGAG	21576	cCas9-v17	24	0
266	GAAAGC	CCACCCAAGAAATCCCGAGAG	21577	cCas9-v42	24	0
267	GAAA	CACCCAAGAAATCCCGAGAG	21578	SpyCas9-3var-NRRH	24	0
268	GAAA	ccACCCAAGAAATCCCGAGAG	21579	iSpyMacCas9	24	0
269	GGAAA	GCCACCCAAGAAATCCCGAGA	21580	SauCas9KKH	25	0
270	GG	CCACCCAAGAAATCCCGAGA	21581	SpyCas9-NG	25	0
271	GG	CCACCCAAGAAATCCCGAGA	21582	SpyCas9-xCas	25	0
272	GG	CCACCCAAGAAATCCCGAGA	21583	SpyCas9-xCas-NG	25	0
273	GGA	CCACCCAAGAAATCCCGAGA	21584	SpyCas9-SpG	25	0
274	GGA	CCACCCAAGAAATCCCGAGA	21585	SpyCas9-SpRY	25	0
275	GCT	TCTTTCTTCTTTTCATCCCA	21586	SpyCas9-SpRY	25	0
276	GGAAAG	GCCACCCAAGAAATCCCGAGA	21587	cCas9-v17	25	0
277	GGAAAG	GCCACCCAAGAAATCCCGAGA	21588	cCas9-v42	25	0
278	GCTTGCAC	ttTTCTTTCTTCTTTTCATCCCA	21589	CjeCas9	25	0
279	GGAA	CCACCCAAGAAATCCCGAGA	21590	SpyCas9-3var-NRRH	25	0
280	GGAA	CCACCCAAGAAATCCCGAGA	21591	SpyCas9-VQR	25	0

281	AGGAA	caGGCCACCCAAGAAATCCCGAG	21592	SauCas9	26	0
282	AGGAA	GGCCACCCAAGAAATCCCGAG	21593	SauCas9KKH	26	0
283	AGG	GCCACCCAAGAAATCCCGAG	21594	ScaCas9	26	0
284	AGG	GCCACCCAAGAAATCCCGAG	21595	ScaCas9-HiFi-Sc++	26	0
285	AGG	GCCACCCAAGAAATCCCGAG	21596	ScaCas9-Sc++	26	0
286	AGG	GCCACCCAAGAAATCCCGAG	21597	SpyCas9	26	0
287	AGG	GCCACCCAAGAAATCCCGAG	21598	SpyCas9-HF1	26	0
288	AGG	GCCACCCAAGAAATCCCGAG	21599	SpyCas9-SpG	26	0
289	AGG	GCCACCCAAGAAATCCCGAG	21600	SpyCas9-SpRY	26	0
290	AG	GCCACCCAAGAAATCCCGAG	21601	SpyCas9-NG	26	0
291	AG	GCCACCCAAGAAATCCCGAG	21602	SpyCas9-xCas	26	0
292	AG	GCCACCCAAGAAATCCCGAG	21603	SpyCas9-xCas-NG	26	0
293	AG	TTCTTTCTTCTTTTCATCCC	21604	SpyCas9-NG	26	0
294	AG	TTCTTTCTTCTTTTCATCCC	21605	SpyCas9-xCas	26	0
295	AG	TTCTTTCTTCTTTTCATCCC	21606	SpyCas9-xCas-NG	26	0
296	AGC	TTCTTTCTTCTTTTCATCCC	21607	SpyCas9-SpG	26	0
297	AGC	TTCTTTCTTCTTTTCATCCC	21608	SpyCas9-SpRY	26	0
298	AGGAAA	GCCACCCAAGAAATCCCGAG	21609	St1Cas9-TH1477	26	0
299	AGGAAA	GGCCACCCAAGAAATCCCGAG	21610	cCas9-v17	26	0
300	AGGAAA	GGCCACCCAAGAAATCCCGAG	21611	cCas9-v42	26	0
301	AGGA	GCCACCCAAGAAATCCCGAG	21612	SpyCas9-3var-NRRH	26	0
302	AGCT	TTCTTTCTTCTTTTCATCCC	21613	SpyCas9-3var-NRCH	26	0
303	GAGGA	ccAGGCCACCCAAGAAATCCCGA	21614	SauCas9	27	0
304	GAGGA	AGGCCACCCAAGAAATCCCGA	21615	SauCas9KKH	27	0
305	GAGG	AGGCCACCCAAGAAATCCCGA	21616	SauriCas9	27	0
306	GAGG	AGGCCACCCAAGAAATCCCGA	21617	SauriCas9-KKH	27	0
307	GAG	GGCCACCCAAGAAATCCCGA	21618	ScaCas9	27	0

308	GAG	GGCCACCCAAGAAATCCCGA	21619	ScaCas9-HiFi-Sc++	27	0
309	GAG	GGCCACCCAAGAAATCCCGA	21620	ScaCas9-Sc++	27	0
310	GAG	GGCCACCCAAGAAATCCCGA	21621	SpyCas9-SpRY	27	0
311	CAG	TTTCTTTCTTCTTTTCATCC	21622	ScaCas9	27	0
312	CAG	TTTCTTTCTTCTTTTCATCC	21623	ScaCas9-HiFi-Sc++	27	0
313	CAG	TTTCTTTCTTCTTTTCATCC	21624	ScaCas9-Sc++	27	0
314	CAG	TTTCTTTCTTCTTTTCATCC	21625	SpyCas9-SpRY	27	0
315	GAGGAAA	GGCCACCCAAGAAATCCCGA	21626	St1Cas9	27	0
316	GAGGAA	AGGCCACCCAAGAAATCCCGA	21627	cCas9-v17	27	0
317	GAGGAA	AGGCCACCCAAGAAATCCCGA	21628	cCas9-v42	27	0
318	CAGC	TTTCTTTCTTCTTTTCATCC	21629	SpyCas9-3var-NRRH	27	0
319	AGAGG	CAGGCCACCCAAGAAATCCCG	21630	SauCas9KKH	28	0
320	AGAG	CAGGCCACCCAAGAAATCCCG	21631	SauriCas9-KKH	28	0
321	AGAG	AGGCCACCCAAGAAATCCCG	21632	SpyCas9-VQR	28	0
322	CCAG	GTTTTCTTTCTTCTTTTCATC	21633	SauriCas9-KKH	28	0
323	AG	AGGCCACCCAAGAAATCCCG	21634	SpyCas9-NG	28	0
324	AG	AGGCCACCCAAGAAATCCCG	21635	SpyCas9-xCas	28	0
325	AG	AGGCCACCCAAGAAATCCCG	21636	SpyCas9-xCas-NG	28	0
326	AGA	AGGCCACCCAAGAAATCCCG	21637	SpyCas9-SpG	28	0
327	AGA	AGGCCACCCAAGAAATCCCG	21638	SpyCas9-SpRY	28	0
328	CCA	TTTTCTTTCTTCTTTTCATC	21639	SpyCas9-SpRY	28	0
329	AGAGGAA	AGGCCACCCAAGAAATCCCG	21640	St1Cas9	28	0
330	CCAGCTTG	gagtTTTCTTTCTTCTTTTCATC	21641	BlatCas9	28	0
331	CCAGC	gagtTTTCTTTCTTCTTTTCATC	21642	BlatCas9	28	0
332	CCAGCT	GTTTTCTTTCTTCTTTTCATC	21643	cCas9-v16	28	0
333	CCAGCT	GTTTTCTTTCTTCTTTTCATC	21644	cCas9-v21	28	0
334	AGAGGA	CAGGCCACCCAAGAAATCCCG	21645	cCas9-v17	28	0

335	AGAGGA	CAGGCCACCCAAGAAATCCCG	21646	cCas9-v42	28	0
336	GAGAG	ggCCAGGCCACCCAAGAAATCCC	21647	SauCas9	29	0
337	GAGAG	CCAGGCCACCCAAGAAATCCC	21648	SauCas9KKH	29	0
338	CCCAG	AGTTTTCTTTCTTCTTTTCAT	21649	SauCas9KKH	29	0
339	GAG	CAGGCCACCCAAGAAATCCC	21650	ScaCas9	29	0
340	GAG	CAGGCCACCCAAGAAATCCC	21651	ScaCas9-HiFi-Sc++	29	0
341	GAG	CAGGCCACCCAAGAAATCCC	21652	ScaCas9-Sc++	29	0
342	GAG	CAGGCCACCCAAGAAATCCC	21653	SpyCas9-SpRY	29	0
343	CCC	GTTTTCTTTCTTCTTTTCAT	21654	SpyCas9-SpRY	29	0
344	GAGAGG	CCAGGCCACCCAAGAAATCCC	21655	cCas9-v17	29	0
345	GAGAGG	CCAGGCCACCCAAGAAATCCC	21656	cCas9-v42	29	0
346	CCCAGC	AGTTTTCTTTCTTCTTTTCAT	21657	cCas9-v17	29	0
347	CCCAGC	AGTTTTCTTTCTTCTTTTCAT	21658	cCas9-v42	29	0
348	CCCAGCTT	ttgaGTTTTCTTTCTTCTTTTCAT	21659	NmeCas9	29	0
349	GAGA	CAGGCCACCCAAGAAATCCC	21660	SpyCas9-3var-NRRH	29	0
350	CGAGA	GCCAGGCCACCCAAGAAATCC	21661	SauCas9KKH	30	0
351	CGAG	GCCAGGCCACCCAAGAAATCC	21662	SauriCas9-KKH	30	0
352	CGAG	CCAGGCCACCCAAGAAATCC	21663	SpyCas9-VQR	30	0
353	CG	CCAGGCCACCCAAGAAATCC	21664	SpyCas9-NG	30	0
354	CG	CCAGGCCACCCAAGAAATCC	21665	SpyCas9-xCas	30	0
355	CG	CCAGGCCACCCAAGAAATCC	21666	SpyCas9-xCas-NG	30	0
356	CGA	CCAGGCCACCCAAGAAATCC	21667	SpyCas9-SpG	30	0
357	CGA	CCAGGCCACCCAAGAAATCC	21668	SpyCas9-SpRY	30	0
358	TCC	AGTTTTCTTTCTTCTTTTCA	21669	SpyCas9-SpRY	30	0
359	CGAGAG	GCCAGGCCACCCAAGAAATCC	21670	cCas9-v17	30	0
360	CGAGAG	GCCAGGCCACCCAAGAAATCC	21671	cCas9-v42	30	0
361	CCGAG	aaGGCCAGGCCACCCAAGAAATC	21672	SauCas9	31	0

362	CCGAG	GGCCAGGCCACCCAAGAAATC	21673	SauCas9KKH	31	0
363	CCG	GCCAGGCCACCCAAGAAATC	21674	ScaCas9	31	0
364	CCG	GCCAGGCCACCCAAGAAATC	21675	ScaCas9-HiFi-Sc++	31	0
365	CCG	GCCAGGCCACCCAAGAAATC	21676	ScaCas9-Sc++	31	0
366	CCG	GCCAGGCCACCCAAGAAATC	21677	SpyCas9-SpRY	31	0
367	ATC	GAGTTTTCTTTCTTCTTTTC	21678	SpyCas9-SpRY	31	0
368	ATCCC	tttgAGTTTTCTTTCTTCTTTTC	21679	BlatCas9	31	0
369	CCGAGA	GGCCAGGCCACCCAAGAAATC	21680	cCas9-v17	31	0
370	CCGAGA	GGCCAGGCCACCCAAGAAATC	21681	cCas9-v42	31	0
371	CATCCC	gcTTTGAGTTTTCTTTCTTCTTTT	21682	Nme2Cas9	32	0
372	CCCGA	AGGCCAGGCCACCCAAGAAAT	21683	SauCas9KKH	32	0
373	CAT	TGAGTTTTCTTTCTTCTTTT	21684	SpyCas9-SpRY	32	0
374	CCC	GGCCAGGCCACCCAAGAAAT	21685	SpyCas9-SpRY	32	0
375	CATCCCAG	ctttGAGTTTTCTTTCTTCTTTT	21686	BlatCas9	32	0
376	CATCC	ctttGAGTTTTCTTTCTTCTTTT	21687	BlatCas9	32	0
377	CCCGAG	AGGCCAGGCCACCCAAGAAAT	21688	cCas9-v17	32	0
378	CCCGAG	AGGCCAGGCCACCCAAGAAAT	21689	cCas9-v42	32	0
379	CATC	TGAGTTTTCTTTCTTCTTTT	21690	SpyCas9-3var-NRTH	32	0
380	TCATCC	agCTTTGAGTTTTCTTTCTTCTTT	21691	Nme2Cas9	33	0
381	TCC	AGGCCAGGCCACCCAAGAAA	21692	SpyCas9-SpRY	33	0
382	TCA	TTGAGTTTTCTTTCTTCTTT	21693	SpyCas9-SpRY	33	0
383	TCATC	gcttTGAGTTTTCTTTCTTCTTT	21694	BlatCas9	33	0
384	TCATCCC	CTTTGAGTTTTCTTTCTTCTTT	21695	CdiCas9	33	0
385	ATC	AAGGCCAGGCCACCCAAGAA	21696	SpyCas9-SpRY	34	0
386	TTC	TTTGAGTTTTCTTTCTTCTT	21697	SpyCas9-SpRY	34	0
387	ATCCCGAG	cggaAGGCCAGGCCACCCAAGAA	21698	BlatCas9	34	0
388	ATCCC	cggaAGGCCAGGCCACCCAAGAA	21699	BlatCas9	34	0

389	AATCCC	ctCGGAAGGCCAGGCCACCCAAGA	21700	Nme2Cas9	35	0
390	AAT	GAAGGCCAGGCCACCCAAGA	21701	SpyCas9-SpRY	35	0
391	TTT	CTTTGAGTTTTCTTTCTTCT	21702	SpyCas9-SpRY	35	0
392	AATCCCGA	tcggAAGGCCAGGCCACCCAAGA	21703	BlatCas9	35	0
393	AATCC	tcggAAGGCCAGGCCACCCAAGA	21704	BlatCas9	35	0
394	AATC	GAAGGCCAGGCCACCCAAGA	21705	SpyCas9-3var-NRTH	35	0
395	AAATCC	acTCGGAAGGCCAGGCCACCCAAG	21706	Nme2Cas9	36	0
396	AAA	GGAAGGCCAGGCCACCCAAG	21707	SpyCas9-SpRY	36	0
397	TTT	GCTTTGAGTTTTCTTTCTTC	21708	SpyCas9-SpRY	36	0
398	AAATC	ctcgGAAGGCCAGGCCACCCAAG	21709	BlatCas9	36	0
399	TTTTC	tgagCTTTGAGTTTTCTTTCTTC	21710	BlatCas9	36	0
400	AAATCCC	TCGGAAGGCCAGGCCACCCAAG	21711	CdiCas9	36	0
401	AAAT	GGAAGGCCAGGCCACCCAAG	21712	SpyCas9-3var-NRRH	36	0
402	AAAT	cgGAAGGCCAGGCCACCCAAG	21713	iSpyMacCas9	36	0
403	GAA	CGGAAGGCCAGGCCACCCAA	21714	SpyCas9-SpRY	37	0
404	GAA	CGGAAGGCCAGGCCACCCAA	21715	SpyCas9-xCas	37	0
405	CTT	AGCTTTGAGTTTTCTTTCTT	21716	SpyCas9-SpRY	37	0
406	GAAATCC	CTCGGAAGGCCAGGCCACCCAA	21717	CdiCas9	37	0
407	GAAA	CGGAAGGCCAGGCCACCCAA	21718	SpyCas9-3var-NRRH	37	0
408	GAAA	tcGGAAGGCCAGGCCACCCAA	21719	iSpyMacCas9	37	0
409	AGAAA	CTCGGAAGGCCAGGCCACCCA	21720	SauCas9KKH	38	0
410	AGAAAT	CTCGGAAGGCCAGGCCACCCA	21721	SauCas9KKH	38	0
411	AGAAAT	CTCGGAAGGCCAGGCCACCCA	21722	cCas9-v17	38	0
412	AGAAAT	CTCGGAAGGCCAGGCCACCCA	21723	cCas9-v42	38	0
413	AG	TCGGAAGGCCAGGCCACCCA	21724	SpyCas9-NG	38	0
414	AG	TCGGAAGGCCAGGCCACCCA	21725	SpyCas9-xCas	38	0
415	AG	TCGGAAGGCCAGGCCACCCA	21726	SpyCas9-xCas-NG	38	0

416	AGA	TCGGAAGGCCAGGCCACCCA	21727	SpyCas9-SpG	38	0
417	AGA	TCGGAAGGCCAGGCCACCCA	21728	SpyCas9-SpRY	38	0
418	TCT	GAGCTTTGAGTTTTCTTTCT	21729	SpyCas9-SpRY	38	0
419	AGAAATC	ACTCGGAAGGCCAGGCCACCCA	21730	CdiCas9	38	0
420	AGAA	TCGGAAGGCCAGGCCACCCA	21731	SpyCas9-3var-NRRH	38	0
421	AGAA	TCGGAAGGCCAGGCCACCCA	21732	SpyCas9-VQR	38	0
422	AAGAA	agACTCGGAAGGCCAGGCCACCC	21733	SauCas9	39	0
423	AAGAA	ACTCGGAAGGCCAGGCCACCC	21734	SauCas9KKH	39	0
424	AAG	CTCGGAAGGCCAGGCCACCC	21735	ScaCas9	39	0
425	AAG	CTCGGAAGGCCAGGCCACCC	21736	ScaCas9-HiFi-Sc++	39	0
426	AAG	CTCGGAAGGCCAGGCCACCC	21737	ScaCas9-Sc++	39	0
427	AAG	CTCGGAAGGCCAGGCCACCC	21738	SpyCas9-SpRY	39	0
428	TTC	TGAGCTTTGAGTTTTCTTTC	21739	SpyCas9-SpRY	39	0
429	AAGAAA	CTCGGAAGGCCAGGCCACCC	21740	St1Cas9-TH1477	39	0
430	AAGAAA	ACTCGGAAGGCCAGGCCACCC	21741	cCas9-v17	39	0
431	AAGAAA	ACTCGGAAGGCCAGGCCACCC	21742	cCas9-v42	39	0
432	AAGAAAT	GACTCGGAAGGCCAGGCCACCC	21743	CdiCas9	39	0
433	AAGAAAT	GACTCGGAAGGCCAGGCCACCC	21744	CdiCas9	39	0
434	AAGA	CTCGGAAGGCCAGGCCACCC	21745	SpyCas9-3var-NRRH	39	0
435	CAAGA	GACTCGGAAGGCCAGGCCACC	21746	SauCas9KKH	40	0
436	CAAG	GACTCGGAAGGCCAGGCCACC	21747	SauriCas9-KKH	40	0
437	CAAG	ACTCGGAAGGCCAGGCCACC	21748	SpyCas9-QQR1	40	0
438	CAAG	gaCTCGGAAGGCCAGGCCACC	21749	iSpyMacCas9	40	0
439	CAA	ACTCGGAAGGCCAGGCCACC	21750	SpyCas9-SpRY	40	0
440	CTT	ATGAGCTTTGAGTTTTCTTT	21751	SpyCas9-SpRY	40	0
441	CAAGAAA	ACTCGGAAGGCCAGGCCACC	21752	St1Cas9	40	0
442	CAAGAA	GACTCGGAAGGCCAGGCCACC	21753	cCas9-v17	40	0

443	CAAGAA	GACTCGGAAGGCCAGGCCACC	21754	cCas9-v42	40	0
444	CCAAG	AGACTCGGAAGGCCAGGCCAC	21755	SauCas9KKH	41	0
445	CCA	GACTCGGAAGGCCAGGCCAC	21756	SpyCas9-SpRY	41	0
446	TCT	GATGAGCTTTGAGTTTTCTT	21757	SpyCas9-SpRY	41	0
447	TCTTCTTT	ggtgATGAGCTTTGAGTTTTCTT	21758	BlatCas9	41	0
448	TCTTC	ggtgATGAGCTTTGAGTTTTCTT	21759	BlatCas9	41	0
449	CCAAGA	AGACTCGGAAGGCCAGGCCAC	21760	cCas9-v17	41	0
450	CCAAGA	AGACTCGGAAGGCCAGGCCAC	21761	cCas9-v42	41	0
451	CCCAA	AAGACTCGGAAGGCCAGGCCA	21762	SauCas9KKH	42	0
452	CCC	AGACTCGGAAGGCCAGGCCA	21763	SpyCas9-SpRY	42	0
453	TTC	TGATGAGCTTTGAGTTTTCT	21764	SpyCas9-SpRY	42	0
454	CCCAAG	AAGACTCGGAAGGCCAGGCCA	21765	cCas9-v17	42	0
455	CCCAAG	AAGACTCGGAAGGCCAGGCCA	21766	cCas9-v42	42	0
456	ACC	AAGACTCGGAAGGCCAGGCC	21767	SpyCas9-SpRY	43	0
457	TTT	GTGATGAGCTTTGAGTTTTC	21768	SpyCas9-SpRY	43	0
458	CAC	GAAGACTCGGAAGGCCAGGC	21769	SpyCas9-SpRY	44	0
459	CTT	GGTGATGAGCTTTGAGTTTT	21770	SpyCas9-SpRY	44	0
460	CACCCAAG	gtggAAGACTCGGAAGGCCAGGC	21771	BlatCas9	44	0
461	CACCC	gtggAAGACTCGGAAGGCCAGGC	21772	BlatCas9	44	0
462	CTTTC	agtgGTGATGAGCTTTGAGTTTT	21773	BlatCas9	44	0
463	CACC	GAAGACTCGGAAGGCCAGGC	21774	SpyCas9-3var-NRCH	44	0
464	CCACCC	caGTGGAAGACTCGGAAGGCCAGG	21775	Nme2Cas9	45	0
465	CCA	GGAAGACTCGGAAGGCCAGG	21776	SpyCas9-SpRY	45	0
466	TCT	TGGTGATGAGCTTTGAGTTT	21777	SpyCas9-SpRY	45	0
467	CCACCCAA	agtgGAAGACTCGGAAGGCCAGG	21778	BlatCas9	45	0
468	CCACCCAA	agtgGAAGACTCGGAAGGCCAGG	21779	BlatCas9	45	0
469	CCACC	agtgGAAGACTCGGAAGGCCAGG	21780	BlatCas9	45	0

470	GCCACC	gcAGTGGAAGACTCGGAAGGCCAG	21781	Nme2Cas9	46	0
471	GCC	TGGAAGACTCGGAAGGCCAG	21782	SpyCas9-SpRY	46	0
472	TTC	GTGGTGATGAGCTTTGAGTT	21783	SpyCas9-SpRY	46	0
473	GCCAC	cagtGGAAGACTCGGAAGGCCAG	21784	BlatCas9	46	0
474	GG	GTGGAAGACTCGGAAGGCCA	21785	SpyCas9-NG	47	0
475	GG	GTGGAAGACTCGGAAGGCCA	21786	SpyCas9-xCas	47	0
476	GG	GTGGAAGACTCGGAAGGCCA	21787	SpyCas9-xCas-NG	47	0
477	GGC	GTGGAAGACTCGGAAGGCCA	21788	SpyCas9-SpG	47	0
478	GGC	GTGGAAGACTCGGAAGGCCA	21789	SpyCas9-SpRY	47	0
479	TTT	AGTGGTGATGAGCTTTGAGT	21790	SpyCas9-SpRY	47	0
480	GGCC	GTGGAAGACTCGGAAGGCCA	21791	SpyCas9-3var-NRCH	47	0
481	AGG	AGTGGAAGACTCGGAAGGCC	21792	ScaCas9	48	0
482	AGG	AGTGGAAGACTCGGAAGGCC	21793	ScaCas9-HiFi-Sc++	48	0
483	AGG	AGTGGAAGACTCGGAAGGCC	21794	ScaCas9-Sc++	48	0
484	AGG	AGTGGAAGACTCGGAAGGCC	21795	SpyCas9	48	0
485	AGG	AGTGGAAGACTCGGAAGGCC	21796	SpyCas9-HF1	48	0
486	AGG	AGTGGAAGACTCGGAAGGCC	21797	SpyCas9-SpG	48	0
487	AGG	AGTGGAAGACTCGGAAGGCC	21798	SpyCas9-SpRY	48	0
488	AG	AGTGGAAGACTCGGAAGGCC	21799	SpyCas9-NG	48	0
489	AG	AGTGGAAGACTCGGAAGGCC	21800	SpyCas9-xCas	48	0
490	AG	AGTGGAAGACTCGGAAGGCC	21801	SpyCas9-xCas-NG	48	0
491	TTT	CAGTGGTGATGAGCTTTGAG	21802	SpyCas9-SpRY	48	0
492	TTTTCTTT	actcAGTGGTGATGAGCTTTGAG	21803	BlatCas9	48	0
493	AGGCC	tgcaGTGGAAGACTCGGAAGGCC	21804	BlatCas9	48	0
494	TTTTC	actcAGTGGTGATGAGCTTTGAG	21805	BlatCas9	48	0
495	AGGCCAC	GCAGTGGAAGACTCGGAAGGCC	21806	CdiCas9	48	0
496	AGGC	AGTGGAAGACTCGGAAGGCC	21807	SpyCas9-3var-NRRH	48	0

497	CAGGCC	tgTGCAGTGGAAGACTCGGAAGGC	21808	Nme2Cas9	49	0
498	CAGG	GCAGTGGAAGACTCGGAAGGC	21809	SauriCas9	49	0
499	CAGG	GCAGTGGAAGACTCGGAAGGC	21810	SauriCas9-KKH	49	0
500	CAG	CAGTGGAAGACTCGGAAGGC	21811	ScaCas9	49	0
501	CAG	CAGTGGAAGACTCGGAAGGC	21812	ScaCas9-HiFi-Sc++	49	0
502	CAG	CAGTGGAAGACTCGGAAGGC	21813	ScaCas9-Sc++	49	0
503	CAG	CAGTGGAAGACTCGGAAGGC	21814	SpyCas9-SpRY	49	0
504	GTT	TCAGTGGTGATGAGCTTTGA	21815	SpyCas9-SpRY	49	0
505	CAGGC	gtgcAGTGGAAGACTCGGAAGGC	21816	BlatCas9	49	0
506	CCAGG	TGCAGTGGAAGACTCGGAAGG	21817	SauCas9KKH	50	0
507	CCAG	TGCAGTGGAAGACTCGGAAGG	21818	SauriCas9-KKH	50	0
508	AG	CTCAGTGGTGATGAGCTTTG	21819	SpyCas9-NG	50	0
509	AG	CTCAGTGGTGATGAGCTTTG	21820	SpyCas9-xCas	50	0
510	AG	CTCAGTGGTGATGAGCTTTG	21821	SpyCas9-xCas-NG	50	0
511	AGT	CTCAGTGGTGATGAGCTTTG	21822	SpyCas9-SpG	50	0
512	AGT	CTCAGTGGTGATGAGCTTTG	21823	SpyCas9-SpRY	50	0
513	CCA	GCAGTGGAAGACTCGGAAGG	21824	SpyCas9-SpRY	50	0
514	CCAGGC	TGCAGTGGAAGACTCGGAAGG	21825	cCas9-v17	50	0
515	CCAGGC	TGCAGTGGAAGACTCGGAAGG	21826	cCas9-v42	50	0
516	AGTT	CTCAGTGGTGATGAGCTTTG	21827	SpyCas9-3var-NRTH	50	0
517	GCCAG	GTGCAGTGGAAGACTCGGAAG	21828	SauCas9KKH	51	0
518	GAG	ACTCAGTGGTGATGAGCTTT	21829	ScaCas9	51	0
519	GAG	ACTCAGTGGTGATGAGCTTT	21830	ScaCas9-HiFi-Sc++	51	0
520	GAG	ACTCAGTGGTGATGAGCTTT	21831	ScaCas9-Sc++	51	0
521	GAG	ACTCAGTGGTGATGAGCTTT	21832	SpyCas9-SpRY	51	0
522	GCC	TGCAGTGGAAGACTCGGAAG	21833	SpyCas9-SpRY	51	0
523	GCCAGG	GTGCAGTGGAAGACTCGGAAG	21834	cCas9-v17	51	0

524	GCCAGG	GTGCAGTGGAAGACTCGGAAG	21835	cCas9-v42	51	0
525	GAGTTTT	TGACTCAGTGGTGATGAGCTTT	21836	CdiCas9	51	0
526	GAGT	ACTCAGTGGTGATGAGCTTT	21837	SpyCas9-3var-NRRH	51	0
527	TGAG	TGACTCAGTGGTGATGAGCTT	21838	SauriCas9-KKH	52	0
528	TGAG	GACTCAGTGGTGATGAGCTT	21839	SpyCas9-VQR	52	0
529	GG	GTGCAGTGGAAGACTCGGAA	21840	SpyCas9-NG	52	0
530	GG	GTGCAGTGGAAGACTCGGAA	21841	SpyCas9-xCas	52	0
531	GG	GTGCAGTGGAAGACTCGGAA	21842	SpyCas9-xCas-NG	52	0
532	TG	GACTCAGTGGTGATGAGCTT	21843	SpyCas9-NG	52	0
533	TG	GACTCAGTGGTGATGAGCTT	21844	SpyCas9-xCas	52	0
534	TG	GACTCAGTGGTGATGAGCTT	21845	SpyCas9-xCas-NG	52	0
535	GGC	GTGCAGTGGAAGACTCGGAA	21846	SpyCas9-SpG	52	0
536	GGC	GTGCAGTGGAAGACTCGGAA	21847	SpyCas9-SpRY	52	0
537	TGA	GACTCAGTGGTGATGAGCTT	21848	SpyCas9-SpG	52	0
538	TGA	GACTCAGTGGTGATGAGCTT	21849	SpyCas9-SpRY	52	0
539	TGAGTT	TGACTCAGTGGTGATGAGCTT	21850	cCas9-v16	52	0
540	TGAGTT	TGACTCAGTGGTGATGAGCTT	21851	cCas9-v21	52	0
541	GGCC	GTGCAGTGGAAGACTCGGAA	21852	SpyCas9-3var-NRCH	52	0
542	TTGAGTT	cctCTGACTCAGTGGTGATGAGCT	21853	PpnCas9	53	0
543	TTGAG	ctCTGACTCAGTGGTGATGAGCT	21854	SauCas9	53	0
544	TTGAG	CTGACTCAGTGGTGATGAGCT	21855	SauCas9KKH	53	0
545	TTGAGT	ctCTGACTCAGTGGTGATGAGCT	21856	SauCas9	53	0
546	TTGAGT	CTGACTCAGTGGTGATGAGCT	21857	SauCas9KKH	53	0
547	TTGAGT	CTGACTCAGTGGTGATGAGCT	21858	cCas9-v17	53	0
548	TTGAGT	CTGACTCAGTGGTGATGAGCT	21859	cCas9-v42	53	0
549	AGG	TGTGCAGTGGAAGACTCGGA	21860	ScaCas9	53	0
550	AGG	TGTGCAGTGGAAGACTCGGA	21861	ScaCas9-HiFi-Sc++	53	0

551	AGG	TGTGCAGTGGAAGACTCGGA	21862	ScaCas9-Sc++	53	0
552	AGG	TGTGCAGTGGAAGACTCGGA	21863	SpyCas9	53	0
553	AGG	TGTGCAGTGGAAGACTCGGA	21864	SpyCas9-HF1	53	0
554	AGG	TGTGCAGTGGAAGACTCGGA	21865	SpyCas9-SpG	53	0
555	AGG	TGTGCAGTGGAAGACTCGGA	21866	SpyCas9-SpRY	53	0
556	TTG	TGACTCAGTGGTGATGAGCT	21867	ScaCas9	53	0
557	TTG	TGACTCAGTGGTGATGAGCT	21868	ScaCas9-HiFi-Sc++	53	0
558	TTG	TGACTCAGTGGTGATGAGCT	21869	ScaCas9-Sc++	53	0
559	TTG	TGACTCAGTGGTGATGAGCT	21870	SpyCas9-SpRY	53	0
560	AG	TGTGCAGTGGAAGACTCGGA	21871	SpyCas9-NG	53	0
561	AG	TGTGCAGTGGAAGACTCGGA	21872	SpyCas9-xCas	53	0
562	AG	TGTGCAGTGGAAGACTCGGA	21873	SpyCas9-xCas-NG	53	0
563	AGGCCAGG	ctgtGTGCAGTGGAAGACTCGGA	21874	BlatCas9	53	0
564	AGGCC	ctgtGTGCAGTGGAAGACTCGGA	21875	BlatCas9	53	0
565	TTGAGTTT	cctcTGACTCAGTGGTGATGAGCT	21876	NmeCas9	53	0
566	AGGC	TGTGCAGTGGAAGACTCGGA	21877	SpyCas9-3var-NRRH	53	0
567	AAGGCC	taCTGTGTGCAGTGGAAGACTCGG	21878	Nme2Cas9	54	0
568	TTTGA	TCTGACTCAGTGGTGATGAGC	21879	SauCas9KKH	54	0
569	AAGG	TGTGTGCAGTGGAAGACTCGG	21880	SauriCas9	54	0
570	AAGG	TGTGTGCAGTGGAAGACTCGG	21881	SauriCas9-KKH	54	0
571	AAG	GTGTGCAGTGGAAGACTCGG	21882	ScaCas9	54	0
572	AAG	GTGTGCAGTGGAAGACTCGG	21883	ScaCas9-HiFi-Sc++	54	0
573	AAG	GTGTGCAGTGGAAGACTCGG	21884	ScaCas9-Sc++	54	0
574	AAG	GTGTGCAGTGGAAGACTCGG	21885	SpyCas9-SpRY	54	0
575	TTT	CTGACTCAGTGGTGATGAGC	21886	SpyCas9-SpRY	54	0
576	AAGGCCAG	actgTGTGCAGTGGAAGACTCGG	21887	BlatCas9	54	0
577	AAGGC	actgTGTGCAGTGGAAGACTCGG	21888	BlatCas9	54	0

578	GAAGG	CTGTGTGCAGTGGAAGACTCG	21889	SauCas9KKH	55	0
579	GAAG	CTGTGTGCAGTGGAAGACTCG	21890	SauriCas9-KKH	55	0
580	GAAG	TGTGTGCAGTGGAAGACTCG	21891	SpyCas9-QQR1	55	0
581	GAAG	ctGTGTGCAGTGGAAGACTCG	21892	iSpyMacCas9	55	0
582	GAA	TGTGTGCAGTGGAAGACTCG	21893	SpyCas9-SpRY	55	0
583	GAA	TGTGTGCAGTGGAAGACTCG	21894	SpyCas9-xCas	55	0
584	CTT	TCTGACTCAGTGGTGATGAG	21895	SpyCas9-SpRY	55	0
585	GAAGGC	CTGTGTGCAGTGGAAGACTCG	21896	cCas9-v17	55	0
586	GAAGGC	CTGTGTGCAGTGGAAGACTCG	21897	cCas9-v42	55	0
587	GGAAG	ACTGTGTGCAGTGGAAGACTC	21898	SauCas9KKH	56	0
588	GG	CTGTGTGCAGTGGAAGACTC	21899	SpyCas9-NG	56	0
589	GG	CTGTGTGCAGTGGAAGACTC	21900	SpyCas9-xCas	56	0
590	GG	CTGTGTGCAGTGGAAGACTC	21901	SpyCas9-xCas-NG	56	0
591	GGA	CTGTGTGCAGTGGAAGACTC	21902	SpyCas9-SpG	56	0
592	GGA	CTGTGTGCAGTGGAAGACTC	21903	SpyCas9-SpRY	56	0
593	GCT	CTCTGACTCAGTGGTGATGA	21904	SpyCas9-SpRY	56	0
594	GGAAGG	ACTGTGTGCAGTGGAAGACTC	21905	cCas9-v17	56	0
595	GGAAGG	ACTGTGTGCAGTGGAAGACTC	21906	cCas9-v42	56	0
596	GGAA	CTGTGTGCAGTGGAAGACTC	21907	SpyCas9-3var-NRRH	56	0
597	GGAA	CTGTGTGCAGTGGAAGACTC	21908	SpyCas9-VQR	56	0
598	CGGAA	tgTACTGTGTGCAGTGGAAGACT	21909	SauCas9	57	0
599	CGGAA	TACTGTGTGCAGTGGAAGACT	21910	SauCas9KKH	57	0
600	CGG	ACTGTGTGCAGTGGAAGACT	21911	ScaCas9	57	0
601	CGG	ACTGTGTGCAGTGGAAGACT	21912	ScaCas9-HiFi-Sc++	57	0
602	CGG	ACTGTGTGCAGTGGAAGACT	21913	ScaCas9-Sc++	57	0
603	CGG	ACTGTGTGCAGTGGAAGACT	21914	SpyCas9	57	0
604	CGG	ACTGTGTGCAGTGGAAGACT	21915	SpyCas9-HF1	57	0

605	CGG	ACTGTGTGCAGTGGAAGACT	21916	SpyCas9-SpG	57	0
606	CGG	ACTGTGTGCAGTGGAAGACT	21917	SpyCas9-SpRY	57	0
607	CG	ACTGTGTGCAGTGGAAGACT	21918	SpyCas9-NG	57	0
608	CG	ACTGTGTGCAGTGGAAGACT	21919	SpyCas9-xCas	57	0
609	CG	ACTGTGTGCAGTGGAAGACT	21920	SpyCas9-xCas-NG	57	0
610	AG	CCTCTGACTCAGTGGTGATG	21921	SpyCas9-NG	57	0
611	AG	CCTCTGACTCAGTGGTGATG	21922	SpyCas9-xCas	57	0
612	AG	CCTCTGACTCAGTGGTGATG	21923	SpyCas9-xCas-NG	57	0
613	AGC	CCTCTGACTCAGTGGTGATG	21924	SpyCas9-SpG	57	0
614	AGC	CCTCTGACTCAGTGGTGATG	21925	SpyCas9-SpRY	57	0
615	CGGAAG	TACTGTGTGCAGTGGAAGACT	21926	cCas9-v17	57	0
616	CGGAAG	TACTGTGTGCAGTGGAAGACT	21927	cCas9-v42	57	0
617	CGGA	ACTGTGTGCAGTGGAAGACT	21928	SpyCas9-3var-NRRH	57	0
618	AGCT	CCTCTGACTCAGTGGTGATG	21929	SpyCas9-3var-NRCH	57	0
619	TCGGA	atGTACTGTGTGCAGTGGAAGAC	21930	SauCas9	58	0
620	TCGGA	GTACTGTGTGCAGTGGAAGAC	21931	SauCas9KKH	58	0
621	TCGG	GTACTGTGTGCAGTGGAAGAC	21932	SauriCas9	58	0
622	TCGG	GTACTGTGTGCAGTGGAAGAC	21933	SauriCas9-KKH	58	0
623	TCG	TACTGTGTGCAGTGGAAGAC	21934	ScaCas9	58	0
624	TCG	TACTGTGTGCAGTGGAAGAC	21935	ScaCas9-HiFi-Sc++	58	0
625	TCG	TACTGTGTGCAGTGGAAGAC	21936	ScaCas9-Sc++	58	0
626	TCG	TACTGTGTGCAGTGGAAGAC	21937	SpyCas9-SpRY	58	0
627	GAG	GCCTCTGACTCAGTGGTGAT	21938	ScaCas9	58	0
628	GAG	GCCTCTGACTCAGTGGTGAT	21939	ScaCas9-HiFi-Sc++	58	0
629	GAG	GCCTCTGACTCAGTGGTGAT	21940	ScaCas9-Sc++	58	0
630	GAG	GCCTCTGACTCAGTGGTGAT	21941	SpyCas9-SpRY	58	0
631	TCGGAA	GTACTGTGTGCAGTGGAAGAC	21942	cCas9-v17	58	0

632	TCGGAA	GTACTGTGTGCAGTGGAAGAC	21943	cCas9-v42	58	0
633	GAGCTTT	GTGCCTCTGACTCAGTGGTGAT	21944	CdiCas9	58	0
634	GAGC	GCCTCTGACTCAGTGGTGAT	21945	SpyCas9-3var-NRRH	58	0
635	CTCGG	TGTACTGTGTGCAGTGGAAGA	21946	SauCas9KKH	59	0
636	TGAG	GTGCCTCTGACTCAGTGGTGA	21947	SauriCas9-KKH	59	0
637	TGAG	TGCCTCTGACTCAGTGGTGA	21948	SpyCas9-VQR	59	0
638	TG	TGCCTCTGACTCAGTGGTGA	21949	SpyCas9-NG	59	0
639	TG	TGCCTCTGACTCAGTGGTGA	21950	SpyCas9-xCas	59	0
640	TG	TGCCTCTGACTCAGTGGTGA	21951	SpyCas9-xCas-NG	59	0
641	TGA	TGCCTCTGACTCAGTGGTGA	21952	SpyCas9-SpG	59	0
642	TGA	TGCCTCTGACTCAGTGGTGA	21953	SpyCas9-SpRY	59	0
643	CTC	GTACTGTGTGCAGTGGAAGA	21954	SpyCas9-SpRY	59	0
644	TGAGCTTT	tagtGCCTCTGACTCAGTGGTGA	21955	BlatCas9	59	0
645	TGAGC	tagtGCCTCTGACTCAGTGGTGA	21956	BlatCas9	59	0
646	TGAGCT	GTGCCTCTGACTCAGTGGTGA	21957	cCas9-v16	59	0
647	TGAGCT	GTGCCTCTGACTCAGTGGTGA	21958	cCas9-v21	59	0
648	CTCGGA	TGTACTGTGTGCAGTGGAAGA	21959	cCas9-v17	59	0
649	CTCGGA	TGTACTGTGTGCAGTGGAAGA	21960	cCas9-v42	59	0
650	ATGAG	ctAGTGCCTCTGACTCAGTGGTG	21961	SauCas9	60	0
651	ATGAG	AGTGCCTCTGACTCAGTGGTG	21962	SauCas9KKH	60	0
652	ATG	GTGCCTCTGACTCAGTGGTG	21963	ScaCas9	60	0
653	ATG	GTGCCTCTGACTCAGTGGTG	21964	ScaCas9-HiFi-Sc++	60	0
654	ATG	GTGCCTCTGACTCAGTGGTG	21965	ScaCas9-Sc++	60	0
655	ATG	GTGCCTCTGACTCAGTGGTG	21966	SpyCas9-SpRY	60	0
656	ACT	TGTACTGTGTGCAGTGGAAG	21967	SpyCas9-SpRY	60	0
657	ATGAGC	AGTGCCTCTGACTCAGTGGTG	21968	cCas9-v17	60	0
658	ATGAGC	AGTGCCTCTGACTCAGTGGTG	21969	cCas9-v42	60	0

659	ATGAGCTT	cctaGTGCCTCTGACTCAGTGGTG	21970	NmeCas9	60	0
660	GATGA	TAGTGCCTCTGACTCAGTGGT	21971	SauCas9KKH	61	0
661	GAC	ATGTACTGTGTGCAGTGGAA	21972	SpyCas9-SpRY	61	0
662	GAT	AGTGCCTCTGACTCAGTGGT	21973	SpyCas9-SpRY	61	0
663	GAT	AGTGCCTCTGACTCAGTGGT	21974	SpyCas9-xCas	61	0
664	GACTCGGA	ctgaTGTACTGTGTGCAGTGGAA	21975	BlatCas9	61	0
665	GACTC	ctgaTGTACTGTGTGCAGTGGAA	21976	BlatCas9	61	0
666	GACT	ATGTACTGTGTGCAGTGGAA	21977	SpyCas9-3var-NRCH	61	0
667	AG	GATGTACTGTGTGCAGTGGA	21978	SpyCas9-NG	62	0
668	AG	GATGTACTGTGTGCAGTGGA	21979	SpyCas9-xCas	62	0
669	AG	GATGTACTGTGTGCAGTGGA	21980	SpyCas9-xCas-NG	62	0
670	TG	TAGTGCCTCTGACTCAGTGG	21981	SpyCas9-NG	62	0
671	TG	TAGTGCCTCTGACTCAGTGG	21982	SpyCas9-xCas	62	0
672	TG	TAGTGCCTCTGACTCAGTGG	21983	SpyCas9-xCas-NG	62	0
673	AGA	GATGTACTGTGTGCAGTGGA	21984	SpyCas9-SpG	62	0
674	AGA	GATGTACTGTGTGCAGTGGA	21985	SpyCas9-SpRY	62	0
675	TGA	TAGTGCCTCTGACTCAGTGG	21986	SpyCas9-SpG	62	0
676	TGA	TAGTGCCTCTGACTCAGTGG	21987	SpyCas9-SpRY	62	0
677	AGAC	GATGTACTGTGTGCAGTGGA	21988	SpyCas9-3var-NRRH	62	0
678	AGAC	GATGTACTGTGTGCAGTGGA	21989	SpyCas9-VQR	62	0
679	TGAT	TAGTGCCTCTGACTCAGTGG	21990	SpyCas9-3var-NRRH	62	0
680	TGAT	TAGTGCCTCTGACTCAGTGG	21991	SpyCas9-VQR	62	0
681	AAG	TGATGTACTGTGTGCAGTGG	21992	ScaCas9	63	0
682	AAG	TGATGTACTGTGTGCAGTGG	21993	ScaCas9-HiFi-Sc++	63	0
683	AAG	TGATGTACTGTGTGCAGTGG	21994	ScaCas9-Sc++	63	0
684	AAG	TGATGTACTGTGTGCAGTGG	21995	SpyCas9-SpRY	63	0
685	GTG	CTAGTGCCTCTGACTCAGTG	21996	ScaCas9	63	0

686	GTG	CTAGTGCCTCTGACTCAGTG	21997	ScaCas9-HiFi-Sc++	63	0
687	GTG	CTAGTGCCTCTGACTCAGTG	21998	ScaCas9-Sc++	63	0
688	GTG	CTAGTGCCTCTGACTCAGTG	21999	SpyCas9-SpRY	63	0
689	AAGAC	gtctGATGTACTGTGTGCAGTGG	22000	BlatCas9	63	0
690	AAGACT	CTGATGTACTGTGTGCAGTGG	22001	cCas9-v16	63	0
691	AAGACT	CTGATGTACTGTGTGCAGTGG	22002	cCas9-v21	63	0
692	GTGATGA	CCTAGTGCCTCTGACTCAGTG	22003	cCas9-v16	63	0
693	GTGATGA	CCTAGTGCCTCTGACTCAGTG	22004	cCas9-v21	63	0
694	AAGACTC	TCTGATGTACTGTGTGCAGTGG	22005	CdiCas9	63	0
695	AAGA	TGATGTACTGTGTGCAGTGG	22006	SpyCas9-3var-NRRH	63	0
696	GAAGA	TCTGATGTACTGTGTGCAGTG	22007	SauCas9KKH	64	0
697	GGTGA	TCCTAGTGCCTCTGACTCAGT	22008	SauCas9KKH	64	0
698	GGTGAT	TCCTAGTGCCTCTGACTCAGT	22009	SauCas9KKH	64	0
699	GAAG	TCTGATGTACTGTGTGCAGTG	22010	SauriCas9-KKH	64	0
700	GAAG	CTGATGTACTGTGTGCAGTG	22011	SpyCas9-QQR1	64	0
701	GAAG	tcTGATGTACTGTGTGCAGTG	22012	iSpyMacCas9	64	0
702	GG	CCTAGTGCCTCTGACTCAGT	22013	SpyCas9-NG	64	0
703	GG	CCTAGTGCCTCTGACTCAGT	22014	SpyCas9-xCas	64	0
704	GG	CCTAGTGCCTCTGACTCAGT	22015	SpyCas9-xCas-NG	64	0
705	GAA	CTGATGTACTGTGTGCAGTG	22016	SpyCas9-SpRY	64	0
706	GAA	CTGATGTACTGTGTGCAGTG	22017	SpyCas9-xCas	64	0
707	GGT	CCTAGTGCCTCTGACTCAGT	22018	SpyCas9-SpG	64	0
708	GGT	CCTAGTGCCTCTGACTCAGT	22019	SpyCas9-SpRY	64	0
709	GAAGAC	TCTGATGTACTGTGTGCAGTG	22020	cCas9-v17	64	0
710	GAAGAC	TCTGATGTACTGTGTGCAGTG	22021	cCas9-v42	64	0
711	GGAAG	GTCTGATGTACTGTGTGCAGT	22022	SauCas9KKH	65	0
712	TGG	TCCTAGTGCCTCTGACTCAG	22023	ScaCas9	65	0

713	TGG	TCCTAGTGCCTCTGACTCAG	22024	ScaCas9-HiFi-Sc++	65	0
714	TGG	TCCTAGTGCCTCTGACTCAG	22025	ScaCas9-Sc++	65	0
715	TGG	TCCTAGTGCCTCTGACTCAG	22026	SpyCas9	65	0
716	TGG	TCCTAGTGCCTCTGACTCAG	22027	SpyCas9-HF1	65	0
717	TGG	TCCTAGTGCCTCTGACTCAG	22028	SpyCas9-SpG	65	0
718	TGG	TCCTAGTGCCTCTGACTCAG	22029	SpyCas9-SpRY	65	0
719	GG	TCTGATGTACTGTGTGCAGT	22030	SpyCas9-NG	65	0
720	GG	TCTGATGTACTGTGTGCAGT	22031	SpyCas9-xCas	65	0
721	GG	TCTGATGTACTGTGTGCAGT	22032	SpyCas9-xCas-NG	65	0
722	TG	TCCTAGTGCCTCTGACTCAG	22033	SpyCas9-NG	65	0
723	TG	TCCTAGTGCCTCTGACTCAG	22034	SpyCas9-xCas	65	0
724	TG	TCCTAGTGCCTCTGACTCAG	22035	SpyCas9-xCas-NG	65	0
725	GGA	TCTGATGTACTGTGTGCAGT	22036	SpyCas9-SpG	65	0
726	GGA	TCTGATGTACTGTGTGCAGT	22037	SpyCas9-SpRY	65	0
727	GGAAGA	GTCTGATGTACTGTGTGCAGT	22038	cCas9-v17	65	0
728	GGAAGA	GTCTGATGTACTGTGTGCAGT	22039	cCas9-v42	65	0
729	GGAAGACT	catgTCTGATGTACTGTGTGCAGT	22040	NmeCas9	65	0
730	GGAA	TCTGATGTACTGTGTGCAGT	22041	SpyCas9-3var-NRRH	65	0
731	GGAA	TCTGATGTACTGTGTGCAGT	22042	SpyCas9-VQR	65	0
732	TGGT	TCCTAGTGCCTCTGACTCAG	22043	SpyCas9-3var-NRRH	65	0
733	TGGAA	caTGTCTGATGTACTGTGTGCAG	22044	SauCas9	66	0
734	TGGAA	TGTCTGATGTACTGTGTGCAG	22045	SauCas9KKH	66	0
735	GTGG	TCTCCTAGTGCCTCTGACTCA	22046	SauriCas9	66	0
736	GTGG	TCTCCTAGTGCCTCTGACTCA	22047	SauriCas9-KKH	66	0
737	TGG	GTCTGATGTACTGTGTGCAG	22048	ScaCas9	66	0
738	TGG	GTCTGATGTACTGTGTGCAG	22049	ScaCas9-HiFi-Sc++	66	0
739	TGG	GTCTGATGTACTGTGTGCAG	22050	ScaCas9-Sc++	66	0

740	TGG	GTCTGATGTACTGTGTGCAG	22051	SpyCas9	66	0
741	TGG	GTCTGATGTACTGTGTGCAG	22052	SpyCas9-HF1	66	0
742	TGG	GTCTGATGTACTGTGTGCAG	22053	SpyCas9-SpG	66	0
743	TGG	GTCTGATGTACTGTGTGCAG	22054	SpyCas9-SpRY	66	0
744	GTG	CTCCTAGTGCCTCTGACTCA	22055	ScaCas9	66	0
745	GTG	CTCCTAGTGCCTCTGACTCA	22056	ScaCas9-HiFi-Sc++	66	0
746	GTG	CTCCTAGTGCCTCTGACTCA	22057	ScaCas9-Sc++	66	0
747	GTG	CTCCTAGTGCCTCTGACTCA	22058	SpyCas9-SpRY	66	0
748	TG	GTCTGATGTACTGTGTGCAG	22059	SpyCas9-NG	66	0
749	TG	GTCTGATGTACTGTGTGCAG	22060	SpyCas9-xCas	66	0
750	TG	GTCTGATGTACTGTGTGCAG	22061	SpyCas9-xCas-NG	66	0
751	GTGGTG	TCTCCTAGTGCCTCTGACTCA	22062	cCas9-v16	66	0
752	GTGGTG	TCTCCTAGTGCCTCTGACTCA	22063	cCas9-v21	66	0
753	TGGAAG	TGTCTGATGTACTGTGTGCAG	22064	cCas9-v17	66	0
754	TGGAAG	TGTCTGATGTACTGTGTGCAG	22065	cCas9-v42	66	0
755	TGGA	GTCTGATGTACTGTGTGCAG	22066	SpyCas9-3var-NRRH	66	0
756	GTGGA	ccATGTCTGATGTACTGTGTGCA	22067	SauCas9	67	0
757	GTGGA	ATGTCTGATGTACTGTGTGCA	22068	SauCas9KKH	67	0
758	AGTGG	GTCTCCTAGTGCCTCTGACTC	22069	SauCas9KKH	67	0
759	AGTGGT	GTCTCCTAGTGCCTCTGACTC	22070	SauCas9KKH	67	0
760	GTGG	ATGTCTGATGTACTGTGTGCA	22071	SauriCas9	67	0
761	GTGG	ATGTCTGATGTACTGTGTGCA	22072	SauriCas9-KKH	67	0
762	GTG	TGTCTGATGTACTGTGTGCA	22073	ScaCas9	67	0
763	GTG	TGTCTGATGTACTGTGTGCA	22074	ScaCas9-HiFi-Sc++	67	0
764	GTG	TGTCTGATGTACTGTGTGCA	22075	ScaCas9-Sc++	67	0
765	GTG	TGTCTGATGTACTGTGTGCA	22076	SpyCas9-SpRY	67	0
766	AG	TCTCCTAGTGCCTCTGACTC	22077	SpyCas9-NG	67	0

767	AG	TCTCCTAGTGCCTCTGACTC	22078	SpyCas9-xCas	67	0
768	AG	TCTCCTAGTGCCTCTGACTC	22079	SpyCas9-xCas-NG	67	0
769	AGT	TCTCCTAGTGCCTCTGACTC	22080	SpyCas9-SpG	67	0
770	AGT	TCTCCTAGTGCCTCTGACTC	22081	SpyCas9-SpRY	67	0
771	GTGGAA	ATGTCTGATGTACTGTGTGCA	22082	cCas9-v17	67	0
772	GTGGAA	ATGTCTGATGTACTGTGTGCA	22083	cCas9-v42	67	0
773	AGTGG	CATGTCTGATGTACTGTGTGC	22084	SauCas9KKH	68	0
774	CAG	GTCTCCTAGTGCCTCTGACT	22085	ScaCas9	68	0
775	CAG	GTCTCCTAGTGCCTCTGACT	22086	ScaCas9-HiFi-Sc++	68	0
776	CAG	GTCTCCTAGTGCCTCTGACT	22087	ScaCas9-Sc++	68	0
777	CAG	GTCTCCTAGTGCCTCTGACT	22088	SpyCas9-SpRY	68	0
778	AG	ATGTCTGATGTACTGTGTGC	22089	SpyCas9-NG	68	0
779	AG	ATGTCTGATGTACTGTGTGC	22090	SpyCas9-xCas	68	0
780	AG	ATGTCTGATGTACTGTGTGC	22091	SpyCas9-xCas-NG	68	0
781	AGT	ATGTCTGATGTACTGTGTGC	22092	SpyCas9-SpG	68	0
782	AGT	ATGTCTGATGTACTGTGTGC	22093	SpyCas9-SpRY	68	0
783	CAGT	GTCTCCTAGTGCCTCTGACT	22094	SpyCas9-3var-NRRH	68	0
784	TCAG	AGGTCTCCTAGTGCCTCTGAC	22095	SauriCas9-KKH	69	0
785	CAG	CATGTCTGATGTACTGTGTG	22096	ScaCas9	69	0
786	CAG	CATGTCTGATGTACTGTGTG	22097	ScaCas9-HiFi-Sc++	69	0
787	CAG	CATGTCTGATGTACTGTGTG	22098	ScaCas9-Sc++	69	0
788	CAG	CATGTCTGATGTACTGTGTG	22099	SpyCas9-SpRY	69	0
789	TCA	GGTCTCCTAGTGCCTCTGAC	22100	SpyCas9-SpRY	69	0
790	TCAGTG	AGGTCTCCTAGTGCCTCTGAC	22101	cCas9-v16	69	0
791	TCAGTG	AGGTCTCCTAGTGCCTCTGAC	22102	cCas9-v21	69	0
792	CAGT	CATGTCTGATGTACTGTGTG	22103	SpyCas9-3var-NRRH	69	0
793	CTCAG	AAGGTCTCCTAGTGCCTCTGA	22104	SauCas9KKH	70	0

794	CTCAGT	AAGGTCTCCTAGTGCCTCTGA	22105	SauCas9KKH	70	0
795	CTCAGT	AAGGTCTCCTAGTGCCTCTGA	22106	cCas9-v17	70	0
796	CTCAGT	AAGGTCTCCTAGTGCCTCTGA	22107	cCas9-v42	70	0
797	GCAG	TCCATGTCTGATGTACTGTGT	22108	SauriCas9-KKH	70	0
798	GCA	CCATGTCTGATGTACTGTGT	22109	SpyCas9-SpRY	70	0
799	CTC	AGGTCTCCTAGTGCCTCTGA	22110	SpyCas9-SpRY	70	0
800	GCAGTG	TCCATGTCTGATGTACTGTGT	22111	cCas9-v16	70	0
801	GCAGTG	TCCATGTCTGATGTACTGTGT	22112	cCas9-v21	70	0
802	TGCAG	ATCCATGTCTGATGTACTGTG	22113	SauCas9KKH	71	0
803	TGCAGT	ATCCATGTCTGATGTACTGTG	22114	SauCas9KKH	71	0
804	TGCAGT	ATCCATGTCTGATGTACTGTG	22115	cCas9-v17	71	0
805	TGCAGT	ATCCATGTCTGATGTACTGTG	22116	cCas9-v42	71	0
806	TG	TCCATGTCTGATGTACTGTG	22117	SpyCas9-NG	71	0
807	TG	TCCATGTCTGATGTACTGTG	22118	SpyCas9-xCas	71	0
808	TG	TCCATGTCTGATGTACTGTG	22119	SpyCas9-xCas-NG	71	0
809	TGC	TCCATGTCTGATGTACTGTG	22120	SpyCas9-SpG	71	0
810	TGC	TCCATGTCTGATGTACTGTG	22121	SpyCas9-SpRY	71	0
811	ACT	AAGGTCTCCTAGTGCCTCTG	22122	SpyCas9-SpRY	71	0
812	TGCA	TCCATGTCTGATGTACTGTG	22123	SpyCas9-3var-NRCH	71	0
813	GTG	ATCCATGTCTGATGTACTGT	22124	ScaCas9	72	0
814	GTG	ATCCATGTCTGATGTACTGT	22125	ScaCas9-HiFi-Sc++	72	0
815	GTG	ATCCATGTCTGATGTACTGT	22126	ScaCas9-Sc++	72	0
816	GTG	ATCCATGTCTGATGTACTGT	22127	SpyCas9-SpRY	72	0
817	GAC	AAAGGTCTCCTAGTGCCTCT	22128	SpyCas9-SpRY	72	0
818	GACTCAGT	cctaAAGGTCTCCTAGTGCCTCT	22129	BlatCas9	72	0
819	GACTC	cctaAAGGTCTCCTAGTGCCTCT	22130	BlatCas9	72	0
820	GACT	AAAGGTCTCCTAGTGCCTCT	22131	SpyCas9-3var-NRCH	72	0

821	TG	GATCCATGTCTGATGTACTG	22132	SpyCas9-NG	73	0
822	TG	GATCCATGTCTGATGTACTG	22133	SpyCas9-xCas	73	0
823	TG	GATCCATGTCTGATGTACTG	22134	SpyCas9-xCas-NG	73	0
824	TG	TAAAGGTCTCCTAGTGCCTC	22135	SpyCas9-NG	73	0
825	TG	TAAAGGTCTCCTAGTGCCTC	22136	SpyCas9-xCas	73	0
826	TG	TAAAGGTCTCCTAGTGCCTC	22137	SpyCas9-xCas-NG	73	0
827	TGT	GATCCATGTCTGATGTACTG	22138	SpyCas9-SpG	73	0
828	TGT	GATCCATGTCTGATGTACTG	22139	SpyCas9-SpRY	73	0
829	TGA	TAAAGGTCTCCTAGTGCCTC	22140	SpyCas9-SpG	73	0
830	TGA	TAAAGGTCTCCTAGTGCCTC	22141	SpyCas9-SpRY	73	0
831	TGTGCAGT	ttggATCCATGTCTGATGTACTG	22142	BlatCas9	73	0
832	TGTGC	ttggATCCATGTCTGATGTACTG	22143	BlatCas9	73	0
833	TGAC	TAAAGGTCTCCTAGTGCCTC	22144	SpyCas9-3var-NRRH	73	0
834	TGAC	TAAAGGTCTCCTAGTGCCTC	22145	SpyCas9-VQR	73	0
835	GTG	GGATCCATGTCTGATGTACT	22146	ScaCas9	74	0
836	GTG	GGATCCATGTCTGATGTACT	22147	ScaCas9-HiFi-Sc++	74	0
837	GTG	GGATCCATGTCTGATGTACT	22148	ScaCas9-Sc++	74	0
838	GTG	GGATCCATGTCTGATGTACT	22149	SpyCas9-SpRY	74	0
839	CTG	CTAAAGGTCTCCTAGTGCCT	22150	ScaCas9	74	0
840	CTG	CTAAAGGTCTCCTAGTGCCT	22151	ScaCas9-HiFi-Sc++	74	0
841	CTG	CTAAAGGTCTCCTAGTGCCT	22152	ScaCas9-Sc++	74	0
842	CTG	CTAAAGGTCTCCTAGTGCCT	22153	SpyCas9-SpRY	74	0
843	CTGAC	taccTAAAGGTCTCCTAGTGCCT	22154	BlatCas9	74	0
844	CTGACT	CCTAAAGGTCTCCTAGTGCCT	22155	cCas9-v16	74	0
845	CTGACT	CCTAAAGGTCTCCTAGTGCCT	22156	cCas9-v21	74	0
846	CTGACTC	ACCTAAAGGTCTCCTAGTGCCT	22157	CdiCas9	74	0
847	TCTGA	ACCTAAAGGTCTCCTAGTGCC	22158	SauCas9KKH	75	0

848	TG	TGGATCCATGTCTGATGTAC	22159	SpyCas9-NG	75	0
849	TG	TGGATCCATGTCTGATGTAC	22160	SpyCas9-xCas	75	0
850	TG	TGGATCCATGTCTGATGTAC	22161	SpyCas9-xCas-NG	75	0
851	TGT	TGGATCCATGTCTGATGTAC	22162	SpyCas9-SpG	75	0
852	TGT	TGGATCCATGTCTGATGTAC	22163	SpyCas9-SpRY	75	0
853	TCT	CCTAAAGGTCTCCTAGTGCC	22164	SpyCas9-SpRY	75	0
854	CTG	TTGGATCCATGTCTGATGTA	22165	ScaCas9	76	0
855	CTG	TTGGATCCATGTCTGATGTA	22166	ScaCas9-HiFi-Sc++	76	0
856	CTG	TTGGATCCATGTCTGATGTA	22167	ScaCas9-Sc++	76	0
857	CTG	TTGGATCCATGTCTGATGTA	22168	SpyCas9-SpRY	76	0
858	CTC	ACCTAAAGGTCTCCTAGTGC	22169	SpyCas9-SpRY	76	0
859	CTCTGACT	cactACCTAAAGGTCTCCTAGTGC	22170	NmeCas9	76	0
860	ACT	CTTGGATCCATGTCTGATGT	22171	SpyCas9-SpRY	77	0
861	CCT	TACCTAAAGGTCTCCTAGTG	22172	SpyCas9-SpRY	77	0
862	TAC	GCTTGGATCCATGTCTGATG	22173	SpyCas9-SpRY	78	0
863	GCC	CTACCTAAAGGTCTCCTAGT	22174	SpyCas9-SpRY	78	0
864	GCCTCTGA	ccacTACCTAAAGGTCTCCTAGT	22175	BlatCas9	78	0
865	GCCTC	ccacTACCTAAAGGTCTCCTAGT	22176	BlatCas9	78	0
866	TACT	GCTTGGATCCATGTCTGATG	22177	SpyCas9-3var-NRCH	78	0
867	TG	ACTACCTAAAGGTCTCCTAG	22178	SpyCas9-NG	79	0
868	TG	ACTACCTAAAGGTCTCCTAG	22179	SpyCas9-xCas	79	0
869	TG	ACTACCTAAAGGTCTCCTAG	22180	SpyCas9-xCas-NG	79	0
870	TGC	ACTACCTAAAGGTCTCCTAG	22181	SpyCas9-SpG	79	0
871	TGC	ACTACCTAAAGGTCTCCTAG	22182	SpyCas9-SpRY	79	0
872	GTA	GGCTTGGATCCATGTCTGAT	22183	SpyCas9-SpRY	79	0
873	TGCC	ACTACCTAAAGGTCTCCTAG	22184	SpyCas9-3var-NRCH	79	0
874	GTG	CACTACCTAAAGGTCTCCTA	22185	ScaCas9	80	0

875	GTG	CACTACCTAAAGGTCTCCTA	22186	ScaCas9-HiFi-Sc++	80	0
876	GTG	CACTACCTAAAGGTCTCCTA	22187	ScaCas9-Sc++	80	0
877	GTG	CACTACCTAAAGGTCTCCTA	22188	SpyCas9-SpRY	80	0
878	TG	GGGCTTGGATCCATGTCTGA	22189	SpyCas9-NG	80	0
879	TG	GGGCTTGGATCCATGTCTGA	22190	SpyCas9-xCas	80	0
880	TG	GGGCTTGGATCCATGTCTGA	22191	SpyCas9-xCas-NG	80	0
881	TGT	GGGCTTGGATCCATGTCTGA	22192	SpyCas9-SpG	80	0
882	TGT	GGGCTTGGATCCATGTCTGA	22193	SpyCas9-SpRY	80	0
883	TGTACTGT	catgGGCTTGGATCCATGTCTGA	22194	BlatCas9	80	0
884	TGTAC	catgGGCTTGGATCCATGTCTGA	22195	BlatCas9	80	0
885	GTGCC	ctccACTACCTAAAGGTCTCCTA	22196	BlatCas9	80	0
886	GTGCCTC	TCCACTACCTAAAGGTCTCCTA	22197	CdiCas9	80	0
887	TGTA	GGGCTTGGATCCATGTCTGA	22198	SpyCas9-3var-NRTH	80	0
888	AGTGCC	taCTCCACTACCTAAAGGTCTCCT	22199	Nme2Cas9	81	0
889	ATG	TGGGCTTGGATCCATGTCTG	22200	ScaCas9	81	0
890	ATG	TGGGCTTGGATCCATGTCTG	22201	ScaCas9-HiFi-Sc++	81	0
891	ATG	TGGGCTTGGATCCATGTCTG	22202	ScaCas9-Sc++	81	0
892	ATG	TGGGCTTGGATCCATGTCTG	22203	SpyCas9-SpRY	81	0
893	AG	CCACTACCTAAAGGTCTCCT	22204	SpyCas9-NG	81	0
894	AG	CCACTACCTAAAGGTCTCCT	22205	SpyCas9-xCas	81	0
895	AG	CCACTACCTAAAGGTCTCCT	22206	SpyCas9-xCas-NG	81	0
896	AGT	CCACTACCTAAAGGTCTCCT	22207	SpyCas9-SpG	81	0
897	AGT	CCACTACCTAAAGGTCTCCT	22208	SpyCas9-SpRY	81	0
898	AGTGC	actcCACTACCTAAAGGTCTCCT	22209	BlatCas9	81	0
899	ATGTACT	CATGGGCTTGGATCCATGTCTG	22210	CdiCas9	81	0
900	TAG	TCCACTACCTAAAGGTCTCC	22211	ScaCas9	82	0
901	TAG	TCCACTACCTAAAGGTCTCC	22212	ScaCas9-HiFi-Sc++	82	0

902	TAG	TCCACTACCTAAAGGTCTCC	22213	ScaCas9-Sc++	82	0
903	TAG	TCCACTACCTAAAGGTCTCC	22214	SpyCas9-SpRY	82	0
904	GAT	ATGGGCTTGGATCCATGTCT	22215	SpyCas9-SpRY	82	0
905	GAT	ATGGGCTTGGATCCATGTCT	22216	SpyCas9-xCas	82	0
906	TAGT	TCCACTACCTAAAGGTCTCC	22217	SpyCas9-3var-NRRH	82	0
907	CTAG	ACTCCACTACCTAAAGGTCTC	22218	SauriCas9-KKH	83	0
908	TG	CATGGGCTTGGATCCATGTC	22219	SpyCas9-NG	83	0
909	TG	CATGGGCTTGGATCCATGTC	22220	SpyCas9-xCas	83	0
910	TG	CATGGGCTTGGATCCATGTC	22221	SpyCas9-xCas-NG	83	0
911	TGA	CATGGGCTTGGATCCATGTC	22222	SpyCas9-SpG	83	0
912	TGA	CATGGGCTTGGATCCATGTC	22223	SpyCas9-SpRY	83	0
913	CTA	CTCCACTACCTAAAGGTCTC	22224	SpyCas9-SpRY	83	0
914	CTAGTG	ACTCCACTACCTAAAGGTCTC	22225	cCas9-v16	83	0
915	CTAGTG	ACTCCACTACCTAAAGGTCTC	22226	cCas9-v21	83	0
916	TGATGTAC	atACATGGGCTTGGATCCATGTC	22227	CjeCas9	83	0
917	TGAT	CATGGGCTTGGATCCATGTC	22228	SpyCas9-3var-NRRH	83	0
918	TGAT	CATGGGCTTGGATCCATGTC	22229	SpyCas9-VQR	83	0
919	CCTAG	TACTCCACTACCTAAAGGTCT	22230	SauCas9KKH	84	0
920	CCTAGT	TACTCCACTACCTAAAGGTCT	22231	SauCas9KKH	84	0
921	CTG	ACATGGGCTTGGATCCATGT	22232	ScaCas9	84	0
922	CTG	ACATGGGCTTGGATCCATGT	22233	ScaCas9-HiFi-Sc++	84	0
923	CTG	ACATGGGCTTGGATCCATGT	22234	ScaCas9-Sc++	84	0
924	CTG	ACATGGGCTTGGATCCATGT	22235	SpyCas9-SpRY	84	0
925	CCT	ACTCCACTACCTAAAGGTCT	22236	SpyCas9-SpRY	84	0
926	TCTGA	ATACATGGGCTTGGATCCATG	22237	SauCas9KKH	85	0
927	TCTGAT	ATACATGGGCTTGGATCCATG	22238	SauCas9KKH	85	0
928	TCT	TACATGGGCTTGGATCCATG	22239	SpyCas9-SpRY	85	0

929	TCC	TACTCCACTACCTAAAGGTC	22240	SpyCas9-SpRY	85	0
930	GTC	ATACATGGGCTTGGATCCAT	22241	SpyCas9-SpRY	86	0
931	CTC	CTACTCCACTACCTAAAGGT	22242	SpyCas9-SpRY	86	0
932	TG	TATACATGGGCTTGGATCCA	22243	SpyCas9-NG	87	0
933	TG	TATACATGGGCTTGGATCCA	22244	SpyCas9-xCas	87	0
934	TG	TATACATGGGCTTGGATCCA	22245	SpyCas9-xCas-NG	87	0
935	TGT	TATACATGGGCTTGGATCCA	22246	SpyCas9-SpG	87	0
936	TGT	TATACATGGGCTTGGATCCA	22247	SpyCas9-SpRY	87	0
937	TCT	ACTACTCCACTACCTAAAGG	22248	SpyCas9-SpRY	87	0
938	TCTCCTAG	tgtaCTACTCCACTACCTAAAGG	22249	BlatCas9	87	0
939	TCTCC	tgtaCTACTCCACTACCTAAAGG	22250	BlatCas9	87	0
940	TGTC	TATACATGGGCTTGGATCCA	22251	SpyCas9-3var-NRTH	87	0
941	GTCTCC	tgTGTACTACTCCACTACCTAAAG	22252	Nme2Cas9	88	0
942	ATG	GTATACATGGGCTTGGATCC	22253	ScaCas9	88	0
943	ATG	GTATACATGGGCTTGGATCC	22254	ScaCas9-HiFi-Sc++	88	0
944	ATG	GTATACATGGGCTTGGATCC	22255	ScaCas9-Sc++	88	0
945	ATG	GTATACATGGGCTTGGATCC	22256	SpyCas9-SpRY	88	0
946	GTC	TACTACTCCACTACCTAAAG	22257	SpyCas9-SpRY	88	0
947	ATGTCTGA	ggggTATACATGGGCTTGGATCC	22258	BlatCas9	88	0
948	GTCTCCTA	gtgtACTACTCCACTACCTAAAG	22259	BlatCas9	88	0
949	ATGTC	ggggTATACATGGGCTTGGATCC	22260	BlatCas9	88	0
950	GTCTC	gtgtACTACTCCACTACCTAAAG	22261	BlatCas9	88	0
951	GG	GTACTACTCCACTACCTAAA	22262	SpyCas9-NG	89	0
952	GG	GTACTACTCCACTACCTAAA	22263	SpyCas9-xCas	89	0
953	GG	GTACTACTCCACTACCTAAA	22264	SpyCas9-xCas-NG	89	0
954	CAT	GGTATACATGGGCTTGGATC	22265	SpyCas9-SpRY	89	0
955	GGT	GTACTACTCCACTACCTAAA	22266	SpyCas9-SpG	89	0

956	GGT	GTACTACTCCACTACCTAAA	22267	SpyCas9-SpRY	89	0
957	GGTC	GTACTACTCCACTACCTAAA	22268	SpyCas9-3var-NRTH	89	0
958	AGG	TGTACTACTCCACTACCTAA	22269	ScaCas9	90	0
959	AGG	TGTACTACTCCACTACCTAA	22270	ScaCas9-HiFi-Sc++	90	0
960	AGG	TGTACTACTCCACTACCTAA	22271	ScaCas9-Sc++	90	0
961	AGG	TGTACTACTCCACTACCTAA	22272	SpyCas9	90	0
962	AGG	TGTACTACTCCACTACCTAA	22273	SpyCas9-HF1	90	0
963	AGG	TGTACTACTCCACTACCTAA	22274	SpyCas9-SpG	90	0
964	AGG	TGTACTACTCCACTACCTAA	22275	SpyCas9-SpRY	90	0
965	AG	TGTACTACTCCACTACCTAA	22276	SpyCas9-NG	90	0
966	AG	TGTACTACTCCACTACCTAA	22277	SpyCas9-xCas	90	0
967	AG	TGTACTACTCCACTACCTAA	22278	SpyCas9-xCas-NG	90	0
968	CCA	GGGTATACATGGGCTTGGAT	22279	SpyCas9-SpRY	90	0
969	AGGTC	atgtGTACTACTCCACTACCTAA	22280	BlatCas9	90	0
970	AGGTCTC	TGTGTACTACTCCACTACCTAA	22281	CdiCas9	90	0
971	CCATGTCT	tcggGGGTATACATGGGCTTGGAT	22282	NmeCas9	90	0
972	AGGT	TGTACTACTCCACTACCTAA	22283	SpyCas9-3var-NRRH	90	0
973	AAGG	TGTGTACTACTCCACTACCTA	22284	SauriCas9	91	0
974	AAGG	TGTGTACTACTCCACTACCTA	22285	SauriCas9-KKH	91	0
975	AAG	GTGTACTACTCCACTACCTA	22286	ScaCas9	91	0
976	AAG	GTGTACTACTCCACTACCTA	22287	ScaCas9-HiFi-Sc++	91	0
977	AAG	GTGTACTACTCCACTACCTA	22288	ScaCas9-Sc++	91	0
978	AAG	GTGTACTACTCCACTACCTA	22289	SpyCas9-SpRY	91	0
979	TCC	GGGGTATACATGGGCTTGGA	22290	SpyCas9-SpRY	91	0
980	AAAGG	ATGTGTACTACTCCACTACCT	22291	SauCas9KKH	92	0
981	AAAGGT	ATGTGTACTACTCCACTACCT	22292	SauCas9KKH	92	0
982	AAAGGT	ATGTGTACTACTCCACTACCT	22293	cCas9-v17	92	0

983	AAAGGT	ATGTGTACTACTCCACTACCT	22294	cCas9-v42	92	0
984	AAAG	ATGTGTACTACTCCACTACCT	22295	SauriCas9-KKH	92	0
985	AAAG	TGTGTACTACTCCACTACCT	22296	SpyCas9-QQR1	92	0
986	AAAG	atGTGTACTACTCCACTACCT	22297	iSpyMacCas9	92	0
987	AAA	TGTGTACTACTCCACTACCT	22298	SpyCas9-SpRY	92	0
988	ATC	GGGGGTATACATGGGCTTGG	22299	SpyCas9-SpRY	92	0
989	AAAGGTCT	gttaTGTGTACTACTCCACTACCT	22300	NmeCas9	92	0
990	TAAAG	TATGTGTACTACTCCACTACC	22301	SauCas9KKH	93	0
991	GAT	CGGGGGTATACATGGGCTTG	22302	SpyCas9-SpRY	93	0
992	GAT	CGGGGGTATACATGGGCTTG	22303	SpyCas9-xCas	93	0
993	TAA	ATGTGTACTACTCCACTACC	22304	SpyCas9-SpRY	93	0
994	GATCCATG	gttcGGGGGTATACATGGGCTTG	22305	BlatCas9	93	0
995	GATCC	gttcGGGGGTATACATGGGCTTG	22306	BlatCas9	93	0
996	TAAAGG	TATGTGTACTACTCCACTACC	22307	cCas9-v17	93	0
997	TAAAGG	TATGTGTACTACTCCACTACC	22308	cCas9-v42	93	0
998	TAAA	ATGTGTACTACTCCACTACC	22309	SpyCas9-3var-NRRH	93	0
999	TAAA	taTGTGTACTACTCCACTACC	22310	iSpyMacCas9	93	0
1000	GATC	CGGGGGTATACATGGGCTTG	22311	SpyCas9-3var-NRTH	93	0
1001	GGATCC	cgGTTCGGGGGTATACATGGGCTT	22312	Nme2Cas9	94	0
1002	CTAAA	TTATGTGTACTACTCCACTAC	22313	SauCas9KKH	94	0
1003	GG	TCGGGGGTATACATGGGCTT	22314	SpyCas9-NG	94	0
1004	GG	TCGGGGGTATACATGGGCTT	22315	SpyCas9-xCas	94	0
1005	GG	TCGGGGGTATACATGGGCTT	22316	SpyCas9-xCas-NG	94	0
1006	GGA	TCGGGGGTATACATGGGCTT	22317	SpyCas9-SpG	94	0
1007	GGA	TCGGGGGTATACATGGGCTT	22318	SpyCas9-SpRY	94	0
1008	CTA	TATGTGTACTACTCCACTAC	22319	SpyCas9-SpRY	94	0
1009	GGATCCAT	ggttCGGGGGTATACATGGGCTT	22320	BlatCas9	94	0

1010	GGATC	ggttCGGGGGTATACATGGGCTT	22321	BlatCas9	94	0
1011	CTAAAG	TTATGTGTACTACTCCACTAC	22322	cCas9-v17	94	0
1012	CTAAAG	TTATGTGTACTACTCCACTAC	22323	cCas9-v42	94	0
1013	GGAT	TCGGGGGTATACATGGGCTT	22324	SpyCas9-3var-NRRH	94	0
1014	GGAT	TCGGGGGTATACATGGGCTT	22325	SpyCas9-VQR	94	0
1015	CCTAA	GTTATGTGTACTACTCCACTA	22326	SauCas9KKH	95	0
1016	TGG	TTCGGGGGTATACATGGGCT	22327	ScaCas9	95	0
1017	TGG	TTCGGGGGTATACATGGGCT	22328	ScaCas9-HiFi-Sc++	95	0
1018	TGG	TTCGGGGGTATACATGGGCT	22329	ScaCas9-Sc++	95	0
1019	TGG	TTCGGGGGTATACATGGGCT	22330	SpyCas9	95	0
1020	TGG	TTCGGGGGTATACATGGGCT	22331	SpyCas9-HF1	95	0
1021	TGG	TTCGGGGGTATACATGGGCT	22332	SpyCas9-SpG	95	0
1022	TGG	TTCGGGGGTATACATGGGCT	22333	SpyCas9-SpRY	95	0
1023	TG	TTCGGGGGTATACATGGGCT	22334	SpyCas9-NG	95	0
1024	TG	TTCGGGGGTATACATGGGCT	22335	SpyCas9-xCas	95	0
1025	TG	TTCGGGGGTATACATGGGCT	22336	SpyCas9-xCas-NG	95	0
1026	CCT	TTATGTGTACTACTCCACTA	22337	SpyCas9-SpRY	95	0
1027	TGGATCC	GGTTCGGGGGTATACATGGGCT	22338	CdiCas9	95	0
1028	TGGA	TTCGGGGGTATACATGGGCT	22339	SpyCas9-3var-NRRH	95	0
1029	TTGGA	acGGTTCGGGGGTATACATGGGC	22340	SauCas9	96	0
1030	TTGGA	GGTTCGGGGGTATACATGGGC	22341	SauCas9KKH	96	0
1031	TTGGAT	acGGTTCGGGGGTATACATGGGC	22342	SauCas9	96	0
1032	TTGGAT	GGTTCGGGGGTATACATGGGC	22343	SauCas9KKH	96	0
1033	TTGGAT	GGTTCGGGGGTATACATGGGC	22344	cCas9-v17	96	0
1034	TTGGAT	GGTTCGGGGGTATACATGGGC	22345	cCas9-v42	96	0
1035	TTGG	GGTTCGGGGGTATACATGGGC	22346	SauriCas9	96	0
1036	TTGG	GGTTCGGGGGTATACATGGGC	22347	SauriCas9-KKH	96	0

1037	TTG	GTTCGGGGGTATACATGGGC	22348	ScaCas9	96	0
1038	TTG	GTTCGGGGGTATACATGGGC	22349	ScaCas9-HiFi-Sc++	96	0
1039	TTG	GTTCGGGGGTATACATGGGC	22350	ScaCas9-Sc++	96	0
1040	TTG	GTTCGGGGGTATACATGGGC	22351	SpyCas9-SpRY	96	0
1041	ACC	GTTATGTGTACTACTCCACT	22352	SpyCas9-SpRY	96	0
1042	CTTGG	CGGTTCGGGGGTATACATGGG	22353	SauCas9KKH	97	0
1043	TAC	AGTTATGTGTACTACTCCAC	22354	SpyCas9-SpRY	97	0
1044	CTT	GGTTCGGGGGTATACATGGG	22355	SpyCas9-SpRY	97	0
1045	TACC	AGTTATGTGTACTACTCCAC	22356	SpyCas9-3var-NRCH	97	0
1046	GCT	CGGTTCGGGGGTATACATGG	22357	SpyCas9-SpRY	98	0
1047	CTA	CAGTTATGTGTACTACTCCA	22358	SpyCas9-SpRY	98	0
1048	CTACCTAA	gggcAGTTATGTGTACTACTCCA	22359	BlatCas9	98	0
1049	CTACCTAA	gggcAGTTATGTGTACTACTCCA	22360	BlatCas9	98	0
1050	CTACC	gggcAGTTATGTGTACTACTCCA	22361	BlatCas9	98	0
1051	ACTACC	ctGGGCAGTTATGTGTACTACTCC	22362	Nme2Cas9	99	0
1052	GG	ACGGTTCGGGGGTATACATG	22363	SpyCas9-NG	99	0
1053	GG	ACGGTTCGGGGGTATACATG	22364	SpyCas9-xCas	99	0
1054	GG	ACGGTTCGGGGGTATACATG	22365	SpyCas9-xCas-NG	99	0
1055	GGC	ACGGTTCGGGGGTATACATG	22366	SpyCas9-SpG	99	0
1056	GGC	ACGGTTCGGGGGTATACATG	22367	SpyCas9-SpRY	99	0
1057	ACT	GCAGTTATGTGTACTACTCC	22368	SpyCas9-SpRY	99	0
1058	ACTACCTA	tgggCAGTTATGTGTACTACTCC	22369	BlatCas9	99	0
1059	ACTAC	tgggCAGTTATGTGTACTACTCC	22370	BlatCas9	99	0
1060	GGCT	ACGGTTCGGGGGTATACATG	22371	SpyCas9-3var-NRCH	99	0
1061	GGG	CACGGTTCGGGGGTATACAT	22372	ScaCas9	100	0
1062	GGG	CACGGTTCGGGGGTATACAT	22373	ScaCas9-HiFi-Sc++	100	0
1063	GGG	CACGGTTCGGGGGTATACAT	22374	ScaCas9-Sc++	100	0

1064	GGG	CACGGTTCGGGGGTATACAT	22375	SpyCas9	100	0
1065	GGG	CACGGTTCGGGGGTATACAT	22376	SpyCas9-HF1	100	0
1066	GGG	CACGGTTCGGGGGTATACAT	22377	SpyCas9-SpG	100	0
1067	GGG	CACGGTTCGGGGGTATACAT	22378	SpyCas9-SpRY	100	0
1068	GG	CACGGTTCGGGGGTATACAT	22379	SpyCas9-NG	100	0
1069	GG	CACGGTTCGGGGGTATACAT	22380	SpyCas9-xCas	100	0
1070	GG	CACGGTTCGGGGGTATACAT	22381	SpyCas9-xCas-NG	100	0
1071	CAC	GGCAGTTATGTGTACTACTC	22382	SpyCas9-SpRY	100	0
1072	GGGC	CACGGTTCGGGGGTATACAT	22383	SpyCas9-3var-NRRH	100	0
1073	CACT	GGCAGTTATGTGTACTACTC	22384	SpyCas9-3var-NRCH	100	0

Table 1D: Exemplary gRNA spacer Cas pairs for correcting the pathogenic IVS10-11G>A mutation

Table 1D provides a gRNA database for correcting the pathogenic IVS10-11G>A mutation in PAH. List of spacers, PAMs, and Cas variants for generating a nick at an appropriate position to enable installation of a desired genomic edit with a gene modifying system. The spacers in this table are designed to be used with a gene modifying polypeptide comprising a nickase variant of the Cas species indicated in the table. Tables 2D, 3D, and 4D detail the other components of the system and are organized such that the ID number shown here in Column 1 ("ID") is meant to correspond to the same ID number in Tables 2D, 2D, and 4D.

ID	PAM sequence	gRNA spacer	SEQ ID NO	Cas species	distance	Overlaps mutation
1	GCC	ATAATAACTTTTCACTTAGG	23599	SpyCas9-SpRY	0	0
2	AGTGA	TAAGCAGTACTGTAGGCCCTA	23600	SauCas9KKH	1	0
3	GG	GATAATAACTTTTCACTTAG	23601	SpyCas9-NG	1	0
4	GG	GATAATAACTTTTCACTTAG	23602	SpyCas9-xCas	1	0
5	GG	GATAATAACTTTTCACTTAG	23603	SpyCas9-xCas-NG	1	0
6	AG	AAGCAGTACTGTAGGCCCTA	23604	SpyCas9-NG	1	0

7	AG	AAGCAGTACTGTAGGCCCTA	23605	SpyCas9-xCas	1	0
8	AG	AAGCAGTACTGTAGGCCCTA	23606	SpyCas9-xCas-NG	1	0
9	GGC	GATAATAACTTTTCACTTAG	23607	SpyCas9-SpG	1	0
10	GGC	GATAATAACTTTTCACTTAG	23608	SpyCas9-SpRY	1	0
11	AGT	AAGCAGTACTGTAGGCCCTA	23609	SpyCas9-SpG	1	0
12	AGT	AAGCAGTACTGTAGGCCCTA	23610	SpyCas9-SpRY	1	0
13	GGCC	GATAATAACTTTTCACTTAG	23611	SpyCas9-3var-NRCH	1	0
14	GGG	TGATAATAACTTTTCACTTA	23612	ScaCas9	2	0
15	GGG	TGATAATAACTTTTCACTTA	23613	ScaCas9-HiFi-Sc++	2	0
16	GGG	TGATAATAACTTTTCACTTA	23614	ScaCas9-Sc++	2	0
17	GGG	TGATAATAACTTTTCACTTA	23615	SpyCas9	2	0
18	GGG	TGATAATAACTTTTCACTTA	23616	SpyCas9-HF1	2	0
19	GGG	TGATAATAACTTTTCACTTA	23617	SpyCas9-SpG	2	0
20	GGG	TGATAATAACTTTTCACTTA	23618	SpyCas9-SpRY	2	0
21	AAG	TAAGCAGTACTGTAGGCCCT	23619	ScaCas9	2	0
22	AAG	TAAGCAGTACTGTAGGCCCT	23620	ScaCas9-HiFi-Sc++	2	0
23	AAG	TAAGCAGTACTGTAGGCCCT	23621	ScaCas9-Sc++	2	0
24	AAG	TAAGCAGTACTGTAGGCCCT	23622	SpyCas9-SpRY	2	0
25	GG	TGATAATAACTTTTCACTTA	23623	SpyCas9-NG	2	0
26	GG	TGATAATAACTTTTCACTTA	23624	SpyCas9-xCas	2	0
27	GG	TGATAATAACTTTTCACTTA	23625	SpyCas9-xCas-NG	2	0
28	GGGCC	cagtGATAATAACTTTTCACTTA	23626	BlatCas9	2	0
29	GGGC	TGATAATAACTTTTCACTTA	23627	SpyCas9-3var-NRRH	2	0
30	AAGT	TAAGCAGTACTGTAGGCCCT	23628	SpyCas9-3var-NRRH	2	0
31	aGGGCC	aaCAGTGATAATAACTTTTCACTT	23629	Nme2Cas9	3	1
32	aGGG	AGTGATAATAACTTTTCACTT	23630	SauriCas9	3	1
33	aGGG	AGTGATAATAACTTTTCACTT	23631	SauriCas9-KKH	3	1
34	tAAG	GATAAGCAGTACTGTAGGCCC	23632	SauriCas9-KKH	3	1
35	tAAG	ATAAGCAGTACTGTAGGCCC	23633	SpyCas9-QQR1	3	1

36	tAAG	gaTAAGCAGTACTGTAGGCCC	23634	iSpyMacCas9	3	1
37	aGG	GTGATAATAACTTTTCACTT	23635	ScaCas9	3	1
38	aGG	GTGATAATAACTTTTCACTT	23636	ScaCas9-HiFi-Sc++	3	1
39	aGG	GTGATAATAACTTTTCACTT	23637	ScaCas9-Sc++	3	1
40	aGG	GTGATAATAACTTTTCACTT	23638	SpyCas9	3	1
41	aGG	GTGATAATAACTTTTCACTT	23639	SpyCas9-HF1	3	1
42	aGG	GTGATAATAACTTTTCACTT	23640	SpyCas9-SpG	3	1
43	aGG	GTGATAATAACTTTTCACTT	23641	SpyCas9-SpRY	3	1
44	aG	GTGATAATAACTTTTCACTT	23642	SpyCas9-NG	3	1
45	aG	GTGATAATAACTTTTCACTT	23643	SpyCas9-xCas	3	1
46	aG	GTGATAATAACTTTTCACTT	23644	SpyCas9-xCas-NG	3	1
47	tAA	ATAAGCAGTACTGTAGGCCC	23645	SpyCas9-SpRY	3	1
48	aGGGCCTA	acagTGATAATAACTTTTCACTT	23646	BlatCas9	3	1
49	aGGGC	acagTGATAATAACTTTTCACTT	23647	BlatCas9	3	1
50	tAAGTG	GATAAGCAGTACTGTAGGCCC	23648	cCas9-v16	3	1
51	tAAGTG	GATAAGCAGTACTGTAGGCCC	23649	cCas9-v21	3	1
52	TaGGG	aaCAGTGATAATAACTTTTCACT	23650	SauCas9	4	1
53	TaGGG	CAGTGATAATAACTTTTCACT	23651	SauCas9KKH	4	1
54	CtAAG	TGATAAGCAGTACTGTAGGCC	23652	SauCas9KKH	4	1
55	CtAAGT	TGATAAGCAGTACTGTAGGCC	23653	SauCas9KKH	4	1
56	CtAAGT	TGATAAGCAGTACTGTAGGCC	23654	cCas9-v17	4	1
57	CtAAGT	TGATAAGCAGTACTGTAGGCC	23655	cCas9-v42	4	1
58	TaGG	CAGTGATAATAACTTTTCACT	23656	SauriCas9	4	1
59	TaGG	CAGTGATAATAACTTTTCACT	23657	SauriCas9-KKH	4	1
60	TaG	AGTGATAATAACTTTTCACT	23658	ScaCas9	4	1
61	TaG	AGTGATAATAACTTTTCACT	23659	ScaCas9-HiFi-Sc++	4	1
62	TaG	AGTGATAATAACTTTTCACT	23660	ScaCas9-Sc++	4	1
63	TaG	AGTGATAATAACTTTTCACT	23661	SpyCas9-SpRY	4	1
64	CtA	GATAAGCAGTACTGTAGGCC	23662	SpyCas9-SpRY	4	1
65	TaGGGC	CAGTGATAATAACTTTTCACT	23663	cCas9-v17	4	1
66	TaGGGC	CAGTGATAATAACTTTTCACT	23664	cCas9-v42	4	1

67	CCtAA	CTGATAAGCAGTACTGTAGGC	23665	SauCas9KKH	5	1
68	TTaGG	ACAGTGATAATAACTTTTCAC	23666	SauCas9KKH	5	1
69	TTaG	ACAGTGATAATAACTTTTCAC	23667	SauriCas9-KKH	5	1
70	CCt	TGATAAGCAGTACTGTAGGC	23668	SpyCas9-SpRY	5	1
71	TTa	CAGTGATAATAACTTTTCAC	23669	SpyCas9-SpRY	5	1
72	TTaGGG	ACAGTGATAATAACTTTTCAC	23670	cCas9-v17	5	1
73	TTaGGG	ACAGTGATAATAACTTTTCAC	23671	cCas9-v42	5	1
74	CTTaG	AACAGTGATAATAACTTTTCA	23672	SauCas9KKH	6	1
75	CCC	CTGATAAGCAGTACTGTAGG	23673	SpyCas9-SpRY	6	0
76	CTT	ACAGTGATAATAACTTTTCA	23674	SpyCas9-SpRY	6	0
77	GCC	TCTGATAAGCAGTACTGTAG	23675	SpyCas9-SpRY	7	0
78	ACT	AACAGTGATAATAACTTTTC	23676	SpyCas9-SpRY	7	0
79	GG	CTCTGATAAGCAGTACTGTA	23677	SpyCas9-NG	8	0
80	GG	CTCTGATAAGCAGTACTGTA	23678	SpyCas9-xCas	8	0
81	GG	CTCTGATAAGCAGTACTGTA	23679	SpyCas9-xCas-NG	8	0
82	GGC	CTCTGATAAGCAGTACTGTA	23680	SpyCas9-SpG	8	0
83	GGC	CTCTGATAAGCAGTACTGTA	23681	SpyCas9-SpRY	8	0
84	CAC	TAACAGTGATAATAACTTTT	23682	SpyCas9-SpRY	8	0
85	GGCCCtAA	cttcTCTGATAAGCAGTACTGTA	23683	BlatCas9	8	1
86	GGCCCtAA	cttcTCTGATAAGCAGTACTGTA	23684	BlatCas9	8	1
87	GGCCC	cttcTCTGATAAGCAGTACTGTA	23685	BlatCas9	8	0
88	GGCC	CTCTGATAAGCAGTACTGTA	23686	SpyCas9-3var-NRCH	8	0
89	CACT	TAACAGTGATAATAACTTTT	23687	SpyCas9-3var-NRCH	8	0
90	AGGCCC	ggCTTCTCTGATAAGCAGTACTGT	23688	Nme2Cas9	9	0
91	AGG	TCTCTGATAAGCAGTACTGT	23689	ScaCas9	9	0
92	AGG	TCTCTGATAAGCAGTACTGT	23690	ScaCas9-HiFi-Sc++	9	0
93	AGG	TCTCTGATAAGCAGTACTGT	23691	ScaCas9-Sc++	9	0
94	AGG	TCTCTGATAAGCAGTACTGT	23692	SpyCas9	9	0
95	AGG	TCTCTGATAAGCAGTACTGT	23693	SpyCas9-HF1	9	0

96	AGG	TCTCTGATAAGCAGTACTGT	23694	SpyCas9-SpG	9	0
97	AGG	TCTCTGATAAGCAGTACTGT	23695	SpyCas9-SpRY	9	0
98	AG	TCTCTGATAAGCAGTACTGT	23696	SpyCas9-NG	9	0
99	AG	TCTCTGATAAGCAGTACTGT	23697	SpyCas9-xCas	9	0
100	AG	TCTCTGATAAGCAGTACTGT	23698	SpyCas9-xCas-NG	9	0
101	TCA	TTAACAGTGATAATAACTTT	23699	SpyCas9-SpRY	9	0
102	AGGCCCtA	gcttCTCTGATAAGCAGTACTGT	23700	BlatCas9	9	1
103	AGGCC	gcttCTCTGATAAGCAGTACTGT	23701	BlatCas9	9	0
104	AGGCCCt	CTTCTCTGATAAGCAGTACTGT	23702	CdiCas9	9	1
105	AGGC	TCTCTGATAAGCAGTACTGT	23703	SpyCas9-3var-NRRH	9	0
106	TAGGCC	tgGCTTCTCTGATAAGCAGTACTG	23704	Nme2Cas9	10	0
107	TAGG	CTTCTCTGATAAGCAGTACTG	23705	SauriCas9	10	0
108	TAGG	CTTCTCTGATAAGCAGTACTG	23706	SauriCas9-KKH	10	0
109	TAG	TTCTCTGATAAGCAGTACTG	23707	ScaCas9	10	0
110	TAG	TTCTCTGATAAGCAGTACTG	23708	ScaCas9-HiFi-Sc++	10	0
111	TAG	TTCTCTGATAAGCAGTACTG	23709	ScaCas9-Sc++	10	0
112	TAG	TTCTCTGATAAGCAGTACTG	23710	SpyCas9-SpRY	10	0
113	TTC	TTTAACAGTGATAATAACTT	23711	SpyCas9-SpRY	10	0
114	TTCACTTa	tgatTTAACAGTGATAATAACTT	23712	BlatCas9	10	1
115	TAGGC	ggctTCTCTGATAAGCAGTACTG	23713	BlatCas9	10	0
116	TTCAC	tgatTTAACAGTGATAATAACTT	23714	BlatCas9	10	0
117	TTCACT	ATTTAACAGTGATAATAACTT	23715	cCas9-v16	10	0
118	TTCACT	ATTTAACAGTGATAATAACTT	23716	cCas9-v21	10	0
119	GTAGG	GCTTCTCTGATAAGCAGTACT	23717	SauCas9KKH	11	0
120	GTAG	GCTTCTCTGATAAGCAGTACT	23718	SauriCas9-KKH	11	0
121	GTA	CTTCTCTGATAAGCAGTACT	23719	SpyCas9-SpRY	11	0
122	TTT	ATTTAACAGTGATAATAACT	23720	SpyCas9-SpRY	11	0
123	GTAGGC	GCTTCTCTGATAAGCAGTACT	23721	cCas9-v17	11	0
124	GTAGGC	GCTTCTCTGATAAGCAGTACT	23722	cCas9-v42	11	0
125	TGTAG	GGCTTCTCTGATAAGCAGTAC	23723	SauCas9KKH	12	0
126	TG	GCTTCTCTGATAAGCAGTAC	23724	SpyCas9-NG	12	0
127	TG	GCTTCTCTGATAAGCAGTAC	23725	SpyCas9-xCas	12	0

128	TG	GCTTCTCTGATAAGCAGTAC	23726	SpyCas9-xCas-NG	12	0
129	TGT	GCTTCTCTGATAAGCAGTAC	23727	SpyCas9-SpG	12	0
130	TGT	GCTTCTCTGATAAGCAGTAC	23728	SpyCas9-SpRY	12	0
131	TTT	GATTTAACAGTGATAATAAC	23729	SpyCas9-SpRY	12	0
132	TTTTC	cctgATTTAACAGTGATAATAAC	23730	BlatCas9	12	0
133	TGTA	GCTTCTCTGATAAGCAGTAC	23731	SpyCas9-3var-NRTH	12	0
134	CTG	GGCTTCTCTGATAAGCAGTA	23732	ScaCas9	13	0
135	CTG	GGCTTCTCTGATAAGCAGTA	23733	ScaCas9-HiFi-Sc++	13	0
136	CTG	GGCTTCTCTGATAAGCAGTA	23734	ScaCas9-Sc++	13	0
137	CTG	GGCTTCTCTGATAAGCAGTA	23735	SpyCas9-SpRY	13	0
138	CTT	TGATTTAACAGTGATAATAA	23736	SpyCas9-SpRY	13	0
139	ACT	TGGCTTCTCTGATAAGCAGT	23737	SpyCas9-SpRY	14	0
140	ACT	CTGATTTAACAGTGATAATA	23738	SpyCas9-SpRY	14	0
141	TAC	TTGGCTTCTCTGATAAGCAG	23739	SpyCas9-SpRY	15	0
142	AAC	CCTGATTTAACAGTGATAAT	23740	SpyCas9-SpRY	15	0
143	TACT	TTGGCTTCTCTGATAAGCAG	23741	SpyCas9-3var-NRCH	15	0
144	AACT	CCTGATTTAACAGTGATAAT	23742	SpyCas9-3var-NRCH	15	0
145	TAA	TCCTGATTTAACAGTGATAA	23743	SpyCas9-SpRY	16	0
146	GTA	TTTGGCTTCTCTGATAAGCA	23744	SpyCas9-SpRY	16	0
147	TAACTTT	GATCCTGATTTAACAGTGATAA	23745	CdiCas9	16	0
148	TAAC	TCCTGATTTAACAGTGATAA	23746	SpyCas9-3var-NRRH	16	0
149	TAAC	atCCTGATTTAACAGTGATAA	23747	iSpyMacCas9	16	0
150	AG	CTTTGGCTTCTCTGATAAGC	23748	SpyCas9-NG	17	0
151	AG	CTTTGGCTTCTCTGATAAGC	23749	SpyCas9-xCas	17	0
152	AG	CTTTGGCTTCTCTGATAAGC	23750	SpyCas9-xCas-NG	17	0
153	AGT	CTTTGGCTTCTCTGATAAGC	23751	SpyCas9-SpG	17	0
154	AGT	CTTTGGCTTCTCTGATAAGC	23752	SpyCas9-SpRY	17	0
155	ATA	ATCCTGATTTAACAGTGATA	23753	SpyCas9-SpRY	17	0

156	AGTACTGT	aagcTTTGGCTTCTCTGATAAGC	23754	BlatCas9	17	0
157	ATAACTTT	ctgaTCCTGATTTAACAGTGATA	23755	BlatCas9	17	0
158	AGTAC	aagcTTTGGCTTCTCTGATAAGC	23756	BlatCas9	17	0
159	ATAAC	ctgaTCCTGATTTAACAGTGATA	23757	BlatCas9	17	0
160	ATAACT	GATCCTGATTTAACAGTGATA	23758	cCas9-v16	17	0
161	ATAACT	GATCCTGATTTAACAGTGATA	23759	cCas9-v21	17	0
162	ATAACTT	TGATCCTGATTTAACAGTGATA	23760	CdiCas9	17	0
163	AGTA	CTTTGGCTTCTCTGATAAGC	23761	SpyCas9-3var-NRTH	17	0
164	AATAA	TGATCCTGATTTAACAGTGAT	23762	SauCas9KKH	18	0
165	CAG	GCTTTGGCTTCTCTGATAAG	23763	ScaCas9	18	0
166	CAG	GCTTTGGCTTCTCTGATAAG	23764	ScaCas9-HiFi-Sc++	18	0
167	CAG	GCTTTGGCTTCTCTGATAAG	23765	ScaCas9-Sc++	18	0
168	CAG	GCTTTGGCTTCTCTGATAAG	23766	SpyCas9-SpRY	18	0
169	AAT	GATCCTGATTTAACAGTGAT	23767	SpyCas9-SpRY	18	0
170	CAGTACT	AAGCTTTGGCTTCTCTGATAAG	23768	CdiCas9	18	0
171	CAGT	GCTTTGGCTTCTCTGATAAG	23769	SpyCas9-3var-NRRH	18	0
172	AATA	GATCCTGATTTAACAGTGAT	23770	SpyCas9-3var-NRTH	18	0
173	GCAG	AAGCTTTGGCTTCTCTGATAA	23771	SauriCas9-KKH	19	0
174	TAA	TGATCCTGATTTAACAGTGA	23772	SpyCas9-SpRY	19	0
175	GCA	AGCTTTGGCTTCTCTGATAA	23773	SpyCas9-SpRY	19	0
176	TAATAAC	ACTGATCCTGATTTAACAGTGA	23774	CdiCas9	19	0
177	TAAT	TGATCCTGATTTAACAGTGA	23775	SpyCas9-3var-NRRH	19	0
178	TAAT	ctGATCCTGATTTAACAGTGA	23776	iSpyMacCas9	19	0
179	AGCAG	GAAGCTTTGGCTTCTCTGATA	23777	SauCas9KKH	20	0
180	AGCAGT	GAAGCTTTGGCTTCTCTGATA	23778	SauCas9KKH	20	0
181	AGCAGT	GAAGCTTTGGCTTCTCTGATA	23779	cCas9-v17	20	0
182	AGCAGT	GAAGCTTTGGCTTCTCTGATA	23780	cCas9-v42	20	0
183	AG	AAGCTTTGGCTTCTCTGATA	23781	SpyCas9-NG	20	0
184	AG	AAGCTTTGGCTTCTCTGATA	23782	SpyCas9-xCas	20	0
185	AG	AAGCTTTGGCTTCTCTGATA	23783	SpyCas9-xCas-NG	20	0
186	AGC	AAGCTTTGGCTTCTCTGATA	23784	SpyCas9-SpG	20	0

187	AGC	AAGCTTTGGCTTCTCTGATA	23785	SpyCas9-SpRY	20	0
188	ATA	CTGATCCTGATTTAACAGTG	23786	SpyCas9-SpRY	20	0
189	AGCAGTAC	gaGAAGCTTTGGCTTCTCTGATA	23787	CjeCas9	20	0
190	AGCA	AAGCTTTGGCTTCTCTGATA	23788	SpyCas9-3var-NRCH	20	0
191	GATAA	TACTGATCCTGATTTAACAGT	23789	SauCas9KKH	21	0
192	GATAAT	TACTGATCCTGATTTAACAGT	23790	SauCas9KKH	21	0
193	AAG	GAAGCTTTGGCTTCTCTGAT	23791	ScaCas9	21	0
194	AAG	GAAGCTTTGGCTTCTCTGAT	23792	ScaCas9-HiFi-Sc++	21	0
195	AAG	GAAGCTTTGGCTTCTCTGAT	23793	ScaCas9-Sc++	21	0
196	AAG	GAAGCTTTGGCTTCTCTGAT	23794	SpyCas9-SpRY	21	0
197	GAT	ACTGATCCTGATTTAACAGT	23795	SpyCas9-SpRY	21	0
198	GAT	ACTGATCCTGATTTAACAGT	23796	SpyCas9-xCas	21	0
199	AAGC	GAAGCTTTGGCTTCTCTGAT	23797	SpyCas9-3var-NRRH	21	0
200	GATA	ACTGATCCTGATTTAACAGT	23798	SpyCas9-3var-NRTH	21	0
201	TAAG	GAGAAGCTTTGGCTTCTCTGA	23799	SauriCas9-KKH	22	0
202	TAAG	AGAAGCTTTGGCTTCTCTGA	23800	SpyCas9-QQR1	22	0
203	TAAG	gaGAAGCTTTGGCTTCTCTGA	23801	iSpyMacCas9	22	0
204	TG	TACTGATCCTGATTTAACAG	23802	SpyCas9-NG	22	0
205	TG	TACTGATCCTGATTTAACAG	23803	SpyCas9-xCas	22	0
206	TG	TACTGATCCTGATTTAACAG	23804	SpyCas9-xCas-NG	22	0
207	TAA	AGAAGCTTTGGCTTCTCTGA	23805	SpyCas9-SpRY	22	0
208	TGA	TACTGATCCTGATTTAACAG	23806	SpyCas9-SpG	22	0
209	TGA	TACTGATCCTGATTTAACAG	23807	SpyCas9-SpRY	22	0
210	TAAGCAGT	gggaGAAGCTTTGGCTTCTCTGA	23808	BlatCas9	22	0
211	TAAGC	gggaGAAGCTTTGGCTTCTCTGA	23809	BlatCas9	22	0
212	TGATAAT	AATACTGATCCTGATTTAACAG	23810	CdiCas9	22	0
213	TGAT	TACTGATCCTGATTTAACAG	23811	SpyCas9-3var-NRRH	22	0
214	TGAT	TACTGATCCTGATTTAACAG	23812	SpyCas9-VQR	22	0

215	ATAAG	GGAGAAGCTTTGGCTTCTCTG	23813	SauCas9KKH	23	0
216	GTG	ATACTGATCCTGATTTAACA	23814	ScaCas9	23	0
217	GTG	ATACTGATCCTGATTTAACA	23815	ScaCas9-HiFi-Sc++	23	0
218	GTG	ATACTGATCCTGATTTAACA	23816	ScaCas9-Sc++	23	0
219	GTG	ATACTGATCCTGATTTAACA	23817	SpyCas9-SpRY	23	0
220	ATA	GAGAAGCTTTGGCTTCTCTG	23818	SpyCas9-SpRY	23	0
221	ATAAGC	GGAGAAGCTTTGGCTTCTCTG	23819	cCas9-v17	23	0
222	ATAAGC	GGAGAAGCTTTGGCTTCTCTG	23820	cCas9-v42	23	0
223	GATAA	GGGAGAAGCTTTGGCTTCTCT	23821	SauCas9KKH	24	0
224	AGTGA	GAATACTGATCCTGATTTAAC	23822	SauCas9KKH	24	0
225	AGTGAT	GAATACTGATCCTGATTTAAC	23823	SauCas9KKH	24	0
226	AG	AATACTGATCCTGATTTAAC	23824	SpyCas9-NG	24	0
227	AG	AATACTGATCCTGATTTAAC	23825	SpyCas9-xCas	24	0
228	AG	AATACTGATCCTGATTTAAC	23826	SpyCas9-xCas-NG	24	0
229	GAT	GGAGAAGCTTTGGCTTCTCT	23827	SpyCas9-SpRY	24	0
230	GAT	GGAGAAGCTTTGGCTTCTCT	23828	SpyCas9-xCas	24	0
231	AGT	AATACTGATCCTGATTTAAC	23829	SpyCas9-SpG	24	0
232	AGT	AATACTGATCCTGATTTAAC	23830	SpyCas9-SpRY	24	0
233	GATA	GGAGAAGCTTTGGCTTCTCT	23831	SpyCas9-3var-NRTH	24	0
234	CAG	GAATACTGATCCTGATTTAA	23832	ScaCas9	25	0
235	CAG	GAATACTGATCCTGATTTAA	23833	ScaCas9-HiFi-Sc++	25	0
236	CAG	GAATACTGATCCTGATTTAA	23834	ScaCas9-Sc++	25	0
237	CAG	GAATACTGATCCTGATTTAA	23835	SpyCas9-SpRY	25	0
238	TG	GGGAGAAGCTTTGGCTTCTC	23836	SpyCas9-NG	25	0
239	TG	GGGAGAAGCTTTGGCTTCTC	23837	SpyCas9-xCas	25	0
240	TG	GGGAGAAGCTTTGGCTTCTC	23838	SpyCas9-xCas-NG	25	0
241	TGA	GGGAGAAGCTTTGGCTTCTC	23839	SpyCas9-SpG	25	0
242	TGA	GGGAGAAGCTTTGGCTTCTC	23840	SpyCas9-SpRY	25	0
243	CAGTGATA	caggGAATACTGATCCTGATTTAA	23841	NmeCas9	25	0

244	TGAT	GGGAGAAGCTTTGGCTTCTC	23842	SpyCas9-3var-NRRH	25	0
245	TGAT	GGGAGAAGCTTTGGCTTCTC	23843	SpyCas9-VQR	25	0
246	CAGT	GAATACTGATCCTGATTTAA	23844	SpyCas9-3var-NRRH	25	0
247	ACAG	GGGAATACTGATCCTGATTTA	23845	SauriCas9-KKH	26	0
248	CTG	GGGGAGAAGCTTTGGCTTCT	23846	ScaCas9	26	0
249	CTG	GGGGAGAAGCTTTGGCTTCT	23847	ScaCas9-HiFi-Sc++	26	0
250	CTG	GGGGAGAAGCTTTGGCTTCT	23848	ScaCas9-Sc++	26	0
251	CTG	GGGGAGAAGCTTTGGCTTCT	23849	SpyCas9-SpRY	26	0
252	ACA	GGAATACTGATCCTGATTTA	23850	SpyCas9-SpRY	26	0
253	ACAGTG	GGGAATACTGATCCTGATTTA	23851	cCas9-v16	26	0
254	ACAGTG	GGGAATACTGATCCTGATTTA	23852	cCas9-v21	26	0
255	TCTGA	AGGGGGAGAAGCTTTGGCTTC	23853	SauCas9KKH	27	0
256	AACAG	AGGGAATACTGATCCTGATTT	23854	SauCas9KKH	27	0
257	TCTGAT	AGGGGGAGAAGCTTTGGCTTC	23855	SauCas9KKH	27	0
258	AACAGT	AGGGAATACTGATCCTGATTT	23856	SauCas9KKH	27	0
259	AACAGT	AGGGAATACTGATCCTGATTT	23857	cCas9-v17	27	0
260	AACAGT	AGGGAATACTGATCCTGATTT	23858	cCas9-v42	27	0
261	AAC	GGGAATACTGATCCTGATTT	23859	SpyCas9-SpRY	27	0
262	TCT	GGGGGAGAAGCTTTGGCTTC	23860	SpyCas9-SpRY	27	0
263	AACA	GGGAATACTGATCCTGATTT	23861	SpyCas9-3var-NRCH	27	0
264	TAA	AGGGAATACTGATCCTGATT	23862	SpyCas9-SpRY	28	0
265	CTC	AGGGGGAGAAGCTTTGGCTT	23863	SpyCas9-SpRY	28	0
266	TAAC	AGGGAATACTGATCCTGATT	23864	SpyCas9-3var-NRRH	28	0
267	TAAC	caGGGAATACTGATCCTGATT	23865	iSpyMacCas9	28	0
268	CTCTGATA	ctccAGGGGGAGAAGCTTTGGCTT	23866	NmeCas9	28	0
269	TCT	CAGGGGGAGAAGCTTTGGCT	23867	SpyCas9-SpRY	29	0
270	TTA	CAGGGAATACTGATCCTGAT	23868	SpyCas9-SpRY	29	0
271	TTAACAGT	cagcAGGGAATACTGATCCTGAT	23869	BlatCas9	29	0
272	TTAAC	cagcAGGGAATACTGATCCTGAT	23870	BlatCas9	29	0

273	TTTAA	AGCAGGGAATACTGATCCTGA	23871	SauCas9KKH	30	0
274	TTC	CCAGGGGGAGAAGCTTTGGC	23872	SpyCas9-SpRY	30	0
275	TTT	GCAGGGAATACTGATCCTGA	23873	SpyCas9-SpRY	30	0
276	TTCTCTGA	gctcCAGGGGGAGAAGCTTTGGC	23874	BlatCas9	30	0
277	TTCTC	gctcCAGGGGGAGAAGCTTTGGC	23875	BlatCas9	30	0
278	CTT	TCCAGGGGGAGAAGCTTTGG	23876	SpyCas9-SpRY	31	0
279	ATT	AGCAGGGAATACTGATCCTG	23877	SpyCas9-SpRY	31	0
280	GAT	CAGCAGGGAATACTGATCCT	23878	SpyCas9-SpRY	32	0
281	GAT	CAGCAGGGAATACTGATCCT	23879	SpyCas9-xCas	32	0
282	GCT	CTCCAGGGGGAGAAGCTTTG	23880	SpyCas9-SpRY	32	0
283	GCTTC	cagcTCCAGGGGGAGAAGCTTTG	23881	BlatCas9	32	0
284	GATT	CAGCAGGGAATACTGATCCT	23882	SpyCas9-3var-NRTH	32	0
285	GG	GCTCCAGGGGGAGAAGCTTT	23883	SpyCas9-NG	33	0
286	GG	GCTCCAGGGGGAGAAGCTTT	23884	SpyCas9-xCas	33	0
287	GG	GCTCCAGGGGGAGAAGCTTT	23885	SpyCas9-xCas-NG	33	0
288	TG	GCAGCAGGGAATACTGATCC	23886	SpyCas9-NG	33	0
289	TG	GCAGCAGGGAATACTGATCC	23887	SpyCas9-xCas	33	0
290	TG	GCAGCAGGGAATACTGATCC	23888	SpyCas9-xCas-NG	33	0
291	GGC	GCTCCAGGGGGAGAAGCTTT	23889	SpyCas9-SpG	33	0
292	GGC	GCTCCAGGGGGAGAAGCTTT	23890	SpyCas9-SpRY	33	0
293	TGA	GCAGCAGGGAATACTGATCC	23891	SpyCas9-SpG	33	0
294	TGA	GCAGCAGGGAATACTGATCC	23892	SpyCas9-SpRY	33	0
295	TGAT	GCAGCAGGGAATACTGATCC	23893	SpyCas9-3var-NRRH	33	0
296	TGAT	GCAGCAGGGAATACTGATCC	23894	SpyCas9-VQR	33	0
297	GGCT	GCTCCAGGGGGAGAAGCTTT	23895	SpyCas9-3var-NRCH	33	0
298	TGG	AGCTCCAGGGGGAGAAGCTT	23896	ScaCas9	34	0
299	TGG	AGCTCCAGGGGGAGAAGCTT	23897	ScaCas9-HiFi-Sc++	34	0
300	TGG	AGCTCCAGGGGGAGAAGCTT	23898	ScaCas9-Sc++	34	0
301	TGG	AGCTCCAGGGGGAGAAGCTT	23899	SpyCas9	34	0

302	TGG	AGCTCCAGGGGGAGAAGCTT	23900	SpyCas9-HF1	34	0
303	TGG	AGCTCCAGGGGGAGAAGCTT	23901	SpyCas9-SpG	34	0
304	TGG	AGCTCCAGGGGGAGAAGCTT	23902	SpyCas9-SpRY	34	0
305	CTG	TGCAGCAGGGAATACTGATC	23903	ScaCas9	34	0
306	CTG	TGCAGCAGGGAATACTGATC	23904	ScaCas9-HiFi-Sc++	34	0
307	CTG	TGCAGCAGGGAATACTGATC	23905	ScaCas9-Sc++	34	0
308	CTG	TGCAGCAGGGAATACTGATC	23906	SpyCas9-SpRY	34	0
309	TG	AGCTCCAGGGGGAGAAGCTT	23907	SpyCas9-NG	34	0
310	TG	AGCTCCAGGGGGAGAAGCTT	23908	SpyCas9-xCas	34	0
311	TG	AGCTCCAGGGGGAGAAGCTT	23909	SpyCas9-xCas-NG	34	0
312	CTGATT	ATGCAGCAGGGAATACTGATC	23910	cCas9-v16	34	0
313	CTGATT	ATGCAGCAGGGAATACTGATC	23911	cCas9-v21	34	0
314	TGGCTTC	CCAGCTCCAGGGGGAGAAGCTT	23912	CdiCas9	34	0
315	CTGATTT	GATGCAGCAGGGAATACTGATC	23913	CdiCas9	34	0
316	TGGC	AGCTCCAGGGGGAGAAGCTT	23914	SpyCas9-3var-NRRH	34	0
317	CCTGATT	tggGATGCAGCAGGGAATACTGAT	23915	PpnCas9	35	0
318	CCTGA	GATGCAGCAGGGAATACTGAT	23916	SauCas9KKH	35	0
319	CCTGAT	GATGCAGCAGGGAATACTGAT	23917	SauCas9KKH	35	0
320	TTGG	CCAGCTCCAGGGGGAGAAGCT	23918	SauriCas9	35	0
321	TTGG	CCAGCTCCAGGGGGAGAAGCT	23919	SauriCas9-KKH	35	0
322	TTG	CAGCTCCAGGGGGAGAAGCT	23920	ScaCas9	35	0
323	TTG	CAGCTCCAGGGGGAGAAGCT	23921	ScaCas9-HiFi-Sc++	35	0
324	TTG	CAGCTCCAGGGGGAGAAGCT	23922	ScaCas9-Sc++	35	0
325	TTG	CAGCTCCAGGGGGAGAAGCT	23923	SpyCas9-SpRY	35	0
326	CCT	ATGCAGCAGGGAATACTGAT	23924	SpyCas9-SpRY	35	0
327	TTGGC	ctccAGCTCCAGGGGGAGAAGCT	23925	BlatCas9	35	0
328	TTGGCT	CCAGCTCCAGGGGGAGAAGCT	23926	cCas9-v16	35	0
329	TTGGCT	CCAGCTCCAGGGGGAGAAGCT	23927	cCas9-v21	35	0
330	TTTGG	TCCAGCTCCAGGGGGAGAAGC	23928	SauCas9KKH	36	0
331	TTT	CCAGCTCCAGGGGGAGAAGC	23929	SpyCas9-SpRY	36	0

332	TCC	GATGCAGCAGGGAATACTGA	23930	SpyCas9-SpRY	36	0
333	TCCTGATT	atggGATGCAGCAGGGAATACTGA	23931	NmeCas9	36	0
334	TTTGGCTT	ttctCCAGCTCCAGGGGGAGAAGC	23932	NmeCas9	36	0
335	CTT	TCCAGCTCCAGGGGGAGAAG	23933	SpyCas9-SpRY	37	0
336	ATC	GGATGCAGCAGGGAATACTG	23934	SpyCas9-SpRY	37	0
337	GAT	GGGATGCAGCAGGGAATACT	23935	SpyCas9-SpRY	38	0
338	GAT	GGGATGCAGCAGGGAATACT	23936	SpyCas9-xCas	38	0
339	GCT	CTCCAGCTCCAGGGGGAGAA	23937	SpyCas9-SpRY	38	0
340	GATCCTGA	tatgGGATGCAGCAGGGAATACT	23938	BlatCas9	38	0
341	GATCC	tatgGGATGCAGCAGGGAATACT	23939	BlatCas9	38	0
342	GATC	GGGATGCAGCAGGGAATACT	23940	SpyCas9-3var-NRTH	38	0
343	TGATCC	ccTATGGGATGCAGCAGGGAATAC	23941	Nme2Cas9	39	0
344	AG	TCTCCAGCTCCAGGGGGAGA	23942	SpyCas9-NG	39	0
345	AG	TCTCCAGCTCCAGGGGGAGA	23943	SpyCas9-xCas	39	0
346	AG	TCTCCAGCTCCAGGGGGAGA	23944	SpyCas9-xCas-NG	39	0
347	TG	TGGGATGCAGCAGGGAATAC	23945	SpyCas9-NG	39	0
348	TG	TGGGATGCAGCAGGGAATAC	23946	SpyCas9-xCas	39	0
349	TG	TGGGATGCAGCAGGGAATAC	23947	SpyCas9-xCas-NG	39	0
350	AGC	TCTCCAGCTCCAGGGGGAGA	23948	SpyCas9-SpG	39	0
351	AGC	TCTCCAGCTCCAGGGGGAGA	23949	SpyCas9-SpRY	39	0
352	TGA	TGGGATGCAGCAGGGAATAC	23950	SpyCas9-SpG	39	0
353	TGA	TGGGATGCAGCAGGGAATAC	23951	SpyCas9-SpRY	39	0
354	TGATCCTG	ctatGGGATGCAGCAGGGAATAC	23952	BlatCas9	39	0
355	TGATC	ctatGGGATGCAGCAGGGAATAC	23953	BlatCas9	39	0
356	TGATCCT	TATGGGATGCAGCAGGGAATAC	23954	CdiCas9	39	0
357	TGAT	TGGGATGCAGCAGGGAATAC	23955	SpyCas9-3var-NRRH	39	0
358	TGAT	TGGGATGCAGCAGGGAATAC	23956	SpyCas9-VQR	39	0
359	AGCT	TCTCCAGCTCCAGGGGGAGA	23957	SpyCas9-3var-NRCH	39	0
360	AAG	TTCTCCAGCTCCAGGGGGAG	23958	ScaCas9	40	0
361	AAG	TTCTCCAGCTCCAGGGGGAG	23959	ScaCas9-HiFi-Sc++	40	0

362	AAG	TTCTCCAGCTCCAGGGGGAG	23960	ScaCas9-Sc++	40	0
363	AAG	TTCTCCAGCTCCAGGGGGAG	23961	SpyCas9-SpRY	40	0
364	CTG	ATGGGATGCAGCAGGGAATA	23962	ScaCas9	40	0
365	CTG	ATGGGATGCAGCAGGGAATA	23963	ScaCas9-HiFi-Sc++	40	0
366	CTG	ATGGGATGCAGCAGGGAATA	23964	ScaCas9-Sc++	40	0
367	CTG	ATGGGATGCAGCAGGGAATA	23965	SpyCas9-SpRY	40	0
368	AAGCTTT	TCTTCTCCAGCTCCAGGGGGAG	23966	CdiCas9	40	0
369	CTGATCC	CTATGGGATGCAGCAGGGAATA	23967	CdiCas9	40	0
370	AAGC	TTCTCCAGCTCCAGGGGGAG	23968	SpyCas9-3var-NRRH	40	0
371	ACTGA	CTATGGGATGCAGCAGGGAAT	23969	SauCas9KKH	41	0
372	ACTGAT	CTATGGGATGCAGCAGGGAAT	23970	SauCas9KKH	41	0
373	GAAG	TCTTCTCCAGCTCCAGGGGGA	23971	SauriCas9-KKH	41	0
374	GAAG	CTTCTCCAGCTCCAGGGGGA	23972	SpyCas9-QQR1	41	0
375	GAAG	tcTTCTCCAGCTCCAGGGGGA	23973	iSpyMacCas9	41	0
376	GAA	CTTCTCCAGCTCCAGGGGGA	23974	SpyCas9-SpRY	41	0
377	GAA	CTTCTCCAGCTCCAGGGGGA	23975	SpyCas9-xCas	41	0
378	ACT	TATGGGATGCAGCAGGGAAT	23976	SpyCas9-SpRY	41	0
379	GAAGCTT	tgtcTTCTCCAGCTCCAGGGGGA	23977	BlatCas9	41	0
380	GAAGC	tgtcTTCTCCAGCTCCAGGGGGA	23978	BlatCas9	41	0
381	GAAGCT	TCTTCTCCAGCTCCAGGGGGA	23979	cCas9-v16	41	0
382	GAAGCT	TCTTCTCCAGCTCCAGGGGGA	23980	cCas9-v21	41	0
383	AGAAG	GTCTTCTCCAGCTCCAGGGGG	23981	SauCas9KKH	42	0
384	AG	TCTTCTCCAGCTCCAGGGGG	23982	SpyCas9-NG	42	0
385	AG	TCTTCTCCAGCTCCAGGGGG	23983	SpyCas9-xCas	42	0
386	AG	TCTTCTCCAGCTCCAGGGGG	23984	SpyCas9-xCas-NG	42	0
387	AGA	TCTTCTCCAGCTCCAGGGGG	23985	SpyCas9-SpG	42	0
388	AGA	TCTTCTCCAGCTCCAGGGGG	23986	SpyCas9-SpRY	42	0
389	TAC	CTATGGGATGCAGCAGGGAA	23987	SpyCas9-SpRY	42	0
390	AGAAGC	GTCTTCTCCAGCTCCAGGGGG	23988	cCas9-v17	42	0
391	AGAAGC	GTCTTCTCCAGCTCCAGGGGG	23989	cCas9-v42	42	0

392	AGAAGCTT	gctgTCTTCTCCAGCTCCAGGGGG	23990	NmeCas9	42	0
393	AGAA	TCTTCTCCAGCTCCAGGGGG	23991	SpyCas9-3var-NRRH	42	0
394	AGAA	TCTTCTCCAGCTCCAGGGGG	23992	SpyCas9-VQR	42	0
395	TACT	CTATGGGATGCAGCAGGGAA	23993	SpyCas9-3var-NRCH	42	0
396	GAGAA	gcTGTCTTCTCCAGCTCCAGGGG	23994	SauCas9	43	0
397	GAGAA	TGTCTTCTCCAGCTCCAGGGG	23995	SauCas9KKH	43	0
398	GAG	GTCTTCTCCAGCTCCAGGGG	23996	ScaCas9	43	0
399	GAG	GTCTTCTCCAGCTCCAGGGG	23997	ScaCas9-HiFi-Sc++	43	0
400	GAG	GTCTTCTCCAGCTCCAGGGG	23998	ScaCas9-Sc++	43	0
401	GAG	GTCTTCTCCAGCTCCAGGGG	23999	SpyCas9-SpRY	43	0
402	ATA	CCTATGGGATGCAGCAGGGA	24000	SpyCas9-SpRY	43	0
403	GAGAAG	TGTCTTCTCCAGCTCCAGGGG	24001	cCas9-v17	43	0
404	GAGAAG	TGTCTTCTCCAGCTCCAGGGG	24002	cCas9-v42	43	0
405	GAGA	GTCTTCTCCAGCTCCAGGGG	24003	SpyCas9-3var-NRRH	43	0
406	GGAGA	CTGTCTTCTCCAGCTCCAGGG	24004	SauCas9KKH	44	0
407	GGAG	CTGTCTTCTCCAGCTCCAGGG	24005	SauriCas9-KKH	44	0
408	GGAG	TGTCTTCTCCAGCTCCAGGG	24006	SpyCas9-VQR	44	0
409	GG	TGTCTTCTCCAGCTCCAGGG	24007	SpyCas9-NG	44	0
410	GG	TGTCTTCTCCAGCTCCAGGG	24008	SpyCas9-xCas	44	0
411	GG	TGTCTTCTCCAGCTCCAGGG	24009	SpyCas9-xCas-NG	44	0
412	GGA	TGTCTTCTCCAGCTCCAGGG	24010	SpyCas9-SpG	44	0
413	GGA	TGTCTTCTCCAGCTCCAGGG	24011	SpyCas9-SpRY	44	0
414	AAT	GCCTATGGGATGCAGCAGGG	24012	SpyCas9-SpRY	44	0
415	AATACTGA	atggCCTATGGGATGCAGCAGGG	24013	BlatCas9	44	0
416	AATAC	atggCCTATGGGATGCAGCAGGG	24014	BlatCas9	44	0
417	GGAGAA	CTGTCTTCTCCAGCTCCAGGG	24015	cCas9-v17	44	0
418	GGAGAA	CTGTCTTCTCCAGCTCCAGGG	24016	cCas9-v42	44	0
419	AATA	GCCTATGGGATGCAGCAGGG	24017	SpyCas9-3var-NRTH	44	0
420	GGGAG	tgGCTGTCTTCTCCAGCTCCAGG	24018	SauCas9	45	0
421	GGGAG	GCTGTCTTCTCCAGCTCCAGG	24019	SauCas9KKH	45	0

422	GGG	CTGTCTTCTCCAGCTCCAGG	24020	ScaCas9	45	0
423	GGG	CTGTCTTCTCCAGCTCCAGG	24021	ScaCas9-HiFi-Sc++	45	0
424	GGG	CTGTCTTCTCCAGCTCCAGG	24022	ScaCas9-Sc++	45	0
425	GGG	CTGTCTTCTCCAGCTCCAGG	24023	SpyCas9	45	0
426	GGG	CTGTCTTCTCCAGCTCCAGG	24024	SpyCas9-HF1	45	0
427	GGG	CTGTCTTCTCCAGCTCCAGG	24025	SpyCas9-SpG	45	0
428	GGG	CTGTCTTCTCCAGCTCCAGG	24026	SpyCas9-SpRY	45	0
429	GG	CTGTCTTCTCCAGCTCCAGG	24027	SpyCas9-NG	45	0
430	GG	CTGTCTTCTCCAGCTCCAGG	24028	SpyCas9-xCas	45	0
431	GG	CTGTCTTCTCCAGCTCCAGG	24029	SpyCas9-xCas-NG	45	0
432	GAA	GGCCTATGGGATGCAGCAGG	24030	SpyCas9-SpRY	45	0
433	GAA	GGCCTATGGGATGCAGCAGG	24031	SpyCas9-xCas	45	0
434	GGGAGA	GCTGTCTTCTCCAGCTCCAGG	24032	cCas9-v17	45	0
435	GGGAGA	GCTGTCTTCTCCAGCTCCAGG	24033	cCas9-v42	45	0
436	GAATACT	ATGGCCTATGGGATGCAGCAGG	24034	CdiCas9	45	0
437	GAAT	GGCCTATGGGATGCAGCAGG	24035	SpyCas9-3var-NRRH	45	0
438	GAAT	tgGCCTATGGGATGCAGCAGG	24036	iSpyMacCas9	45	0
439	GGGA	CTGTCTTCTCCAGCTCCAGG	24037	SpyCas9-3var-NRRH	45	0
440	GGGGA	atGGCTGTCTTCTCCAGCTCCAG	24038	SauCas9	46	0
441	GGGGA	GGCTGTCTTCTCCAGCTCCAG	24039	SauCas9KKH	46	0
442	GGGG	GGCTGTCTTCTCCAGCTCCAG	24040	SauriCas9	46	0
443	GGGG	GGCTGTCTTCTCCAGCTCCAG	24041	SauriCas9-KKH	46	0
444	GGG	GCTGTCTTCTCCAGCTCCAG	24042	ScaCas9	46	0
445	GGG	GCTGTCTTCTCCAGCTCCAG	24043	ScaCas9-HiFi-Sc++	46	0
446	GGG	GCTGTCTTCTCCAGCTCCAG	24044	ScaCas9-Sc++	46	0
447	GGG	GCTGTCTTCTCCAGCTCCAG	24045	SpyCas9	46	0
448	GGG	GCTGTCTTCTCCAGCTCCAG	24046	SpyCas9-HF1	46	0
449	GGG	GCTGTCTTCTCCAGCTCCAG	24047	SpyCas9-SpG	46	0
450	GGG	GCTGTCTTCTCCAGCTCCAG	24048	SpyCas9-SpRY	46	0
451	GG	GCTGTCTTCTCCAGCTCCAG	24049	SpyCas9-NG	46	0

452	GG	GCTGTCTTCTCCAGCTCCAG	24050	SpyCas9-xCas	46	0
453	GG	GCTGTCTTCTCCAGCTCCAG	24051	SpyCas9-xCas-NG	46	0
454	GG	TGGCCTATGGGATGCAGCAG	24052	SpyCas9-NG	46	0
455	GG	TGGCCTATGGGATGCAGCAG	24053	SpyCas9-xCas	46	0
456	GG	TGGCCTATGGGATGCAGCAG	24054	SpyCas9-xCas-NG	46	0
457	GGA	TGGCCTATGGGATGCAGCAG	24055	SpyCas9-SpG	46	0
458	GGA	TGGCCTATGGGATGCAGCAG	24056	SpyCas9-SpRY	46	0
459	GGGGAG	GGCTGTCTTCTCCAGCTCCAG	24057	cCas9-v17	46	0
460	GGGGAG	GGCTGTCTTCTCCAGCTCCAG	24058	cCas9-v42	46	0
461	GGAATAC	AATGGCCTATGGGATGCAGCAG	24059	CdiCas9	46	0
462	GGAA	TGGCCTATGGGATGCAGCAG	24060	SpyCas9-3var-NRRH	46	0
463	GGAA	TGGCCTATGGGATGCAGCAG	24061	SpyCas9-VQR	46	0
464	GGGGG	gaTGGCTGTCTTCTCCAGCTCCA	24062	SauCas9	47	0
465	GGGGG	TGGCTGTCTTCTCCAGCTCCA	24063	SauCas9KKH	47	0
466	GGGAA	caAATGGCCTATGGGATGCAGCA	24064	SauCas9	47	0
467	GGGAA	AATGGCCTATGGGATGCAGCA	24065	SauCas9KKH	47	0
468	GGGAAT	caAATGGCCTATGGGATGCAGCA	24066	SauCas9	47	0
469	GGGAAT	AATGGCCTATGGGATGCAGCA	24067	SauCas9KKH	47	0
470	GGGAAT	AATGGCCTATGGGATGCAGCA	24068	cCas9-v17	47	0
471	GGGAAT	AATGGCCTATGGGATGCAGCA	24069	cCas9-v42	47	0
472	GGGG	TGGCTGTCTTCTCCAGCTCCA	24070	SauriCas9	47	0
473	GGGG	TGGCTGTCTTCTCCAGCTCCA	24071	SauriCas9-KKH	47	0
474	GGG	GGCTGTCTTCTCCAGCTCCA	24072	ScaCas9	47	0
475	GGG	GGCTGTCTTCTCCAGCTCCA	24073	ScaCas9-HiFi-Sc++	47	0
476	GGG	GGCTGTCTTCTCCAGCTCCA	24074	ScaCas9-Sc++	47	0
477	GGG	GGCTGTCTTCTCCAGCTCCA	24075	SpyCas9	47	0
478	GGG	GGCTGTCTTCTCCAGCTCCA	24076	SpyCas9-HF1	47	0
479	GGG	GGCTGTCTTCTCCAGCTCCA	24077	SpyCas9-SpG	47	0
480	GGG	GGCTGTCTTCTCCAGCTCCA	24078	SpyCas9-SpRY	47	0
481	GGG	ATGGCCTATGGGATGCAGCA	24079	ScaCas9	47	0
482	GGG	ATGGCCTATGGGATGCAGCA	24080	ScaCas9-HiFi-Sc++	47	0

483	GGG	ATGGCCTATGGGATGCAGCA	24081	ScaCas9-Sc++	47	0
484	GGG	ATGGCCTATGGGATGCAGCA	24082	SpyCas9	47	0
485	GGG	ATGGCCTATGGGATGCAGCA	24083	SpyCas9-HF1	47	0
486	GGG	ATGGCCTATGGGATGCAGCA	24084	SpyCas9-SpG	47	0
487	GGG	ATGGCCTATGGGATGCAGCA	24085	SpyCas9-SpRY	47	0
488	GG	GGCTGTCTTCTCCAGCTCCA	24086	SpyCas9-NG	47	0
489	GG	GGCTGTCTTCTCCAGCTCCA	24087	SpyCas9-xCas	47	0
490	GG	GGCTGTCTTCTCCAGCTCCA	24088	SpyCas9-xCas-NG	47	0
491	GG	ATGGCCTATGGGATGCAGCA	24089	SpyCas9-NG	47	0
492	GG	ATGGCCTATGGGATGCAGCA	24090	SpyCas9-xCas	47	0
493	GG	ATGGCCTATGGGATGCAGCA	24091	SpyCas9-xCas-NG	47	0
494	GGGGGA	TGGCTGTCTTCTCCAGCTCCA	24092	cCas9-v17	47	0
495	GGGGGA	TGGCTGTCTTCTCCAGCTCCA	24093	cCas9-v42	47	0
496	GGGAATAC	caAATGGCCTATGGGATGCAGCA	24094	CjeCas9	47	0
497	GGGA	ATGGCCTATGGGATGCAGCA	24095	SpyCas9-3var-NRRH	47	0
498	AGGGG	ggATGGCTGTCTTCTCCAGCTCC	24096	SauCas9	48	0
499	AGGGG	ATGGCTGTCTTCTCCAGCTCC	24097	SauCas9KKH	48	0
500	AGGGA	acAAATGGCCTATGGGATGCAGC	24098	SauCas9	48	0
501	AGGGA	AAATGGCCTATGGGATGCAGC	24099	SauCas9KKH	48	0
502	AGGG	ATGGCTGTCTTCTCCAGCTCC	24100	SauriCas9	48	0
503	AGGG	ATGGCTGTCTTCTCCAGCTCC	24101	SauriCas9-KKH	48	0
504	AGGG	AAATGGCCTATGGGATGCAGC	24102	SauriCas9	48	0
505	AGGG	AAATGGCCTATGGGATGCAGC	24103	SauriCas9-KKH	48	0
506	AGG	TGGCTGTCTTCTCCAGCTCC	24104	ScaCas9	48	0
507	AGG	TGGCTGTCTTCTCCAGCTCC	24105	ScaCas9-HiFi-Sc++	48	0
508	AGG	TGGCTGTCTTCTCCAGCTCC	24106	ScaCas9-Sc++	48	0
509	AGG	TGGCTGTCTTCTCCAGCTCC	24107	SpyCas9	48	0
510	AGG	TGGCTGTCTTCTCCAGCTCC	24108	SpyCas9-HF1	48	0
511	AGG	TGGCTGTCTTCTCCAGCTCC	24109	SpyCas9-SpG	48	0
512	AGG	TGGCTGTCTTCTCCAGCTCC	24110	SpyCas9-SpRY	48	0
513	AGG	AATGGCCTATGGGATGCAGC	24111	ScaCas9	48	0

514	AGG	AATGGCCTATGGGATGCAGC	24112	ScaCas9-HiFi-Sc++	48	0
515	AGG	AATGGCCTATGGGATGCAGC	24113	ScaCas9-Sc++	48	0
516	AGG	AATGGCCTATGGGATGCAGC	24114	SpyCas9	48	0
517	AGG	AATGGCCTATGGGATGCAGC	24115	SpyCas9-HF1	48	0
518	AGG	AATGGCCTATGGGATGCAGC	24116	SpyCas9-SpG	48	0
519	AGG	AATGGCCTATGGGATGCAGC	24117	SpyCas9-SpRY	48	0
520	AG	TGGCTGTCTTCTCCAGCTCC	24118	SpyCas9-NG	48	0
521	AG	TGGCTGTCTTCTCCAGCTCC	24119	SpyCas9-xCas	48	0
522	AG	TGGCTGTCTTCTCCAGCTCC	24120	SpyCas9-xCas-NG	48	0
523	AG	AATGGCCTATGGGATGCAGC	24121	SpyCas9-NG	48	0
524	AG	AATGGCCTATGGGATGCAGC	24122	SpyCas9-xCas	48	0
525	AG	AATGGCCTATGGGATGCAGC	24123	SpyCas9-xCas-NG	48	0
526	AGGGAAT	AATGGCCTATGGGATGCAGC	24124	St1Cas9	48	0
527	AGGGGG	ATGGCTGTCTTCTCCAGCTCC	24125	cCas9-v17	48	0
528	AGGGGG	ATGGCTGTCTTCTCCAGCTCC	24126	cCas9-v42	48	0
529	AGGGAA	AAATGGCCTATGGGATGCAGC	24127	cCas9-v17	48	0
530	AGGGAA	AAATGGCCTATGGGATGCAGC	24128	cCas9-v42	48	0
531	CAGGG	tgGATGGCTGTCTTCTCCAGCTC	24129	SauCas9	49	0
532	CAGGG	GATGGCTGTCTTCTCCAGCTC	24130	SauCas9KKH	49	0
533	CAGGG	caCAAATGGCCTATGGGATGCAG	24131	SauCas9	49	0
534	CAGGG	CAAATGGCCTATGGGATGCAG	24132	SauCas9KKH	49	0
535	CAGG	GATGGCTGTCTTCTCCAGCTC	24133	SauriCas9	49	0
536	CAGG	GATGGCTGTCTTCTCCAGCTC	24134	SauriCas9-KKH	49	0
537	CAGG	CAAATGGCCTATGGGATGCAG	24135	SauriCas9	49	0
538	CAGG	CAAATGGCCTATGGGATGCAG	24136	SauriCas9-KKH	49	0
539	CAG	ATGGCTGTCTTCTCCAGCTC	24137	ScaCas9	49	0
540	CAG	ATGGCTGTCTTCTCCAGCTC	24138	ScaCas9-HiFi-Sc++	49	0
541	CAG	ATGGCTGTCTTCTCCAGCTC	24139	ScaCas9-Sc++	49	0
542	CAG	ATGGCTGTCTTCTCCAGCTC	24140	SpyCas9-SpRY	49	0
543	CAG	AAATGGCCTATGGGATGCAG	24141	ScaCas9	49	0
544	CAG	AAATGGCCTATGGGATGCAG	24142	ScaCas9-HiFi-Sc++	49	0

545	CAG	AAATGGCCTATGGGATGCAG	24143	ScaCas9-Sc++	49	0
546	CAG	AAATGGCCTATGGGATGCAG	24144	SpyCas9-SpRY	49	0
547	CAGGGG	GATGGCTGTCTTCTCCAGCTC	24145	cCas9-v17	49	0
548	CAGGGG	GATGGCTGTCTTCTCCAGCTC	24146	cCas9-v42	49	0
549	CAGGGA	CAAATGGCCTATGGGATGCAG	24147	cCas9-v17	49	0
550	CAGGGA	CAAATGGCCTATGGGATGCAG	24148	cCas9-v42	49	0
551	CCAGG	GGATGGCTGTCTTCTCCAGCT	24149	SauCas9KKH	50	0
552	GCAGG	ACAAATGGCCTATGGGATGCA	24150	SauCas9KKH	50	0
553	CCAG	GGATGGCTGTCTTCTCCAGCT	24151	SauriCas9-KKH	50	0
554	GCAG	ACAAATGGCCTATGGGATGCA	24152	SauriCas9-KKH	50	0
555	CCA	GATGGCTGTCTTCTCCAGCT	24153	SpyCas9-SpRY	50	0
556	GCA	CAAATGGCCTATGGGATGCA	24154	SpyCas9-SpRY	50	0
557	CCAGGG	GGATGGCTGTCTTCTCCAGCT	24155	cCas9-v17	50	0
558	CCAGGG	GGATGGCTGTCTTCTCCAGCT	24156	cCas9-v42	50	0
559	GCAGGG	ACAAATGGCCTATGGGATGCA	24157	cCas9-v17	50	0
560	GCAGGG	ACAAATGGCCTATGGGATGCA	24158	cCas9-v42	50	0
561	TCCAG	TGGATGGCTGTCTTCTCCAGC	24159	SauCas9KKH	51	0
562	AGCAG	CACAAATGGCCTATGGGATGC	24160	SauCas9KKH	51	0
563	AG	ACAAATGGCCTATGGGATGC	24161	SpyCas9-NG	51	0
564	AG	ACAAATGGCCTATGGGATGC	24162	SpyCas9-xCas	51	0
565	AG	ACAAATGGCCTATGGGATGC	24163	SpyCas9-xCas-NG	51	0
566	AGC	ACAAATGGCCTATGGGATGC	24164	SpyCas9-SpG	51	0
567	AGC	ACAAATGGCCTATGGGATGC	24165	SpyCas9-SpRY	51	0
568	TCC	GGATGGCTGTCTTCTCCAGC	24166	SpyCas9-SpRY	51	0
569	TCCAGG	TGGATGGCTGTCTTCTCCAGC	24167	cCas9-v17	51	0
570	TCCAGG	TGGATGGCTGTCTTCTCCAGC	24168	cCas9-v42	51	0
571	AGCAGG	CACAAATGGCCTATGGGATGC	24169	cCas9-v17	51	0
572	AGCAGG	CACAAATGGCCTATGGGATGC	24170	cCas9-v42	51	0
573	AGCA	ACAAATGGCCTATGGGATGC	24171	SpyCas9-3var-NRCH	51	0
574	CAG	CACAAATGGCCTATGGGATG	24172	ScaCas9	52	0
575	CAG	CACAAATGGCCTATGGGATG	24173	ScaCas9-HiFi-Sc++	52	0

576	CAG	CACAAATGGCCTATGGGATG	24174	ScaCas9-Sc++	52	0
577	CAG	CACAAATGGCCTATGGGATG	24175	SpyCas9-SpRY	52	0
578	CTC	TGGATGGCTGTCTTCTCCAG	24176	SpyCas9-SpRY	52	0
579	CAGC	CACAAATGGCCTATGGGATG	24177	SpyCas9-3var-NRRH	52	0
580	GCAG	GGCACAAATGGCCTATGGGAT	24178	SauriCas9-KKH	53	0
581	GCT	TTGGATGGCTGTCTTCTCCA	24179	SpyCas9-SpRY	53	0
582	GCA	GCACAAATGGCCTATGGGAT	24180	SpyCas9-SpRY	53	0
583	GCTCCAGG	atttTGGATGGCTGTCTTCTCCA	24181	BlatCas9	53	0
584	GCAGCAGG	ggggCACAAATGGCCTATGGGAT	24182	BlatCas9	53	0
585	GCTCC	atttTGGATGGCTGTCTTCTCCA	24183	BlatCas9	53	0
586	GCAGC	ggggCACAAATGGCCTATGGGAT	24184	BlatCas9	53	0
587	AGCTCC	taATTTTGGATGGCTGTCTTCTCC	24185	Nme2Cas9	54	0
588	TGCAG	GGGCACAAATGGCCTATGGGA	24186	SauCas9KKH	54	0
589	AG	TTTGGATGGCTGTCTTCTCC	24187	SpyCas9-NG	54	0
590	AG	TTTGGATGGCTGTCTTCTCC	24188	SpyCas9-xCas	54	0
591	AG	TTTGGATGGCTGTCTTCTCC	24189	SpyCas9-xCas-NG	54	0
592	TG	GGCACAAATGGCCTATGGGA	24190	SpyCas9-NG	54	0
593	TG	GGCACAAATGGCCTATGGGA	24191	SpyCas9-xCas	54	0
594	TG	GGCACAAATGGCCTATGGGA	24192	SpyCas9-xCas-NG	54	0
595	AGC	TTTGGATGGCTGTCTTCTCC	24193	SpyCas9-SpG	54	0
596	AGC	TTTGGATGGCTGTCTTCTCC	24194	SpyCas9-SpRY	54	0
597	TGC	GGCACAAATGGCCTATGGGA	24195	SpyCas9-SpG	54	0
598	TGC	GGCACAAATGGCCTATGGGA	24196	SpyCas9-SpRY	54	0
599	AGCTCCAG	aattTTGGATGGCTGTCTTCTCC	24197	BlatCas9	54	0
600	AGCTC	aattTTGGATGGCTGTCTTCTCC	24198	BlatCas9	54	0
601	TGCAGC	GGGCACAAATGGCCTATGGGA	24199	cCas9-v17	54	0
602	TGCAGC	GGGCACAAATGGCCTATGGGA	24200	cCas9-v42	54	0
603	AGCT	TTTGGATGGCTGTCTTCTCC	24201	SpyCas9-3var-NRCH	54	0
604	TGCA	GGCACAAATGGCCTATGGGA	24202	SpyCas9-3var-NRCH	54	0
605	CAG	TTTTGGATGGCTGTCTTCTC	24203	ScaCas9	55	0

606	CAG	TTTTGGATGGCTGTCTTCTC	24204	ScaCas9-HiFi-Sc++	55	0
607	CAG	TTTTGGATGGCTGTCTTCTC	24205	ScaCas9-Sc++	55	0
608	CAG	TTTTGGATGGCTGTCTTCTC	24206	SpyCas9-SpRY	55	0
609	ATG	GGGCACAAATGGCCTATGGG	24207	ScaCas9	55	0
610	ATG	GGGCACAAATGGCCTATGGG	24208	ScaCas9-HiFi-Sc++	55	0
611	ATG	GGGCACAAATGGCCTATGGG	24209	ScaCas9-Sc++	55	0
612	ATG	GGGCACAAATGGCCTATGGG	24210	SpyCas9-SpRY	55	0
613	CAGCTCC	AATTTTGGATGGCTGTCTTCTC	24211	CdiCas9	55	0
614	CAGC	TTTTGGATGGCTGTCTTCTC	24212	SpyCas9-3var-NRRH	55	0
615	CCAG	AATTTTGGATGGCTGTCTTCT	24213	SauriCas9-KKH	56	0
616	GAT	GGGGCACAAATGGCCTATGG	24214	SpyCas9-SpRY	56	0
617	GAT	GGGGCACAAATGGCCTATGG	24215	SpyCas9-xCas	56	0
618	CCA	ATTTTGGATGGCTGTCTTCT	24216	SpyCas9-SpRY	56	0
619	CCAGC	gtaaTTTTGGATGGCTGTCTTCT	24217	BlatCas9	56	0
620	GATGC	gaagGGGCACAAATGGCCTATGG	24218	BlatCas9	56	0
621	CCAGCT	AATTTTGGATGGCTGTCTTCT	24219	cCas9-v16	56	0
622	CCAGCT	AATTTTGGATGGCTGTCTTCT	24220	cCas9-v21	56	0
623	TCCAG	TAATTTTGGATGGCTGTCTTC	24221	SauCas9KKH	57	0
624	GG	AGGGGCACAAATGGCCTATG	24222	SpyCas9-NG	57	0
625	GG	AGGGGCACAAATGGCCTATG	24223	SpyCas9-xCas	57	0
626	GG	AGGGGCACAAATGGCCTATG	24224	SpyCas9-xCas-NG	57	0
627	GGA	AGGGGCACAAATGGCCTATG	24225	SpyCas9-SpG	57	0
628	GGA	AGGGGCACAAATGGCCTATG	24226	SpyCas9-SpRY	57	0
629	TCC	AATTTTGGATGGCTGTCTTC	24227	SpyCas9-SpRY	57	0
630	TCCAGC	TAATTTTGGATGGCTGTCTTC	24228	cCas9-v17	57	0
631	TCCAGC	TAATTTTGGATGGCTGTCTTC	24229	cCas9-v42	57	0
632	GGAT	AGGGGCACAAATGGCCTATG	24230	SpyCas9-3var-NRRH	57	0
633	GGAT	AGGGGCACAAATGGCCTATG	24231	SpyCas9-VQR	57	0
634	GGG	AAGGGGCACAAATGGCCTAT	24232	ScaCas9	58	0
635	GGG	AAGGGGCACAAATGGCCTAT	24233	ScaCas9-HiFi-Sc++	58	0

636	GGG	AAGGGGCACAAATGGCCTAT	24234	ScaCas9-Sc++	58	0
637	GGG	AAGGGGCACAAATGGCCTAT	24235	SpyCas9	58	0
638	GGG	AAGGGGCACAAATGGCCTAT	24236	SpyCas9-HF1	58	0
639	GGG	AAGGGGCACAAATGGCCTAT	24237	SpyCas9-SpG	58	0
640	GGG	AAGGGGCACAAATGGCCTAT	24238	SpyCas9-SpRY	58	0
641	GG	AAGGGGCACAAATGGCCTAT	24239	SpyCas9-NG	58	0
642	GG	AAGGGGCACAAATGGCCTAT	24240	SpyCas9-xCas	58	0
643	GG	AAGGGGCACAAATGGCCTAT	24241	SpyCas9-xCas-NG	58	0
644	CTC	TAATTTTGGATGGCTGTCTT	24242	SpyCas9-SpRY	58	0
645	GGGATGC	GAAGGGGCACAAATGGCCTAT	24243	cCas9-v16	58	0
646	GGGATGC	GAAGGGGCACAAATGGCCTAT	24244	cCas9-v21	58	0
647	GGGA	AAGGGGCACAAATGGCCTAT	24245	SpyCas9-3var-NRRH	58	0
648	TGGGA	agAGAAGGGGCACAAATGGCCTA	24246	SauCas9	59	0
649	TGGGA	AGAAGGGGCACAAATGGCCTA	24247	SauCas9KKH	59	0
650	TGGGAT	agAGAAGGGGCACAAATGGCCTA	24248	SauCas9	59	0
651	TGGGAT	AGAAGGGGCACAAATGGCCTA	24249	SauCas9KKH	59	0
652	TGGGAT	AGAAGGGGCACAAATGGCCTA	24250	cCas9-v17	59	0
653	TGGGAT	AGAAGGGGCACAAATGGCCTA	24251	cCas9-v42	59	0
654	TGGG	AGAAGGGGCACAAATGGCCTA	24252	SauriCas9	59	0
655	TGGG	AGAAGGGGCACAAATGGCCTA	24253	SauriCas9-KKH	59	0
656	TGG	GAAGGGGCACAAATGGCCTA	24254	ScaCas9	59	0
657	TGG	GAAGGGGCACAAATGGCCTA	24255	ScaCas9-HiFi-Sc++	59	0
658	TGG	GAAGGGGCACAAATGGCCTA	24256	ScaCas9-Sc++	59	0
659	TGG	GAAGGGGCACAAATGGCCTA	24257	SpyCas9	59	0
660	TGG	GAAGGGGCACAAATGGCCTA	24258	SpyCas9-HF1	59	0
661	TGG	GAAGGGGCACAAATGGCCTA	24259	SpyCas9-SpG	59	0
662	TGG	GAAGGGGCACAAATGGCCTA	24260	SpyCas9-SpRY	59	0
663	TG	GAAGGGGCACAAATGGCCTA	24261	SpyCas9-NG	59	0
664	TG	GAAGGGGCACAAATGGCCTA	24262	SpyCas9-xCas	59	0
665	TG	GAAGGGGCACAAATGGCCTA	24263	SpyCas9-xCas-NG	59	0
666	TCT	GTAATTTTGGATGGCTGTCT	24264	SpyCas9-SpRY	59	0

667	TCTCC	agtgTAATTTTGGATGGCTGTCT	24265	BlatCas9	59	0
668	TTCTCC	acAGTGTAATTTTGGATGGCTGTC	24266	Nme2Cas9	60	0
669	ATGGG	gaGAGAAGGGGCACAAATGGCCT	24267	SauCas9	60	0
670	ATGGG	GAGAAGGGGCACAAATGGCCT	24268	SauCas9KKH	60	0
671	ATGG	GAGAAGGGGCACAAATGGCCT	24269	SauriCas9	60	0
672	ATGG	GAGAAGGGGCACAAATGGCCT	24270	SauriCas9-KKH	60	0
673	ATG	AGAAGGGGCACAAATGGCCT	24271	ScaCas9	60	0
674	ATG	AGAAGGGGCACAAATGGCCT	24272	ScaCas9-HiFi-Sc++	60	0
675	ATG	AGAAGGGGCACAAATGGCCT	24273	ScaCas9-Sc++	60	0
676	ATG	AGAAGGGGCACAAATGGCCT	24274	SpyCas9-SpRY	60	0
677	TTC	TGTAATTTTGGATGGCTGTC	24275	SpyCas9-SpRY	60	0
678	TTCTCCAG	cagtGTAATTTTGGATGGCTGTC	24276	BlatCas9	60	0
679	TTCTC	cagtGTAATTTTGGATGGCTGTC	24277	BlatCas9	60	0
680	ATGGGA	GAGAAGGGGCACAAATGGCCT	24278	cCas9-v17	60	0
681	ATGGGA	GAGAAGGGGCACAAATGGCCT	24279	cCas9-v42	60	0
682	TATGG	AGAGAAGGGGCACAAATGGCC	24280	SauCas9KKH	61	0
683	TAT	GAGAAGGGGCACAAATGGCC	24281	SpyCas9-SpRY	61	0
684	CTT	GTGTAATTTTGGATGGCTGT	24282	SpyCas9-SpRY	61	0
685	TCT	AGTGTAATTTTGGATGGCTG	24283	SpyCas9-SpRY	62	0
686	CTA	AGAGAAGGGGCACAAATGGC	24284	SpyCas9-SpRY	62	0
687	TCTTC	gacaGTGTAATTTTGGATGGCTG	24285	BlatCas9	62	0
688	GTC	CAGTGTAATTTTGGATGGCT	24286	SpyCas9-SpRY	63	0
689	CCT	GAGAGAAGGGGCACAAATGG	24287	SpyCas9-SpRY	63	0
690	TG	ACAGTGTAATTTTGGATGGC	24288	SpyCas9-NG	64	0
691	TG	ACAGTGTAATTTTGGATGGC	24289	SpyCas9-xCas	64	0
692	TG	ACAGTGTAATTTTGGATGGC	24290	SpyCas9-xCas-NG	64	0
693	TGT	ACAGTGTAATTTTGGATGGC	24291	SpyCas9-SpG	64	0
694	TGT	ACAGTGTAATTTTGGATGGC	24292	SpyCas9-SpRY	64	0
695	GCC	TGAGAGAAGGGGCACAAATG	24293	SpyCas9-SpRY	64	0
696	TGTC	ACAGTGTAATTTTGGATGGC	24294	SpyCas9-3var-NRTH	64	0
697	CTG	GACAGTGTAATTTTGGATGG	24295	ScaCas9	65	0

698	CTG	GACAGTGTAATTTTGGATGG	24296	ScaCas9-HiFi-Sc++	65	0
699	CTG	GACAGTGTAATTTTGGATGG	24297	ScaCas9-Sc++	65	0
700	CTG	GACAGTGTAATTTTGGATGG	24298	SpyCas9-SpRY	65	0
701	GG	ATGAGAGAAGGGGCACAAAT	24299	SpyCas9-NG	65	0
702	GG	ATGAGAGAAGGGGCACAAAT	24300	SpyCas9-xCas	65	0
703	GG	ATGAGAGAAGGGGCACAAAT	24301	SpyCas9-xCas-NG	65	0
704	GGC	ATGAGAGAAGGGGCACAAAT	24302	SpyCas9-SpG	65	0
705	GGC	ATGAGAGAAGGGGCACAAAT	24303	SpyCas9-SpRY	65	0
706	CTGTC	cgtgACAGTGTAATTTTGGATGG	24304	BlatCas9	65	0
707	CTGTCTT	GTGACAGTGTAATTTTGGATGG	24305	CdiCas9	65	0
708	GGCC	ATGAGAGAAGGGGCACAAAT	24306	SpyCas9-3var-NRCH	65	0
709	TGG	GATGAGAGAAGGGGCACAAA	24307	ScaCas9	66	0
710	TGG	GATGAGAGAAGGGGCACAAA	24308	ScaCas9-HiFi-Sc++	66	0
711	TGG	GATGAGAGAAGGGGCACAAA	24309	ScaCas9-Sc++	66	0
712	TGG	GATGAGAGAAGGGGCACAAA	24310	SpyCas9	66	0
713	TGG	GATGAGAGAAGGGGCACAAA	24311	SpyCas9-HF1	66	0
714	TGG	GATGAGAGAAGGGGCACAAA	24312	SpyCas9-SpG	66	0
715	TGG	GATGAGAGAAGGGGCACAAA	24313	SpyCas9-SpRY	66	0
716	TG	GATGAGAGAAGGGGCACAAA	24314	SpyCas9-NG	66	0
717	TG	GATGAGAGAAGGGGCACAAA	24315	SpyCas9-xCas	66	0
718	TG	GATGAGAGAAGGGGCACAAA	24316	SpyCas9-xCas-NG	66	0
719	GCT	TGACAGTGTAATTTTGGATG	24317	SpyCas9-SpRY	66	0
720	TGGCCTAT	tgagATGAGAGAAGGGGCACAAA	24318	BlatCas9	66	0
721	TGGCC	tgagATGAGAGAAGGGGCACAAA	24319	BlatCas9	66	0
722	TGGC	GATGAGAGAAGGGGCACAAA	24320	SpyCas9-3var-NRRH	66	0
723	ATGGCC	ggTGAGATGAGAGAAGGGGCACAA	24321	Nme2Cas9	67	0
724	ATGG	GAGATGAGAGAAGGGGCACAA	24322	SauriCas9	67	0
725	ATGG	GAGATGAGAGAAGGGGCACAA	24323	SauriCas9-KKH	67	0
726	ATG	AGATGAGAGAAGGGGCACAA	24324	ScaCas9	67	0
727	ATG	AGATGAGAGAAGGGGCACAA	24325	ScaCas9-HiFi-Sc++	67	0

728	ATG	AGATGAGAGAAGGGGCACAA	24326	ScaCas9-Sc++	67	0
729	ATG	AGATGAGAGAAGGGGCACAA	24327	SpyCas9-SpRY	67	0
730	GG	GTGACAGTGTAATTTTGGAT	24328	SpyCas9-NG	67	0
731	GG	GTGACAGTGTAATTTTGGAT	24329	SpyCas9-xCas	67	0
732	GG	GTGACAGTGTAATTTTGGAT	24330	SpyCas9-xCas-NG	67	0
733	GGC	GTGACAGTGTAATTTTGGAT	24331	SpyCas9-SpG	67	0
734	GGC	GTGACAGTGTAATTTTGGAT	24332	SpyCas9-SpRY	67	0
735	ATGGCCTA	gtgaGATGAGAGAAGGGGCACAA	24333	BlatCas9	67	0
736	ATGGC	gtgaGATGAGAGAAGGGGCACAA	24334	BlatCas9	67	0
737	GGCTGTCT	ctccGTGACAGTGTAATTTTGGAT	24335	NmeCas9	67	0
738	GGCT	GTGACAGTGTAATTTTGGAT	24336	SpyCas9-3var-NRCH	67	0
739	AATGG	TGAGATGAGAGAAGGGGCACA	24337	SauCas9KKH	68	0
740	TGG	CGTGACAGTGTAATTTTGGA	24338	ScaCas9	68	0
741	TGG	CGTGACAGTGTAATTTTGGA	24339	ScaCas9-HiFi-Sc++	68	0
742	TGG	CGTGACAGTGTAATTTTGGA	24340	ScaCas9-Sc++	68	0
743	TGG	CGTGACAGTGTAATTTTGGA	24341	SpyCas9	68	0
744	TGG	CGTGACAGTGTAATTTTGGA	24342	SpyCas9-HF1	68	0
745	TGG	CGTGACAGTGTAATTTTGGA	24343	SpyCas9-SpG	68	0
746	TGG	CGTGACAGTGTAATTTTGGA	24344	SpyCas9-SpRY	68	0
747	TG	CGTGACAGTGTAATTTTGGA	24345	SpyCas9-NG	68	0
748	TG	CGTGACAGTGTAATTTTGGA	24346	SpyCas9-xCas	68	0
749	TG	CGTGACAGTGTAATTTTGGA	24347	SpyCas9-xCas-NG	68	0
750	AAT	GAGATGAGAGAAGGGGCACA	24348	SpyCas9-SpRY	68	0
751	TGGC	CGTGACAGTGTAATTTTGGA	24349	SpyCas9-3var-NRRH	68	0
752	ATGG	TCCGTGACAGTGTAATTTTGG	24350	SauriCas9	69	0
753	ATGG	TCCGTGACAGTGTAATTTTGG	24351	SauriCas9-KKH	69	0
754	ATG	CCGTGACAGTGTAATTTTGG	24352	ScaCas9	69	0
755	ATG	CCGTGACAGTGTAATTTTGG	24353	ScaCas9-HiFi-Sc++	69	0
756	ATG	CCGTGACAGTGTAATTTTGG	24354	ScaCas9-Sc++	69	0

757	ATG	CCGTGACAGTGTAATTTTGG	24355	SpyCas9-SpRY	69	0
758	AAA	TGAGATGAGAGAAGGGGCAC	24356	SpyCas9-SpRY	69	0
759	ATGGCTGT	actcCGTGACAGTGTAATTTTGG	24357	BlatCas9	69	0
760	ATGGC	actcCGTGACAGTGTAATTTTGG	24358	BlatCas9	69	0
761	ATGGCT	TCCGTGACAGTGTAATTTTGG	24359	cCas9-v16	69	0
762	ATGGCT	TCCGTGACAGTGTAATTTTGG	24360	cCas9-v21	69	0
763	AAAT	TGAGATGAGAGAAGGGGCAC	24361	SpyCas9-3var-NRRH	69	0
764	AAAT	gtGAGATGAGAGAAGGGGCAC	24362	iSpyMacCas9	69	0
765	GATGG	CTCCGTGACAGTGTAATTTTG	24363	SauCas9KKH	70	0
766	GAT	TCCGTGACAGTGTAATTTTG	24364	SpyCas9-SpRY	70	0
767	GAT	TCCGTGACAGTGTAATTTTG	24365	SpyCas9-xCas	70	0
768	CAA	GTGAGATGAGAGAAGGGGCA	24366	SpyCas9-SpRY	70	0
769	CAAA	GTGAGATGAGAGAAGGGGCA	24367	SpyCas9-3var-NRRH	70	0
770	CAAA	ggTGAGATGAGAGAAGGGGCA	24368	iSpyMacCas9	70	0
771	ACAAA	GGGTGAGATGAGAGAAGGGGC	24369	SauCas9KKH	71	0
772	ACAAAT	GGGTGAGATGAGAGAAGGGGC	24370	SauCas9KKH	71	0
773	ACAAAT	GGGTGAGATGAGAGAAGGGGC	24371	cCas9-v17	71	0
774	ACAAAT	GGGTGAGATGAGAGAAGGGGC	24372	cCas9-v42	71	0
775	GG	CTCCGTGACAGTGTAATTTT	24373	SpyCas9-NG	71	0
776	GG	CTCCGTGACAGTGTAATTTT	24374	SpyCas9-xCas	71	0
777	GG	CTCCGTGACAGTGTAATTTT	24375	SpyCas9-xCas-NG	71	0
778	GGA	CTCCGTGACAGTGTAATTTT	24376	SpyCas9-SpG	71	0
779	GGA	CTCCGTGACAGTGTAATTTT	24377	SpyCas9-SpRY	71	0
780	ACA	GGTGAGATGAGAGAAGGGGC	24378	SpyCas9-SpRY	71	0
781	GGAT	CTCCGTGACAGTGTAATTTT	24379	SpyCas9-3var-NRRH	71	0
782	GGAT	CTCCGTGACAGTGTAATTTT	24380	SpyCas9-VQR	71	0
783	CACAA	GGGGTGAGATGAGAGAAGGGG	24381	SauCas9KKH	72	0
784	TGG	ACTCCGTGACAGTGTAATTT	24382	ScaCas9	72	0
785	TGG	ACTCCGTGACAGTGTAATTT	24383	ScaCas9-HiFi-Sc++	72	0

786	TGG	ACTCCGTGACAGTGTAATTT	24384	ScaCas9-Sc++	72	0
787	TGG	ACTCCGTGACAGTGTAATTT	24385	SpyCas9	72	0
788	TGG	ACTCCGTGACAGTGTAATTT	24386	SpyCas9-HF1	72	0
789	TGG	ACTCCGTGACAGTGTAATTT	24387	SpyCas9-SpG	72	0
790	TGG	ACTCCGTGACAGTGTAATTT	24388	SpyCas9-SpRY	72	0
791	TG	ACTCCGTGACAGTGTAATTT	24389	SpyCas9-NG	72	0
792	TG	ACTCCGTGACAGTGTAATTT	24390	SpyCas9-xCas	72	0
793	TG	ACTCCGTGACAGTGTAATTT	24391	SpyCas9-xCas-NG	72	0
794	CAC	GGGTGAGATGAGAGAAGGGG	24392	SpyCas9-SpRY	72	0
795	CACAAA	GGGGTGAGATGAGAGAAGGGG	24393	cCas9-v17	72	0
796	CACAAA	GGGGTGAGATGAGAGAAGGGG	24394	cCas9-v42	72	0
797	TGGA	ACTCCGTGACAGTGTAATTT	24395	SpyCas9-3var-NRRH	72	0
798	CACA	GGGTGAGATGAGAGAAGGGG	24396	SpyCas9-3var-NRCH	72	0
799	TTGGA	tgGAACTCCGTGACAGTGTAATT	24397	SauCas9	73	0
800	TTGGA	GAACTCCGTGACAGTGTAATT	24398	SauCas9KKH	73	0
801	TTGGAT	tgGAACTCCGTGACAGTGTAATT	24399	SauCas9	73	0
802	TTGGAT	GAACTCCGTGACAGTGTAATT	24400	SauCas9KKH	73	0
803	TTGGAT	GAACTCCGTGACAGTGTAATT	24401	cCas9-v17	73	0
804	TTGGAT	GAACTCCGTGACAGTGTAATT	24402	cCas9-v42	73	0
805	TTGG	GAACTCCGTGACAGTGTAATT	24403	SauriCas9	73	0
806	TTGG	GAACTCCGTGACAGTGTAATT	24404	SauriCas9-KKH	73	0
807	TTG	AACTCCGTGACAGTGTAATT	24405	ScaCas9	73	0
808	TTG	AACTCCGTGACAGTGTAATT	24406	ScaCas9-HiFi-Sc++	73	0
809	TTG	AACTCCGTGACAGTGTAATT	24407	ScaCas9-Sc++	73	0
810	TTG	AACTCCGTGACAGTGTAATT	24408	SpyCas9-SpRY	73	0
811	GCA	GGGGTGAGATGAGAGAAGGG	24409	SpyCas9-SpRY	73	0
812	GCACAA	GGGGTGAGATGAGAGAAGGG	24410	St1Cas9-CNRZ1066	73	0
813	TTTGG	GGAACTCCGTGACAGTGTAAT	24411	SauCas9KKH	74	0
814	GG	CGGGGTGAGATGAGAGAAGG	24412	SpyCas9-NG	74	0
815	GG	CGGGGTGAGATGAGAGAAGG	24413	SpyCas9-xCas	74	0

816	GG	CGGGGTGAGATGAGAGAAGG	24414	SpyCas9-xCas-NG	74	0
817	GGC	CGGGGTGAGATGAGAGAAGG	24415	SpyCas9-SpG	74	0
818	GGC	CGGGGTGAGATGAGAGAAGG	24416	SpyCas9-SpRY	74	0
819	TTT	GAACTCCGTGACAGTGTAAT	24417	SpyCas9-SpRY	74	0
820	GGCACAAA	aatcGGGGTGAGATGAGAGAAGG	24418	BlatCas9	74	0
821	GGCACAAA	aatcGGGGTGAGATGAGAGAAGG	24419	BlatCas9	74	0
822	GGCACAAA	aaTCGGGGTGAGATGAGAGAAGG	24420	GeoCas9	74	0
823	GGCAC	aatcGGGGTGAGATGAGAGAAGG	24421	BlatCas9	74	0
824	GGCA	CGGGGTGAGATGAGAGAAGG	24422	SpyCas9-3var-NRCH	74	0
825	GGG	TCGGGGTGAGATGAGAGAAG	24423	ScaCas9	75	0
826	GGG	TCGGGGTGAGATGAGAGAAG	24424	ScaCas9-HiFi-Sc++	75	0
827	GGG	TCGGGGTGAGATGAGAGAAG	24425	ScaCas9-Sc++	75	0
828	GGG	TCGGGGTGAGATGAGAGAAG	24426	SpyCas9	75	0
829	GGG	TCGGGGTGAGATGAGAGAAG	24427	SpyCas9-HF1	75	0
830	GGG	TCGGGGTGAGATGAGAGAAG	24428	SpyCas9-SpG	75	0
831	GGG	TCGGGGTGAGATGAGAGAAG	24429	SpyCas9-SpRY	75	0
832	GG	TCGGGGTGAGATGAGAGAAG	24430	SpyCas9-NG	75	0
833	GG	TCGGGGTGAGATGAGAGAAG	24431	SpyCas9-xCas	75	0
834	GG	TCGGGGTGAGATGAGAGAAG	24432	SpyCas9-xCas-NG	75	0
835	TTT	GGAACTCCGTGACAGTGTAA	24433	SpyCas9-SpRY	75	0
836	GGGC	TCGGGGTGAGATGAGAGAAG	24434	SpyCas9-3var-NRRH	75	0
837	GGGG	AATCGGGGTGAGATGAGAGAA	24435	SauriCas9	76	0
838	GGGG	AATCGGGGTGAGATGAGAGAA	24436	SauriCas9-KKH	76	0
839	GGG	ATCGGGGTGAGATGAGAGAA	24437	ScaCas9	76	0
840	GGG	ATCGGGGTGAGATGAGAGAA	24438	ScaCas9-HiFi-Sc++	76	0
841	GGG	ATCGGGGTGAGATGAGAGAA	24439	ScaCas9-Sc++	76	0
842	GGG	ATCGGGGTGAGATGAGAGAA	24440	SpyCas9	76	0
843	GGG	ATCGGGGTGAGATGAGAGAA	24441	SpyCas9-HF1	76	0
844	GGG	ATCGGGGTGAGATGAGAGAA	24442	SpyCas9-SpG	76	0

845	GGG	ATCGGGGTGAGATGAGAGAA	24443	SpyCas9-SpRY	76	0
846	GG	ATCGGGGTGAGATGAGAGAA	24444	SpyCas9-NG	76	0
847	GG	ATCGGGGTGAGATGAGAGAA	24445	SpyCas9-xCas	76	0
848	GG	ATCGGGGTGAGATGAGAGAA	24446	SpyCas9-xCas-NG	76	0
849	ATT	TGGAACTCCGTGACAGTGTA	24447	SpyCas9-SpRY	76	0
850	GGGGC	ggaaTCGGGGTGAGATGAGAGAA	24448	BlatCas9	76	0
851	AGGGG	agGAATCGGGGTGAGATGAGAGA	24449	SauCas9	77	0
852	AGGGG	GAATCGGGGTGAGATGAGAGA	24450	SauCas9KKH	77	0
853	AGGG	GAATCGGGGTGAGATGAGAGA	24451	SauriCas9	77	0
854	AGGG	GAATCGGGGTGAGATGAGAGA	24452	SauriCas9-KKH	77	0
855	AGG	AATCGGGGTGAGATGAGAGA	24453	ScaCas9	77	0
856	AGG	AATCGGGGTGAGATGAGAGA	24454	ScaCas9-HiFi-Sc++	77	0
857	AGG	AATCGGGGTGAGATGAGAGA	24455	ScaCas9-Sc++	77	0
858	AGG	AATCGGGGTGAGATGAGAGA	24456	SpyCas9	77	0
859	AGG	AATCGGGGTGAGATGAGAGA	24457	SpyCas9-HF1	77	0
860	AGG	AATCGGGGTGAGATGAGAGA	24458	SpyCas9-SpG	77	0
861	AGG	AATCGGGGTGAGATGAGAGA	24459	SpyCas9-SpRY	77	0
862	AG	AATCGGGGTGAGATGAGAGA	24460	SpyCas9-NG	77	0
863	AG	AATCGGGGTGAGATGAGAGA	24461	SpyCas9-xCas	77	0
864	AG	AATCGGGGTGAGATGAGAGA	24462	SpyCas9-xCas-NG	77	0
865	AAT	CTGGAACTCCGTGACAGTGT	24463	SpyCas9-SpRY	77	0
866	AGGGGC	GAATCGGGGTGAGATGAGAGA	24464	cCas9-v17	77	0
867	AGGGGC	GAATCGGGGTGAGATGAGAGA	24465	cCas9-v42	77	0
868	AGGGGCAC	agGAATCGGGGTGAGATGAGAGA	24466	CjeCas9	77	0
869	AATT	CTGGAACTCCGTGACAGTGT	24467	SpyCas9-3var-NRTH	77	0
870	AAGGG	aaGGAATCGGGGTGAGATGAGAG	24468	SauCas9	78	0
871	AAGGG	GGAATCGGGGTGAGATGAGAG	24469	SauCas9KKH	78	0
872	AAGG	GGAATCGGGGTGAGATGAGAG	24470	SauriCas9	78	0
873	AAGG	GGAATCGGGGTGAGATGAGAG	24471	SauriCas9-KKH	78	0
874	AAG	GAATCGGGGTGAGATGAGAG	24472	ScaCas9	78	0

875	AAG	GAATCGGGGTGAGATGAGAG	24473	ScaCas9-HiFi-Sc++	78	0
876	AAG	GAATCGGGGTGAGATGAGAG	24474	ScaCas9-Sc++	78	0
877	AAG	GAATCGGGGTGAGATGAGAG	24475	SpyCas9-SpRY	78	0
878	TAA	GCTGGAACTCCGTGACAGTG	24476	SpyCas9-SpRY	78	0
879	AAGGGG	GGAATCGGGGTGAGATGAGAG	24477	cCas9-v17	78	0
880	AAGGGG	GGAATCGGGGTGAGATGAGAG	24478	cCas9-v42	78	0
881	TAATTTT	GGGCTGGAACTCCGTGACAGTG	24479	CdiCas9	78	0
882	TAAT	GCTGGAACTCCGTGACAGTG	24480	SpyCas9-3var-NRRH	78	0
883	TAAT	ggCTGGAACTCCGTGACAGTG	24481	iSpyMacCas9	78	0
884	GAAGG	AGGAATCGGGGTGAGATGAGA	24482	SauCas9KKH	79	0
885	GAAG	AGGAATCGGGGTGAGATGAGA	24483	SauriCas9-KKH	79	0
886	GAAG	GGAATCGGGGTGAGATGAGA	24484	SpyCas9-QQR1	79	0
887	GAAG	agGAATCGGGGTGAGATGAGA	24485	iSpyMacCas9	79	0
888	GAA	GGAATCGGGGTGAGATGAGA	24486	SpyCas9-SpRY	79	0
889	GAA	GGAATCGGGGTGAGATGAGA	24487	SpyCas9-xCas	79	0
890	GTA	GGCTGGAACTCCGTGACAGT	24488	SpyCas9-SpRY	79	0
891	GTAATT	GGGCTGGAACTCCGTGACAGT	24489	cCas9-v16	79	0
892	GTAATT	GGGCTGGAACTCCGTGACAGT	24490	cCas9-v21	79	0
893	GAAGGG	AGGAATCGGGGTGAGATGAGA	24491	cCas9-v17	79	0
894	GAAGGG	AGGAATCGGGGTGAGATGAGA	24492	cCas9-v42	79	0
895	GTAATTT	GGGGCTGGAACTCCGTGACAGT	24493	CdiCas9	79	0
896	TGTAATT	agaGGGGCTGGAACTCCGTGACAG	24494	PpnCas9	80	0
897	TGTAA	GGGGCTGGAACTCCGTGACAG	24495	SauCas9KKH	80	0
898	AGAAG	AAGGAATCGGGGTGAGATGAG	24496	SauCas9KKH	80	0
899	TGTAAT	GGGGCTGGAACTCCGTGACAG	24497	SauCas9KKH	80	0
900	TG	GGGCTGGAACTCCGTGACAG	24498	SpyCas9-NG	80	0
901	TG	GGGCTGGAACTCCGTGACAG	24499	SpyCas9-xCas	80	0
902	TG	GGGCTGGAACTCCGTGACAG	24500	SpyCas9-xCas-NG	80	0
903	AG	AGGAATCGGGGTGAGATGAG	24501	SpyCas9-NG	80	0
904	AG	AGGAATCGGGGTGAGATGAG	24502	SpyCas9-xCas	80	0

905	AG	AGGAATCGGGGTGAGATGAG	24503	SpyCas9-xCas-NG	80	0
906	TGT	GGGCTGGAACTCCGTGACAG	24504	SpyCas9-SpG	80	0
907	TGT	GGGCTGGAACTCCGTGACAG	24505	SpyCas9-SpRY	80	0
908	AGA	AGGAATCGGGGTGAGATGAG	24506	SpyCas9-SpG	80	0
909	AGA	AGGAATCGGGGTGAGATGAG	24507	SpyCas9-SpRY	80	0
910	AGAAGG	AAGGAATCGGGGTGAGATGAG	24508	cCas9-v17	80	0
911	AGAAGG	AAGGAATCGGGGTGAGATGAG	24509	cCas9-v42	80	0
912	AGAA	AGGAATCGGGGTGAGATGAG	24510	SpyCas9-3var-NRRH	80	0
913	AGAA	AGGAATCGGGGTGAGATGAG	24511	SpyCas9-VQR	80	0
914	TGTA	GGGCTGGAACTCCGTGACAG	24512	SpyCas9-3var-NRTH	80	0
915	GAGAA	taGAAGGAATCGGGGTGAGATGA	24513	SauCas9	81	0
916	GAGAA	GAAGGAATCGGGGTGAGATGA	24514	SauCas9KKH	81	0
917	GTG	GGGGCTGGAACTCCGTGACA	24515	ScaCas9	81	0
918	GTG	GGGGCTGGAACTCCGTGACA	24516	ScaCas9-HiFi-Sc++	81	0
919	GTG	GGGGCTGGAACTCCGTGACA	24517	ScaCas9-Sc++	81	0
920	GTG	GGGGCTGGAACTCCGTGACA	24518	SpyCas9-SpRY	81	0
921	GAG	AAGGAATCGGGGTGAGATGA	24519	ScaCas9	81	0
922	GAG	AAGGAATCGGGGTGAGATGA	24520	ScaCas9-HiFi-Sc++	81	0
923	GAG	AAGGAATCGGGGTGAGATGA	24521	ScaCas9-Sc++	81	0
924	GAG	AAGGAATCGGGGTGAGATGA	24522	SpyCas9-SpRY	81	0
925	GAGAAG	GAAGGAATCGGGGTGAGATGA	24523	cCas9-v17	81	0
926	GAGAAG	GAAGGAATCGGGGTGAGATGA	24524	cCas9-v42	81	0
927	GTGTAAT	GAGGGGCTGGAACTCCGTGACA	24525	CdiCas9	81	0
928	GAGA	AAGGAATCGGGGTGAGATGA	24526	SpyCas9-3var-NRRH	81	0
929	AGAGA	AGAAGGAATCGGGGTGAGATG	24527	SauCas9KKH	82	0
930	AGAG	AGAAGGAATCGGGGTGAGATG	24528	SauriCas9-KKH	82	0
931	AGAG	GAAGGAATCGGGGTGAGATG	24529	SpyCas9-VQR	82	0
932	AG	AGGGGCTGGAACTCCGTGAC	24530	SpyCas9-NG	82	0
933	AG	AGGGGCTGGAACTCCGTGAC	24531	SpyCas9-xCas	82	0
934	AG	AGGGGCTGGAACTCCGTGAC	24532	SpyCas9-xCas-NG	82	0

935	AG	GAAGGAATCGGGGTGAGATG	24533	SpyCas9-NG	82	0
936	AG	GAAGGAATCGGGGTGAGATG	24534	SpyCas9-xCas	82	0
937	AG	GAAGGAATCGGGGTGAGATG	24535	SpyCas9-xCas-NG	82	0
938	AGT	AGGGGCTGGAACTCCGTGAC	24536	SpyCas9-SpG	82	0
939	AGT	AGGGGCTGGAACTCCGTGAC	24537	SpyCas9-SpRY	82	0
940	AGA	GAAGGAATCGGGGTGAGATG	24538	SpyCas9-SpG	82	0
941	AGA	GAAGGAATCGGGGTGAGATG	24539	SpyCas9-SpRY	82	0
942	AGAGAA	AGAAGGAATCGGGGTGAGATG	24540	cCas9-v17	82	0
943	AGAGAA	AGAAGGAATCGGGGTGAGATG	24541	cCas9-v42	82	0
944	GAGAG	tgTAGAAGGAATCGGGGTGAGAT	24542	SauCas9	83	0
945	GAGAG	TAGAAGGAATCGGGGTGAGAT	24543	SauCas9KKH	83	0
946	CAG	GAGGGGCTGGAACTCCGTGA	24544	ScaCas9	83	0
947	CAG	GAGGGGCTGGAACTCCGTGA	24545	ScaCas9-HiFi-Sc++	83	0
948	CAG	GAGGGGCTGGAACTCCGTGA	24546	ScaCas9-Sc++	83	0
949	CAG	GAGGGGCTGGAACTCCGTGA	24547	SpyCas9-SpRY	83	0
950	GAG	AGAAGGAATCGGGGTGAGAT	24548	ScaCas9	83	0
951	GAG	AGAAGGAATCGGGGTGAGAT	24549	ScaCas9-HiFi-Sc++	83	0
952	GAG	AGAAGGAATCGGGGTGAGAT	24550	ScaCas9-Sc++	83	0
953	GAG	AGAAGGAATCGGGGTGAGAT	24551	SpyCas9-SpRY	83	0
954	GAGAGA	TAGAAGGAATCGGGGTGAGAT	24552	cCas9-v17	83	0
955	GAGAGA	TAGAAGGAATCGGGGTGAGAT	24553	cCas9-v42	83	0
956	CAGT	GAGGGGCTGGAACTCCGTGA	24554	SpyCas9-3var-NRRH	83	0
957	GAGA	AGAAGGAATCGGGGTGAGAT	24555	SpyCas9-3var-NRRH	83	0
958	TGAGA	GTAGAAGGAATCGGGGTGAGA	24556	SauCas9KKH	84	0
959	ACAG	TAGAGGGGCTGGAACTCCGTG	24557	SauriCas9-KKH	84	0
960	TGAG	GTAGAAGGAATCGGGGTGAGA	24558	SauriCas9-KKH	84	0
961	TGAG	TAGAAGGAATCGGGGTGAGA	24559	SpyCas9-VQR	84	0
962	TG	TAGAAGGAATCGGGGTGAGA	24560	SpyCas9-NG	84	0
963	TG	TAGAAGGAATCGGGGTGAGA	24561	SpyCas9-xCas	84	0
964	TG	TAGAAGGAATCGGGGTGAGA	24562	SpyCas9-xCas-NG	84	0

965	TGA	TAGAAGGAATCGGGGTGAGA	24563	SpyCas9-SpG	84	0
966	TGA	TAGAAGGAATCGGGGTGAGA	24564	SpyCas9-SpRY	84	0
967	ACA	AGAGGGGCTGGAACTCCGTG	24565	SpyCas9-SpRY	84	0
968	ACAGTG	TAGAGGGGCTGGAACTCCGTG	24566	cCas9-v16	84	0
969	ACAGTG	TAGAGGGGCTGGAACTCCGTG	24567	cCas9-v21	84	0
970	TGAGAG	GTAGAAGGAATCGGGGTGAGA	24568	cCas9-v17	84	0
971	TGAGAG	GTAGAAGGAATCGGGGTGAGA	24569	cCas9-v42	84	0
972	ATGAG	gaTGTAGAAGGAATCGGGGTGAG	24570	SauCas9	85	0
973	ATGAG	TGTAGAAGGAATCGGGGTGAG	24571	SauCas9KKH	85	0
974	GACAG	ATAGAGGGGCTGGAACTCCGT	24572	SauCas9KKH	85	0
975	GACAGT	ATAGAGGGGCTGGAACTCCGT	24573	SauCas9KKH	85	0
976	GACAGT	ATAGAGGGGCTGGAACTCCGT	24574	cCas9-v17	85	0
977	GACAGT	ATAGAGGGGCTGGAACTCCGT	24575	cCas9-v42	85	0
978	ATG	GTAGAAGGAATCGGGGTGAG	24576	ScaCas9	85	0
979	ATG	GTAGAAGGAATCGGGGTGAG	24577	ScaCas9-HiFi-Sc++	85	0
980	ATG	GTAGAAGGAATCGGGGTGAG	24578	ScaCas9-Sc++	85	0
981	ATG	GTAGAAGGAATCGGGGTGAG	24579	SpyCas9-SpRY	85	0
982	GAC	TAGAGGGGCTGGAACTCCGT	24580	SpyCas9-SpRY	85	0
983	ATGAGA	TGTAGAAGGAATCGGGGTGAG	24581	cCas9-v17	85	0
984	ATGAGA	TGTAGAAGGAATCGGGGTGAG	24582	cCas9-v42	85	0
985	GACA	TAGAGGGGCTGGAACTCCGT	24583	SpyCas9-3var-NRCH	85	0
986	GATGA	ATGTAGAAGGAATCGGGGTGA	24584	SauCas9KKH	86	0
987	TG	ATAGAGGGGCTGGAACTCCG	24585	SpyCas9-NG	86	0
988	TG	ATAGAGGGGCTGGAACTCCG	24586	SpyCas9-xCas	86	0
989	TG	ATAGAGGGGCTGGAACTCCG	24587	SpyCas9-xCas-NG	86	0
990	TGA	ATAGAGGGGCTGGAACTCCG	24588	SpyCas9-SpG	86	0
991	TGA	ATAGAGGGGCTGGAACTCCG	24589	SpyCas9-SpRY	86	0
992	GAT	TGTAGAAGGAATCGGGGTGA	24590	SpyCas9-SpRY	86	0
993	GAT	TGTAGAAGGAATCGGGGTGA	24591	SpyCas9-xCas	86	0
994	TGAC	ATAGAGGGGCTGGAACTCCG	24592	SpyCas9-3var-NRRH	86	0

995	TGAC	ATAGAGGGGCTGGAACTCCG	24593	SpyCas9-VQR	86	0
996	GTG	AATAGAGGGGCTGGAACTCC	24594	ScaCas9	87	0
997	GTG	AATAGAGGGGCTGGAACTCC	24595	ScaCas9-HiFi-Sc++	87	0
998	GTG	AATAGAGGGGCTGGAACTCC	24596	ScaCas9-Sc++	87	0
999	GTG	AATAGAGGGGCTGGAACTCC	24597	SpyCas9-SpRY	87	0
1000	AG	ATGTAGAAGGAATCGGGGTG	24598	SpyCas9-NG	87	0
1001	AG	ATGTAGAAGGAATCGGGGTG	24599	SpyCas9-xCas	87	0
1002	AG	ATGTAGAAGGAATCGGGGTG	24600	SpyCas9-xCas-NG	87	0
1003	AGA	ATGTAGAAGGAATCGGGGTG	24601	SpyCas9-SpG	87	0
1004	AGA	ATGTAGAAGGAATCGGGGTG	24602	SpyCas9-SpRY	87	0
1005	GTGACAGT	cgtaATAGAGGGGCTGGAACTCC	24603	BlatCas9	87	0
1006	GTGAC	cgtaATAGAGGGGCTGGAACTCC	24604	BlatCas9	87	0
1007	AGAT	ATGTAGAAGGAATCGGGGTG	24605	SpyCas9-3var-NRRH	87	0
1008	AGAT	ATGTAGAAGGAATCGGGGTG	24606	SpyCas9-VQR	87	0
1009	CGTGA	GTAATAGAGGGGCTGGAACTC	24607	SauCas9KKH	88	0
1010	GAG	GATGTAGAAGGAATCGGGGT	24608	ScaCas9	88	0
1011	GAG	GATGTAGAAGGAATCGGGGT	24609	ScaCas9-HiFi-Sc++	88	0
1012	GAG	GATGTAGAAGGAATCGGGGT	24610	ScaCas9-Sc++	88	0
1013	GAG	GATGTAGAAGGAATCGGGGT	24611	SpyCas9-SpRY	88	0
1014	CG	TAATAGAGGGGCTGGAACTC	24612	SpyCas9-NG	88	0
1015	CG	TAATAGAGGGGCTGGAACTC	24613	SpyCas9-xCas	88	0
1016	CG	TAATAGAGGGGCTGGAACTC	24614	SpyCas9-xCas-NG	88	0
1017	CGT	TAATAGAGGGGCTGGAACTC	24615	SpyCas9-SpG	88	0
1018	CGT	TAATAGAGGGGCTGGAACTC	24616	SpyCas9-SpRY	88	0
1019	GAGATGA	TGATGTAGAAGGAATCGGGGT	24617	cCas9-v16	88	0
1020	GAGATGA	TGATGTAGAAGGAATCGGGGT	24618	cCas9-v21	88	0
1021	GAGA	GATGTAGAAGGAATCGGGGT	24619	SpyCas9-3var-NRRH	88	0
1022	TGAGA	GTGATGTAGAAGGAATCGGGG	24620	SauCas9KKH	89	0
1023	TGAGAT	GTGATGTAGAAGGAATCGGGG	24621	SauCas9KKH	89	0

1024	TGAGAT	GTGATGTAGAAGGAATCGGGG	24622	cCas9-v17	89	0
1025	TGAGAT	GTGATGTAGAAGGAATCGGGG	24623	cCas9-v42	89	0
1026	TGAG	GTGATGTAGAAGGAATCGGGG	24624	SauriCas9-KKH	89	0
1027	TGAG	TGATGTAGAAGGAATCGGGG	24625	SpyCas9-VQR	89	0
1028	CCG	GTAATAGAGGGGCTGGAACT	24626	ScaCas9	89	0
1029	CCG	GTAATAGAGGGGCTGGAACT	24627	ScaCas9-HiFi-Sc++	89	0
1030	CCG	GTAATAGAGGGGCTGGAACT	24628	ScaCas9-Sc++	89	0
1031	CCG	GTAATAGAGGGGCTGGAACT	24629	SpyCas9-SpRY	89	0
1032	TG	TGATGTAGAAGGAATCGGGG	24630	SpyCas9-NG	89	0
1033	TG	TGATGTAGAAGGAATCGGGG	24631	SpyCas9-xCas	89	0
1034	TG	TGATGTAGAAGGAATCGGGG	24632	SpyCas9-xCas-NG	89	0
1035	TGA	TGATGTAGAAGGAATCGGGG	24633	SpyCas9-SpG	89	0
1036	TGA	TGATGTAGAAGGAATCGGGG	24634	SpyCas9-SpRY	89	0
1037	CCGTGACA	ccacGTAATAGAGGGGCTGGAACT	24635	NmeCas9	89	0
1038	GTGAG	gcTGTGATGTAGAAGGAATCGGG	24636	SauCas9	90	0
1039	GTGAG	TGTGATGTAGAAGGAATCGGG	24637	SauCas9KKH	90	0
1040	GTG	GTGATGTAGAAGGAATCGGG	24638	ScaCas9	90	0
1041	GTG	GTGATGTAGAAGGAATCGGG	24639	ScaCas9-HiFi-Sc++	90	0
1042	GTG	GTGATGTAGAAGGAATCGGG	24640	ScaCas9-Sc++	90	0
1043	GTG	GTGATGTAGAAGGAATCGGG	24641	SpyCas9-SpRY	90	0
1044	TCC	CGTAATAGAGGGGCTGGAAC	24642	SpyCas9-SpRY	90	0
1045	TCCGTG	ACGTAATAGAGGGGCTGGAAC	24643	cCas9-v16	90	0
1046	TCCGTG	ACGTAATAGAGGGGCTGGAAC	24644	cCas9-v21	90	0
1047	GTGAGA	TGTGATGTAGAAGGAATCGGG	24645	cCas9-v17	90	0
1048	GTGAGA	TGTGATGTAGAAGGAATCGGG	24646	cCas9-v42	90	0
1049	GGTGA	CTGTGATGTAGAAGGAATCGG	24647	SauCas9KKH	91	0
1050	GG	TGTGATGTAGAAGGAATCGG	24648	SpyCas9-NG	91	0
1051	GG	TGTGATGTAGAAGGAATCGG	24649	SpyCas9-xCas	91	0
1052	GG	TGTGATGTAGAAGGAATCGG	24650	SpyCas9-xCas-NG	91	0
1053	GGT	TGTGATGTAGAAGGAATCGG	24651	SpyCas9-SpG	91	0

1054	GGT	TGTGATGTAGAAGGAATCGG	24652	SpyCas9-SpRY	91	0
1055	CTC	ACGTAATAGAGGGGCTGGAA	24653	SpyCas9-SpRY	91	0
1056	GGG	CTGTGATGTAGAAGGAATCG	24654	ScaCas9	92	0
1057	GGG	CTGTGATGTAGAAGGAATCG	24655	ScaCas9-HiFi-Sc++	92	0
1058	GGG	CTGTGATGTAGAAGGAATCG	24656	ScaCas9-Sc++	92	0
1059	GGG	CTGTGATGTAGAAGGAATCG	24657	SpyCas9	92	0
1060	GGG	CTGTGATGTAGAAGGAATCG	24658	SpyCas9-HF1	92	0
1061	GGG	CTGTGATGTAGAAGGAATCG	24659	SpyCas9-SpG	92	0
1062	GGG	CTGTGATGTAGAAGGAATCG	24660	SpyCas9-SpRY	92	0
1063	GG	CTGTGATGTAGAAGGAATCG	24661	SpyCas9-NG	92	0
1064	GG	CTGTGATGTAGAAGGAATCG	24662	SpyCas9-xCas	92	0
1065	GG	CTGTGATGTAGAAGGAATCG	24663	SpyCas9-xCas-NG	92	0
1066	ACT	CACGTAATAGAGGGGCTGGA	24664	SpyCas9-SpRY	92	0
1067	ACTCCGTG	tgccACGTAATAGAGGGGCTGGA	24665	BlatCas9	92	0
1068	ACTCC	tgccACGTAATAGAGGGGCTGGA	24666	BlatCas9	92	0
1069	GGGT	CTGTGATGTAGAAGGAATCG	24667	SpyCas9-3var-NRRH	92	0
1070	AACTCC	tcTGCCACGTAATAGAGGGGCTGG	24668	Nme2Cas9	93	0
1071	GGGG	GGCTGTGATGTAGAAGGAATC	24669	SauriCas9	93	0
1072	GGGG	GGCTGTGATGTAGAAGGAATC	24670	SauriCas9-KKH	93	0
1073	GGG	GCTGTGATGTAGAAGGAATC	24671	ScaCas9	93	0
1074	GGG	GCTGTGATGTAGAAGGAATC	24672	ScaCas9-HiFi-Sc++	93	0
1075	GGG	GCTGTGATGTAGAAGGAATC	24673	ScaCas9-Sc++	93	0
1076	GGG	GCTGTGATGTAGAAGGAATC	24674	SpyCas9	93	0
1077	GGG	GCTGTGATGTAGAAGGAATC	24675	SpyCas9-HF1	93	0
1078	GGG	GCTGTGATGTAGAAGGAATC	24676	SpyCas9-SpG	93	0
1079	GGG	GCTGTGATGTAGAAGGAATC	24677	SpyCas9-SpRY	93	0
1080	GG	GCTGTGATGTAGAAGGAATC	24678	SpyCas9-NG	93	0
1081	GG	GCTGTGATGTAGAAGGAATC	24679	SpyCas9-xCas	93	0
1082	GG	GCTGTGATGTAGAAGGAATC	24680	SpyCas9-xCas-NG	93	0

1083	AAC	CCACGTAATAGAGGGGCTGG	24681	SpyCas9-SpRY	93	0
1084	AACTCCGT	ctgcCACGTAATAGAGGGGCTGG	24682	BlatCas9	93	0
1085	AACTC	ctgcCACGTAATAGAGGGGCTGG	24683	BlatCas9	93	0
1086	GGGGTG	GGCTGTGATGTAGAAGGAATC	24684	cCas9-v16	93	0
1087	GGGGTG	GGCTGTGATGTAGAAGGAATC	24685	cCas9-v21	93	0
1088	AACT	CCACGTAATAGAGGGGCTGG	24686	SpyCas9-3var-NRCH	93	0
1089	CGGGG	ttGGGCTGTGATGTAGAAGGAAT	24687	SauCas9	94	0
1090	CGGGG	GGGCTGTGATGTAGAAGGAAT	24688	SauCas9KKH	94	0
1091	CGGGGT	ttGGGCTGTGATGTAGAAGGAAT	24689	SauCas9	94	0
1092	CGGGGT	GGGCTGTGATGTAGAAGGAAT	24690	SauCas9KKH	94	0
1093	CGGGGT	GGGCTGTGATGTAGAAGGAAT	24691	cCas9-v17	94	0
1094	CGGGGT	GGGCTGTGATGTAGAAGGAAT	24692	cCas9-v42	94	0
1095	CGGG	GGGCTGTGATGTAGAAGGAAT	24693	SauriCas9	94	0
1096	CGGG	GGGCTGTGATGTAGAAGGAAT	24694	SauriCas9-KKH	94	0
1097	CGG	GGCTGTGATGTAGAAGGAAT	24695	ScaCas9	94	0
1098	CGG	GGCTGTGATGTAGAAGGAAT	24696	ScaCas9-HiFi-Sc++	94	0
1099	CGG	GGCTGTGATGTAGAAGGAAT	24697	ScaCas9-Sc++	94	0
1100	CGG	GGCTGTGATGTAGAAGGAAT	24698	SpyCas9	94	0
1101	CGG	GGCTGTGATGTAGAAGGAAT	24699	SpyCas9-HF1	94	0
1102	CGG	GGCTGTGATGTAGAAGGAAT	24700	SpyCas9-SpG	94	0
1103	CGG	GGCTGTGATGTAGAAGGAAT	24701	SpyCas9-SpRY	94	0
1104	CG	GGCTGTGATGTAGAAGGAAT	24702	SpyCas9-NG	94	0
1105	CG	GGCTGTGATGTAGAAGGAAT	24703	SpyCas9-xCas	94	0
1106	CG	GGCTGTGATGTAGAAGGAAT	24704	SpyCas9-xCas-NG	94	0
1107	GAA	GCCACGTAATAGAGGGGCTG	24705	SpyCas9-SpRY	94	0
1108	GAA	GCCACGTAATAGAGGGGCTG	24706	SpyCas9-xCas	94	0
1109	GAACTCC	CTGCCACGTAATAGAGGGGCTG	24707	CdiCas9	94	0
1110	GAAC	GCCACGTAATAGAGGGGCTG	24708	SpyCas9-3var-NRRH	94	0
1111	GAAC	tgCCACGTAATAGAGGGGCTG	24709	iSpyMacCas9	94	0
1112	TCGGG	ttTGGGCTGTGATGTAGAAGGAA	24710	SauCas9	95	0
1113	TCGGG	TGGGCTGTGATGTAGAAGGAA	24711	SauCas9KKH	95	0

1114	TCGG	TGGGCTGTGATGTAGAAGGAA	24712	SauriCas9	95	0
1115	TCGG	TGGGCTGTGATGTAGAAGGAA	24713	SauriCas9-KKH	95	0
1116	TCG	GGGCTGTGATGTAGAAGGAA	24714	ScaCas9	95	0
1117	TCG	GGGCTGTGATGTAGAAGGAA	24715	ScaCas9-HiFi-Sc++	95	0
1118	TCG	GGGCTGTGATGTAGAAGGAA	24716	ScaCas9-Sc++	95	0
1119	TCG	GGGCTGTGATGTAGAAGGAA	24717	SpyCas9-SpRY	95	0
1120	GG	TGCCACGTAATAGAGGGGCT	24718	SpyCas9-NG	95	0
1121	GG	TGCCACGTAATAGAGGGGCT	24719	SpyCas9-xCas	95	0
1122	GG	TGCCACGTAATAGAGGGGCT	24720	SpyCas9-xCas-NG	95	0
1123	GGA	TGCCACGTAATAGAGGGGCT	24721	SpyCas9-SpG	95	0
1124	GGA	TGCCACGTAATAGAGGGGCT	24722	SpyCas9-SpRY	95	0
1125	GGAAC	ctctGCCACGTAATAGAGGGGCT	24723	BlatCas9	95	0
1126	GGAACT	CTGCCACGTAATAGAGGGGCT	24724	cCas9-v16	95	0
1127	GGAACT	CTGCCACGTAATAGAGGGGCT	24725	cCas9-v21	95	0
1128	TCGGGG	TGGGCTGTGATGTAGAAGGAA	24726	cCas9-v17	95	0
1129	TCGGGG	TGGGCTGTGATGTAGAAGGAA	24727	cCas9-v42	95	0
1130	GGAACTC	TCTGCCACGTAATAGAGGGGCT	24728	CdiCas9	95	0
1131	GGAA	TGCCACGTAATAGAGGGGCT	24729	SpyCas9-3var-NRRH	95	0
1132	GGAA	TGCCACGTAATAGAGGGGCT	24730	SpyCas9-VQR	95	0
1133	TGGAA	tcTCTGCCACGTAATAGAGGGGC	24731	SauCas9	96	0
1134	TGGAA	TCTGCCACGTAATAGAGGGGC	24732	SauCas9KKH	96	0
1135	ATCGG	TTGGGCTGTGATGTAGAAGGA	24733	SauCas9KKH	96	0
1136	TGG	CTGCCACGTAATAGAGGGGC	24734	ScaCas9	96	0
1137	TGG	CTGCCACGTAATAGAGGGGC	24735	ScaCas9-HiFi-Sc++	96	0
1138	TGG	CTGCCACGTAATAGAGGGGC	24736	ScaCas9-Sc++	96	0
1139	TGG	CTGCCACGTAATAGAGGGGC	24737	SpyCas9	96	0
1140	TGG	CTGCCACGTAATAGAGGGGC	24738	SpyCas9-HF1	96	0
1141	TGG	CTGCCACGTAATAGAGGGGC	24739	SpyCas9-SpG	96	0
1142	TGG	CTGCCACGTAATAGAGGGGC	24740	SpyCas9-SpRY	96	0
1143	TG	CTGCCACGTAATAGAGGGGC	24741	SpyCas9-NG	96	0
1144	TG	CTGCCACGTAATAGAGGGGC	24742	SpyCas9-xCas	96	0

1145	TG	CTGCCACGTAATAGAGGGGC	24743	SpyCas9-xCas-NG	96	0
1146	ATC	TGGGCTGTGATGTAGAAGGA	24744	SpyCas9-SpRY	96	0
1147	TGGAAC	TCTGCCACGTAATAGAGGGGC	24745	cCas9-v17	96	0
1148	TGGAAC	TCTGCCACGTAATAGAGGGGC	24746	cCas9-v42	96	0
1149	ATCGGG	TTGGGCTGTGATGTAGAAGGA	24747	cCas9-v17	96	0
1150	ATCGGG	TTGGGCTGTGATGTAGAAGGA	24748	cCas9-v42	96	0
1151	TGGAACT	CTCTGCCACGTAATAGAGGGGC	24749	CdiCas9	96	0
1152	TGGA	CTGCCACGTAATAGAGGGGC	24750	SpyCas9-3var-NRRH	96	0
1153	CTGGA	ctCTCTGCCACGTAATAGAGGGG	24751	SauCas9	97	0
1154	CTGGA	CTCTGCCACGTAATAGAGGGG	24752	SauCas9KKH	97	0
1155	CTGG	CTCTGCCACGTAATAGAGGGG	24753	SauriCas9	97	0
1156	CTGG	CTCTGCCACGTAATAGAGGGG	24754	SauriCas9-KKH	97	0
1157	CTG	TCTGCCACGTAATAGAGGGG	24755	ScaCas9	97	0
1158	CTG	TCTGCCACGTAATAGAGGGG	24756	ScaCas9-HiFi-Sc++	97	0
1159	CTG	TCTGCCACGTAATAGAGGGG	24757	ScaCas9-Sc++	97	0
1160	CTG	TCTGCCACGTAATAGAGGGG	24758	SpyCas9-SpRY	97	0
1161	AAT	TTGGGCTGTGATGTAGAAGG	24759	SpyCas9-SpRY	97	0
1162	CTGGAA	CTCTGCCACGTAATAGAGGGG	24760	cCas9-v17	97	0
1163	CTGGAA	CTCTGCCACGTAATAGAGGGG	24761	cCas9-v42	97	0
1164	AATC	TTGGGCTGTGATGTAGAAGG	24762	SpyCas9-3var-NRTH	97	0
1165	GCTGG	TCTCTGCCACGTAATAGAGGG	24763	SauCas9KKH	98	0
1166	GAA	TTTGGGCTGTGATGTAGAAG	24764	SpyCas9-SpRY	98	0
1167	GAA	TTTGGGCTGTGATGTAGAAG	24765	SpyCas9-xCas	98	0
1168	GCT	CTCTGCCACGTAATAGAGGG	24766	SpyCas9-SpRY	98	0
1169	GAATCGGG	gcatTTGGGCTGTGATGTAGAAG	24767	BlatCas9	98	0
1170	GAATC	gcatTTGGGCTGTGATGTAGAAG	24768	BlatCas9	98	0
1171	GAAT	TTTGGGCTGTGATGTAGAAG	24769	SpyCas9-3var-NRRH	98	0
1172	GAAT	atTTGGGCTGTGATGTAGAAG	24770	iSpyMacCas9	98	0
1173	GG	TCTCTGCCACGTAATAGAGG	24771	SpyCas9-NG	99	0
1174	GG	TCTCTGCCACGTAATAGAGG	24772	SpyCas9-xCas	99	0
1175	GG	TCTCTGCCACGTAATAGAGG	24773	SpyCas9-xCas-NG	99	0

1176	GG	ATTTGGGCTGTGATGTAGAA	24774	SpyCas9-NG	99	0
1177	GG	ATTTGGGCTGTGATGTAGAA	24775	SpyCas9-xCas	99	0
1178	GG	ATTTGGGCTGTGATGTAGAA	24776	SpyCas9-xCas-NG	99	0
1179	GGC	TCTCTGCCACGTAATAGAGG	24777	SpyCas9-SpG	99	0
1180	GGC	TCTCTGCCACGTAATAGAGG	24778	SpyCas9-SpRY	99	0
1181	GGA	ATTTGGGCTGTGATGTAGAA	24779	SpyCas9-SpG	99	0
1182	GGA	ATTTGGGCTGTGATGTAGAA	24780	SpyCas9-SpRY	99	0
1183	GGAA	ATTTGGGCTGTGATGTAGAA	24781	SpyCas9-3var-NRRH	99	0
1184	GGAA	ATTTGGGCTGTGATGTAGAA	24782	SpyCas9-VQR	99	0
1185	GGCT	TCTCTGCCACGTAATAGAGG	24783	SpyCas9-3var-NRCH	99	0
1186	AGGAA	caGCATTTGGGCTGTGATGTAGA	24784	SauCas9	100	0
1187	AGGAA	GCATTTGGGCTGTGATGTAGA	24785	SauCas9KKH	100	0
1188	AGGAAT	caGCATTTGGGCTGTGATGTAGA	24786	SauCas9	100	0
1189	AGGAAT	GCATTTGGGCTGTGATGTAGA	24787	SauCas9KKH	100	0
1190	AGGAAT	GCATTTGGGCTGTGATGTAGA	24788	cCas9-v17	100	0
1191	AGGAAT	GCATTTGGGCTGTGATGTAGA	24789	cCas9-v42	100	0
1192	GGG	CTCTCTGCCACGTAATAGAG	24790	ScaCas9	100	0
1193	GGG	CTCTCTGCCACGTAATAGAG	24791	ScaCas9-HiFi-Sc++	100	0
1194	GGG	CTCTCTGCCACGTAATAGAG	24792	ScaCas9-Sc++	100	0
1195	GGG	CTCTCTGCCACGTAATAGAG	24793	SpyCas9	100	0
1196	GGG	CTCTCTGCCACGTAATAGAG	24794	SpyCas9-HF1	100	0
1197	GGG	CTCTCTGCCACGTAATAGAG	24795	SpyCas9-SpG	100	0
1198	GGG	CTCTCTGCCACGTAATAGAG	24796	SpyCas9-SpRY	100	0
1199	AGG	CATTTGGGCTGTGATGTAGA	24797	ScaCas9	100	0
1200	AGG	CATTTGGGCTGTGATGTAGA	24798	ScaCas9-HiFi-Sc++	100	0
1201	AGG	CATTTGGGCTGTGATGTAGA	24799	ScaCas9-Sc++	100	0
1202	AGG	CATTTGGGCTGTGATGTAGA	24800	SpyCas9	100	0
1203	AGG	CATTTGGGCTGTGATGTAGA	24801	SpyCas9-HF1	100	0
1204	AGG	CATTTGGGCTGTGATGTAGA	24802	SpyCas9-SpG	100	0
1205	AGG	CATTTGGGCTGTGATGTAGA	24803	SpyCas9-SpRY	100	0

1206	GG	CTCTCTGCCACGTAATAGAG	24804	SpyCas9-NG	100	0
1207	GG	CTCTCTGCCACGTAATAGAG	24805	SpyCas9-xCas	100	0
1208	GG	CTCTCTGCCACGTAATAGAG	24806	SpyCas9-xCas-NG	100	0
1209	AG	CATTTGGGCTGTGATGTAGA	24807	SpyCas9-NG	100	0
1210	AG	CATTTGGGCTGTGATGTAGA	24808	SpyCas9-xCas	100	0
1211	AG	CATTTGGGCTGTGATGTAGA	24809	SpyCas9-xCas-NG	100	0
1212	AGGAATC	AGCATTTGGGCTGTGATGTAGA	24810	CdiCas9	100	0
1213	GGGC	CTCTCTGCCACGTAATAGAG	24811	SpyCas9-3var-NRRH	100	0
1214	AGGA	CATTTGGGCTGTGATGTAGA	24812	SpyCas9-3var-NRRH	100	0

In the exemplary template sequences provided herein, capital letters indicate "core nucleotides" while lower case letters indicate "flanking nucleotides." Herein, when an RNA sequence (e.g., a template RNA sequence) is said to comprise a particular sequence (e.g., a sequence of Tables 1A, 1B, 1C, or 1D or a portion thereof) that comprises thymine (T), it is of course understood that the RNA sequence may (and frequently does) comprise uracil (U) in place of T. For instance, the RNA sequence may comprise U at every position shown as T in the sequence in Tables 1A, 1B, 1C, or 1D. More specifically, the present disclosure provides an RNA sequence according to every gRNA spacer sequence shown in Tables 1A, 1B, 1C, or 1D, wherein the RNA sequence has a U in place of each T in the sequence in Tables 1A, 1B, 1C, or 1D.

In some embodiments of the systems and methods herein, the heterologous object sequence comprises the core nucleotides of an RT template sequence from Table 3A, Table 3B, Table 3C, or Table 3D. In some embodiments, the heterologous object sequence additionally comprises one or more (e.g., 2, 3, 4, 5, 10, 20, 30, 40, or all) consecutive nucleotides starting with the 3' end of the flanking nucleotides of the RT template sequence. In some embodiments, the heterologous object sequence comprises the core nucleotides of the RT template sequence of Table 3A, Table 3B, Table 3C, or Table 3D that corresponds to the gRNA spacer sequence. In the context of the sequence tables, a first component "corresponds to" a second component when both components have the same ID number in the referenced table. For example, for a gRNA spacer of ID #1, the *corresponding* RT template would be the RT template also having ID #1 in a table referencing the same mutation. In some embodiments, the heterologous object sequence

additionally comprises one or more consecutive nucleotides starting with the 3' end of the flanking nucleotides of the RT template sequence.

In some embodiments, the primer binding site (PBS) sequence has a sequence comprising the core nucleotides of a PBS sequence from the same row of Table 3A, Table 3B, Table 3C, or Table 3D as the RT template sequence. In some embodiments, the PBS sequence additionally comprises one or more (e.g., 1, 2, 3, 4, 5, 6, 7, or all) consecutive nucleotides starting with the 5' end of the flanking nucleotides of the primer region.

Table 3A: Exemplary RT sequence (heterologous object sequence) and PBS sequence pairs

Table 3A provides exemplified PBS sequences and heterologous object sequences (reverse transcription template regions) of a template RNA for correcting the pathogenic R408W mutation in PAH. The gRNA spacers from Table 1A were filtered, e.g., filtered by occurrence within 15 nt of the desired editing location and use of a Tier 1 Cas enzyme. PBS sequences and heterologous object sequences (reverse transcription template regions) were designed relative to the nick site directed by the cognate gRNA from Table 1A, as described in this application. For exemplification, these regions were designed to be 8-17 nt (priming) and 1-50 nt extended beyond the location of the edit (RT). Without wishing to be limited by example, given variability of length, sequences are provided that use the maximum length parameters and comprise all templates of shorter length within the given parameters. Sequences are shown with uppercase letters indicating core sequence and lowercase letters indicating flanking sequence that may be truncated within the described length parameters.

ID	RT Template Sequence	SEQ ID NO	PBS Sequence	SEQ ID NO
1	caagacctcaatcctttgggtgtatgggtcgtagcgaactgagaagggcCG	24813	AGGTATTGtggcagcaa	25003
2	tcactcaagcctgtggttttggtcttaggaactttgctgccacaataccTCG	24814	GCCCTTCTcagttcgct	25004
6	tcactcaagcctgtggttttggtcttaggaactttgctgccacaataccTCG	24815	GCCCTTCTcagttcgct	25005
7	caagacctcaatcctttgggtgtatgggtcgtagcgaactgagaagggcCGA	24816	GGTATTGTggcagcaaa	25006
10	tcactcaagcctgtggttttggtcttaggaactttgctgccacaataccTCGG	24817	CCCTTCTCagttcgcta	25007
13	tcactcaagcctgtggttttggtcttaggaactttgctgccacaataccTCGG	24818	CCCTTCTCagttcgcta	25008
14	tcactcaagcctgtggttttggtcttaggaactttgctgccacaataccTCGG	24819	CCCTTCTCagttcgcta	25009
17	tcactcaagcctgtggttttggtcttaggaactttgctgccacaataccTCGG	24820	CCCTTCTCagttcgcta	25010

18	caagacctcaatcctttgggtgtatgggtcgtagcgaactgagaagggcCGAG	24821	GTATTGTGgcagcaaag	25011
21	tcactcaagcctgtggttttggtcttaggaactttgctgccacaataccTCGG	24822	CCCTTCTCagttcgcta	25012
25	caagacctcaatcctttgggtgtatgggtcgtagcgaactgagaagggcCGAG	24823	GTATTGTGgcagcaaag	25013
26	caagacctcaatcctttgggtgtatgggtcgtagcgaactgagaagggcCGAG	24824	GTATTGTGgcagcaaag	25014
29	caagacctcaatcctttgggtgtatgggtcgtagcgaactgagaagggcCGAGG	24825	TATTGTGGcagcaaagt	25015
30	tcactcaagcctgtggttttggtcttaggaactttgctgccacaataccTCGGC	24826	CCTTCTCAgttcgctac	25016
31	tcactcaagcctgtggttttggtcttaggaactttgctgccacaataccTCGGC	24827	CCTTCTCAgttcgctac	25017
34	caagacctcaatcctttgggtgtatgggtcgtagcgaactgagaagggcCGAGG	24828	TATTGTGGcagcaaagt	25018
35	caagacctcaatcctttgggtgtatgggtcgtagcgaactgagaagggcCGAGG	24829	TATTGTGGcagcaaagt	25019
38	caagacctcaatcctttgggtgtatgggtcgtagcgaactgagaagggcCGAGG	24830	TATTGTGGcagcaaagt	25020
41	tcactcaagcctgtggttttggtcttaggaactttgctgccacaataccTCGGC	24831	CCTTCTCAgttcgctac	25021
42	tcactcaagcctgtggttttggtcttaggaactttgctgccacaataccTCGGC	24832	CCTTCTCAgttcgctac	25022
43	caagacctcaatcctttgggtgtatgggtcgtagcgaactgagaagggcCGAGG	24833	TATTGTGGcagcaaagt	25023
46	caagacctcaatcctttgggtgtatgggtcgtagcgaactgagaagggcCGAGG	24834	TATTGTGGcagcaaagt	25024
47	caagacctcaatcctttgggtgtatgggtcgtagcgaactgagaagggcCGAGG	24835	TATTGTGGcagcaaagt	25025
50	caagacctcaatcctttgggtgtatgggtcgtagcgaactgagaagggcCGAGGT	24836	ATTGTGGCagcaaagtt	25026
51	tcactcaagcctgtggttttggtcttaggaactttgctgccacaataccTCGGCC	24837	CTTCTCAGttcgctacg	25027
52	tcactcaagcctgtggttttggtcttaggaactttgctgccacaataccTCGGCC	24838	CTTCTCAGttcgctacg	25028
55	caagacctcaatcctttgggtgtatgggtcgtagcgaactgagaagggcCGAGGT	24839	ATTGTGGCagcaaagtt	25029
56	caagacctcaatcctttgggtgtatgggtcgtagcgaactgagaagggcCGAGGT	24840	ATTGTGGCagcaaagtt	25030
57	tcactcaagcctgtggttttggtcttaggaactttgctgccacaataccTCGGCC	24841	CTTCTCAGttcgctacg	25031
62	caagacctcaatcctttgggtgtatgggtcgtagcgaactgagaagggcCGAGGT	24842	ATTGTGGCagcaaagtt	25032
63	caagacctcaatcctttgggtgtatgggtcgtagcgaactgagaagggcCGAGGT	24843	ATTGTGGCagcaaagtt	25033
64	tcactcaagcctgtggttttggtcttaggaactttgctgccacaataccTCGGCC	24844	CTTCTCAGttcgctacg	25034
65	caagacctcaatcctttgggtgtatgggtcgtagcgaactgagaagggcCGAGGT	24845	ATTGTGGCagcaaagtt	25035
66	tcactcaagcctgtggttttggtcttaggaactttgctgccacaataccTCGGCCC	24846	TTCTCAGTtcgctacga	25036
67	caagacctcaatcctttgggtgtatgggtcgtagcgaactgagaagggcCGAGGTA	24847	TTGTGGCAgcaaagttc	25037

68	tcactcaagcctgtggttttggtcttaggaactttgctgccacaataccTCGGCCC	24848	TTCTCAGTtcgctacga	25038
69	caagacctcaatcctttgggtgtatgggtcgtagcgaactgagaagggcCGAGGTA	24849	TTGTGGCAgcaaagttc	25039
72	tcactcaagcctgtggttttggtcttaggaactttgctgccacaataccTCGGCCCT	24850	TCTCAGTTcgctacgac	25040
73	tcactcaagcctgtggttttggtcttaggaactttgctgccacaataccTCGGCCCT	24851	TCTCAGTTcgctacgac	25041
74	caagacctcaatcctttgggtgtatgggtcgtagcgaactgagaagggcCGAGGTAT	24852	TGTGGCAGcaaagttcc	25042
77	tcactcaagcctgtggttttggtcttaggaactttgctgccacaataccTCGGCCCTT	24853	CTCAGTTCgctacgacc	25043
81	tcactcaagcctgtggttttggtcttaggaactttgctgccacaataccTCGGCCCTT	24854	CTCAGTTCgctacgacc	25044
82	caagacctcaatcctttgggtgtatgggtcgtagcgaactgagaagggcCGAGGTATT	24855	GTGGCAGCaaagttcct	25045
86	tcactcaagcctgtggttttggtcttaggaactttgctgccacaataccTCGGCCCTTC	24856	TCAGTTCGctacgaccc	25046
87	tcactcaagcctgtggttttggtcttaggaactttgctgccacaataccTCGGCCCTTC	24857	TCAGTTCGctacgaccc	25047
90	tcactcaagcctgtggttttggtcttaggaactttgctgccacaataccTCGGCCCTTC	24858	TCAGTTCGctacgaccc	25048
91	tcactcaagcctgtggttttggtcttaggaactttgctgccacaataccTCGGCCCTTC	24859	TCAGTTCGctacgaccc	25049
94	caagacctcaatcctttgggtgtatgggtcgtagcgaactgagaagggcCGAGGTATTG	24860	TGGCAGCAaagttccta	25050
95	tcactcaagcctgtggttttggtcttaggaactttgctgccacaataccTCGGCCCTTC	24861	TCAGTTCGctacgaccc	25051
96	tcactcaagcctgtggttttggtcttaggaactttgctgccacaataccTCGGCCCTTC	24862	TCAGTTCGctacgaccc	25052
99	tcactcaagcctgtggttttggtcttaggaactttgctgccacaataccTCGGCCCTTCT	24863	CAGTTCGCtacgaccca	25053
100	tcactcaagcctgtggttttggtcttaggaactttgctgccacaataccTCGGCCCTTCT	24864	CAGTTCGCtacgaccca	25054
101	tcactcaagcctgtggttttggtcttaggaactttgctgccacaataccTCGGCCCTTCT	24865	CAGTTCGCtacgaccca	25055
104	tcactcaagcctgtggttttggtcttaggaactttgctgccacaataccTCGGCCCTTCT	24866	CAGTTCGCtacgaccca	25056
105	tcactcaagcctgtggttttggtcttaggaactttgctgccacaataccTCGGCCCTTCT	24867	CAGTTCGCtacgaccca	25057
108	tcactcaagcctgtggttttggtcttaggaactttgctgccacaataccTCGGCCCTTCT	24868	CAGTTCGCtacgaccca	25058
109	tcactcaagcctgtggttttggtcttaggaactttgctgccacaataccTCGGCCCTTCT	24869	CAGTTCGCtacgaccca	25059
112	caagacctcaatcctttgggtgtatgggtcgtagcgaactgagaagggcCGAGGTATTGT	24870	GGCAGCAAagttcctaa	25060
113	tcactcaagcctgtggttttggtcttaggaactttgctgccacaataccTCGGCCCTTCT	24871	CAGTTCGCtacgaccca	25061
114	tcactcaagcctgtggttttggtcttaggaactttgctgccacaataccTCGGCCCTTCT	24872	CAGTTCGCtacgaccca	25062
115	caagacctcaatcctttgggtgtatgggtcgtagcgaactgagaagggcCGAGGTATTGT	24873	GGCAGCAAagttcctaa	25063
116	tcactcaagcctgtggttttggtcttaggaactttgctgccacaataccTCGGCCCTTCT	24874	CAGTTCGCtacgaccca	25064

117	caagacctcaatcctttgggtgtatgggtcgtagcgaactgagaagggcCGAGGTATTGT	24875	GGCAGCAAAagttcctaa	25065
119	caagacctcaatcctttgggtgtatgggtcgtagcgaactgagaagggcCGAGGTATTGTG	24876	GCAGCAAAGttcctaag	25066
120	tcactcaagcctgtggttttggtcttaggaactttgctgccacaataccTCGGCCCTTCTC	24877	AGTTCGCTacgacccat	25067
121	tcactcaagcctgtggttttggtcttaggaactttgctgccacaataccTCGGCCCTTCTC	24878	AGTTCGCTacgacccat	25068
122	tcactcaagcctgtggttttggtcttaggaactttgctgccacaataccTCGGCCCTTCTC	24879	AGTTCGCTacgacccat	25069
123	tcactcaagcctgtggttttggtcttaggaactttgctgccacaataccTCGGCCCTTCTC	24880	AGTTCGCTacgacccat	25070
126	tcactcaagcctgtggttttggtcttaggaactttgctgccacaataccTCGGCCCTTCTC	24881	AGTTCGCTacgacccat	25071
127	tcactcaagcctgtggttttggtcttaggaactttgctgccacaataccTCGGCCCTTCTC	24882	AGTTCGCTacgacccat	25072
128	caagacctcaatcctttgggtgtatgggtcgtagcgaactgagaagggcCGAGGTATTGTG	24883	GCAGCAAAGttcctaag	25073
129	caagacctcaatcctttgggtgtatgggtcgtagcgaactgagaagggcCGAGGTATTGTG	24884	GCAGCAAAGttcctaag	25074
130	caagacctcaatcctttgggtgtatgggtcgtagcgaactgagaagggcCGAGGTATTGTG	24885	GCAGCAAAGttcctaag	25075
134	tcactcaagcctgtggttttggtcttaggaactttgctgccacaataccTCGGCCCTTCTCA	24886	GTTCGCTAcgacccata	25076
135	tcactcaagcctgtggttttggtcttaggaactttgctgccacaataccTCGGCCCTTCTCA	24887	GTTCGCTAcgacccata	25077
138	tcactcaagcctgtggttttggtcttaggaactttgctgccacaataccTCGGCCCTTCTCA	24888	GTTCGCTAcgacccata	25078
140	caagacctcaatcctttgggtgtatgggtcgtagcgaactgagaagggcCGAGGTATTGTGG	24889	CAGCAAAGttcctaaga	25079
146	tcactcaagcctgtggttttggtcttaggaactttgctgccacaataccTCGGCCCTTCTCAG	24890	TTCGCTACgacccatac	25080
147	tcactcaagcctgtggttttggtcttaggaactttgctgccacaataccTCGGCCCTTCTCAG	24891	TTCGCTACgacccatac	25081
151	tcactcaagcctgtggttttggtcttaggaactttgctgccacaataccTCGGCCCTTCTCAG	24892	TTCGCTACgacccatac	25082
152	caagacctcaatcctttgggtgtatgggtcgtagcgaactgagaagggcCGAGGTATTGTGGC	24893	AGCAAAGTtcctaagac	25083
158	tcactcaagcctgtggttttggtcttaggaactttgctgccacaataccTCGGCCCTTCTCAGT	24894	TCGCTACGaccataca	25084
159	tcactcaagcctgtggttttggtcttaggaactttgctgccacaataccTCGGCCCTTCTCAGT	24895	TCGCTACGaccataca	25085
160	caagacctcaatcctttgggtgtatgggtcgtagcgaactgagaagggcCGAGGTATTGTGGCA	24896	GCAAAGTTcctaagacc	25086
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167	tcactcaagcctgtggttttggtcttaggaactttgctgccacaataccTCGGCCCTTCTCAGT	24899	TCGCTACGaccataca	25089
168	caagacctcaatcctttgggtgtatgggtcgtagcgaactgagaagggcCGAGGTATTGTGGCA	24900	GCAAAGTTcctaagacc	25090
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177	tcactcaagcctgtggttttggtcttaggaactttgctgccacaataccTCGGCCCTTCTCAGTT	24903	CGCTACGAccatacac	25093
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182	caagacctcaatcctttgggtgtatgggtcgtagcgaactgagaagggcCGAGGTATTGTGGCAG	24905	CAAAGTTCctaagacca	25095
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210	tcactcaagcctgtggttttggtcttaggaactttgctgccacaataccTCGGCCCTTCTCAGTTCGC	24919	TACGACCCatacaccca	25109
211	caagacctcaatcctttgggtgtatgggtcgtagcgaactgagaagggcCGAGGTATTGTGGCAGCAA	24920	AGTTCCTAagaccaaaa	25110
214	caagacctcaatcctttgggtgtatgggtcgtagcgaactgagaagggcCGAGGTATTGTGGCAGCAAA	24921	GTTCCTAAgaccaaaac	25111
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217	caagacctcaatcctttgggtgtatgggtcgtagcgaactgagaagggcCGAGGTATTGTGGCAGCAAA	24923	GTTCCTAAgaccaaaac	25113
218	caagacctcaatcctttgggtgtatgggtcgtagcgaactgagaagggcCGAGGTATTGTGGCAGCAAA	24924	GTTCCTAAgaccaaaac	25114
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230	caagacctcaatcctttgggtgtatgggtcgtagcgaactgagaagggcCGAGGTATTGTGGCAGCAAAG	24928	TTCCTAAGaccaaaacc	25118

231	tcactcaagcctgtggttttggtcttaggaactttgctgccacaataccTCGGCCCTTCTCAGTTCGCTA	24929	CGACCCATacacccaaa	25119
232	tcactcaagcctgtggttttggtcttaggaactttgctgccacaataccTCGGCCCTTCTCAGTTCGCTA	24930	CGACCCATacacccaaa	25120
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242	tcactcaagcctgtggttttggtcttaggaactttgctgccacaataccTCGGCCCTTCTCAGTTCGCTAC	24933	GACCCATAcacccaaag	25123
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246	caagacctcaatccttgggtgtatgggtcgtagcgaactgagaagggcCGAGGTATTGTGGCAGCAAAGT	24935	TCCTAAGAccaaaacca	25125
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257	caagacctcaatccttgggtgtatgggtcgtagcgaactgagaagggcCGAGGTATTGTGGCAGCAAAGTT	24940	CCTAAGACcaaaaccac	25130
258	caagacctcaatccttgggtgtatgggtcgtagcgaactgagaagggcCGAGGTATTGTGGCAGCAAAGTT	24941	CCTAAGACcaaaaccac	25131
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265	tcactcaagcctgtggttttggtcttaggaactttgctgccacaataccTCGGCCCTTCTCAGTTCGCTACGA	24943	CCCATACAccaaagga	25133
266	caagacctcaatccttgggtgtatgggtcgtagcgaactgagaagggcCGAGGTATTGTGGCAGCAAAGTTC	24944	CTAAGACCaaaaccaca	25134
268	tcactcaagcctgtggttttggtcttaggaactttgctgccacaataccTCGGCCCTTCTCAGTTCGCTACGAC	24945	CCATACACccaaaggat	25135
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271	tcactcaagcctgtggttttggtcttaggaactttgctgccacaataccTCGGCCCTTCTCAGTTCGCTACGAC	24948	CCATACACccaaaggat	25138
272	tcactcaagcctgtggttttggtcttaggaactttgctgccacaataccTCGGCCCTTCTCAGTTCGCTACGAC	24949	CCATACACccaaaggat	25139
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275	tcactcaagcctgtggttttggtcttaggaactttgctgccacaataccTCGGCCCTTCTCAGTTCGCTACGACC	24951	CATACACCcaaaggatt	25141
276	tcactcaagcctgtggttttggtcttaggaactttgctgccacaataccTCGGCCCTTCTCAGTTCGCTACGACC	24952	CATACACCcaaaggatt	25142
280	tcactcaagcctgtggttttggtcttaggaactttgctgccacaataccTCGGCCCTTCTCAGTTCGCTACGACC	24953	CATACACCcaaaggatt	25143
281	caagacctcaatccttgggtgtatgggtcgtagcgaactgagaagggcCGAGGTATTGTGGCAGCAAAGTTCCT	24954	AAGACCAAaaccacagg	25144
286	tcactcaagcctgtggttttggtcttaggaactttgctgccacaataccTCGGCCCTTCTCAGTTCGCTACGACCC	24955	ATACACCCaaaggattg	25145

287	tcactcaagcctgtggttttggtcttaggaactttgctgccacaataccTCGGCCCTTCTCAGTTCGCTACGACCC	24956	ATACACCCaaaggattg	25146
288	caagacctcaatcctttgggtgtatgggtcgtagcgaactgagaagggcCGAGGTATTGTGGCAGCAAAGTTCCTA	24957	AGACCAAAaccacaggc	25147
293	caagacctcaatcctttgggtgtatgggtcgtagcgaactgagaagggcCGAGGTATTGTGGCAGCAAAGTTCCTAA	24958	GACCAAAAccacaggct	25148
297	caagacctcaatcctttgggtgtatgggtcgtagcgaactgagaagggcCGAGGTATTGTGGCAGCAAAGTTCCTAA	24959	GACCAAAAccacaggct	25149
298	tcactcaagcctgtggttttggtcttaggaactttgctgccacaataccTCGGCCCTTCTCAGTTCGCTACGACCCA	24960	TACACCCAaaggattga	25150
299	caagacctcaatcctttgggtgtatgggtcgtagcgaactgagaagggcCGAGGTATTGTGGCAGCAAAGTTCCTAA	24961	GACCAAAAccacaggct	25151
300	caagacctcaatcctttgggtgtatgggtcgtagcgaactgagaagggcCGAGGTATTGTGGCAGCAAAGTTCCTAA	24962	GACCAAAAccacaggct	25152
306	caagacctcaatcctttgggtgtatgggtcgtagcgaactgagaagggcCGAGGTATTGTGGCAGCAAAGTTCCTAAG	24963	ACCAAAACcacaggctt	25153
307	caagacctcaatcctttgggtgtatgggtcgtagcgaactgagaagggcCGAGGTATTGTGGCAGCAAAGTTCCTAAG	24964	ACCAAAACcacaggctt	25154
310	caagacctcaatcctttgggtgtatgggtcgtagcgaactgagaagggcCGAGGTATTGTGGCAGCAAAGTTCCTAAG	24965	ACCAAAACcacaggctt	25155
311	caagacctcaatcctttgggtgtatgggtcgtagcgaactgagaagggcCGAGGTATTGTGGCAGCAAAGTTCCTAAG	24966	ACCAAAACcacaggctt	25156
314	caagacctcaatcctttgggtgtatgggtcgtagcgaactgagaagggcCGAGGTATTGTGGCAGCAAAGTTCCTAAG	24967	ACCAAAACcacaggctt	25157
315	tcactcaagcctgtggttttggtcttaggaactttgctgccacaataccTCGGCCCTTCTCAGTTCGCTACGACCCAT	24968	ACACCCAAaggattgag	25158
318	caagacctcaatcctttgggtgtatgggtcgtagcgaactgagaagggcCGAGGTATTGTGGCAGCAAAGTTCCTAAG	24969	ACCAAAACcacaggctt	25159
322	tcactcaagcctgtggttttggtcttaggaactttgctgccacaataccTCGGCCCTTCTCAGTTCGCTACGACCCAT	24970	ACACCCAAaggattgag	25160
328	caagacctcaatcctttgggtgtatgggtcgtagcgaactgagaagggcCGAGGTATTGTGGCAGCAAAGTTCCTAAGA	24971	CCAAAACCacaggcttg	25161
329	caagacctcaatcctttgggtgtatgggtcgtagcgaactgagaagggcCGAGGTATTGTGGCAGCAAAGTTCCTAAGA	24972	CCAAAACCacaggcttg	25162
330	caagacctcaatcctttgggtgtatgggtcgtagcgaactgagaagggcCGAGGTATTGTGGCAGCAAAGTTCCTAAGA	24973	CCAAAACCacaggcttg	25163
331	caagacctcaatcctttgggtgtatgggtcgtagcgaactgagaagggcCGAGGTATTGTGGCAGCAAAGTTCCTAAGA	24974	CCAAAACCacaggcttg	25164
334	tcactcaagcctgtggttttggtcttaggaactttgctgccacaataccTCGGCCCTTCTCAGTTCGCTACGACCCATA	24975	CACCCAAAggattgagg	25165
335	tcactcaagcctgtggttttggtcttaggaactttgctgccacaataccTCGGCCCTTCTCAGTTCGCTACGACCCATA	24976	CACCCAAAggattgagg	25166
338	tcactcaagcctgtggttttggtcttaggaactttgctgccacaataccTCGGCCCTTCTCAGTTCGCTACGACCCATA	24977	CACCCAAAggattgagg	25167
341	caagacctcaatcctttgggtgtatgggtcgtagcgaactgagaagggcCGAGGTATTGTGGCAGCAAAGTTCCTAAGA	24978	CCAAAACCacaggcttg	25168
342	caagacctcaatcctttgggtgtatgggtcgtagcgaactgagaagggcCGAGGTATTGTGGCAGCAAAGTTCCTAAGA	24979	CCAAAACCacaggcttg	25169
343	tcactcaagcctgtggttttggtcttaggaactttgctgccacaataccTCGGCCCTTCTCAGTTCGCTACGACCCATA	24980	CACCCAAAggattgagg	25170
346	tcactcaagcctgtggttttggtcttaggaactttgctgccacaataccTCGGCCCTTCTCAGTTCGCTACGACCCATA	24981	CACCCAAAggattgagg	25171
347	tcactcaagcctgtggttttggtcttaggaactttgctgccacaataccTCGGCCCTTCTCAGTTCGCTACGACCCATA	24982	CACCCAAAggattgagg	25172

351	caagacctcaatcctttgggtgtatgggtcgtagcgaactgagaagggcCGAGGTATTG TGGCAGCAAAGTTCCTAAGAC	24983	CAAAACCAc aggcttga	25173
352	tcactcaagcctgtggttttggtcttaggaactttgctgccacaataccTCGGCCCTTCTC AGTTCGCTACGACCCATAC	24984	ACCCAAAGg attgaggt	25174
353	tcactcaagcctgtggttttggtcttaggaactttgctgccacaataccTCGGCCCTTCTC AGTTCGCTACGACCCATAC	24985	ACCCAAAGg attgaggt	25175
354	caagacctcaatcctttgggtgtatgggtcgtagcgaactgagaagggcCGAGGTATTG TGGCAGCAAAGTTCCTAAGAC	24986	CAAAACCAc aggcttga	25176
357	tcactcaagcctgtggttttggtcttaggaactttgctgccacaataccTCGGCCCTTCTC AGTTCGCTACGACCCATAC	24987	ACCCAAAGg attgaggt	25177
358	tcactcaagcctgtggttttggtcttaggaactttgctgccacaataccTCGGCCCTTCTC AGTTCGCTACGACCCATAC	24988	ACCCAAAGg attgaggt	25178
361	tcactcaagcctgtggttttggtcttaggaactttgctgccacaataccTCGGCCCTTCTC AGTTCGCTACGACCCATAC	24989	ACCCAAAGg attgaggt	25179
362	tcactcaagcctgtggttttggtcttaggaactttgctgccacaataccTCGGCCCTTCTC AGTTCGCTACGACCCATAC	24990	ACCCAAAGg attgaggt	25180
365	caagacctcaatcctttgggtgtatgggtcgtagcgaactgagaagggcCGAGGTATTG TGGCAGCAAAGTTCCTAAGAC	24991	CAAAACCAc aggcttga	25181
366	caagacctcaatcctttgggtgtatgggtcgtagcgaactgagaagggcCGAGGTATTG TGGCAGCAAAGTTCCTAAGAC	24992	CAAAACCAc aggcttga	25182
369	tcactcaagcctgtggttttggtcttaggaactttgctgccacaataccTCGGCCCTTCTC AGTTCGCTACGACCCATACA	24993	CCCAAAGGat tgaggtc	25183
370	tcactcaagcctgtggttttggtcttaggaactttgctgccacaataccTCGGCCCTTCTC AGTTCGCTACGACCCATACA	24994	CCCAAAGGat tgaggtc	25184
371	tcactcaagcctgtggttttggtcttaggaactttgctgccacaataccTCGGCCCTTCTC AGTTCGCTACGACCCATACA	24995	CCCAAAGGat tgaggtc	25185
372	tcactcaagcctgtggttttggtcttaggaactttgctgccacaataccTCGGCCCTTCTC AGTTCGCTACGACCCATACA	24996	CCCAAAGGat tgaggtc	25186
375	caagacctcaatcctttgggtgtatgggtcgtagcgaactgagaagggcCGAGGTATTG TGGCAGCAAAGTTCCTAAGACC	24997	AAAACCACa ggcttgag	25187
376	tcactcaagcctgtggttttggtcttaggaactttgctgccacaataccTCGGCCCTTCTC AGTTCGCTACGACCCATACA	24998	CCCAAAGGat tgaggtc	25188
377	tcactcaagcctgtggttttggtcttaggaactttgctgccacaataccTCGGCCCTTCTC AGTTCGCTACGACCCATACA	24999	CCCAAAGGat tgaggtc	25189
380	tcactcaagcctgtggttttggtcttaggaactttgctgccacaataccTCGGCCCTTCTC AGTTCGCTACGACCCATACA	25000	CCCAAAGGat tgaggtc	25190
381	tcactcaagcctgtggttttggtcttaggaactttgctgccacaataccTCGGCCCTTCTC AGTTCGCTACGACCCATACA	25001	CCCAAAGGat tgaggtc	25191
382	caagacctcaatcctttgggtgtatgggtcgtagcgaactgagaagggcCGAGGTATTG TGGCAGCAAAGTTCCTAAGACC	25002	AAAACCACa ggcttgag	25192

Table 3B: Exemplary RT sequence (heterologous object sequence) and PBS sequence pairs

Table 3B provides exemplified PBS sequences and heterologous object sequences (reverse transcription template regions) of a template RNA for correcting the pathogenic R261Q mutation in PAH. The gRNA spacers from Table 1B were filtered, e.g., filtered by occurrence within 15 nt of the desired editing location and use of a Tier 1 Cas enzyme. PBS sequences and heterologous object sequences (reverse transcription template regions) were designed relative to the nick site directed by the cognate gRNA from Table 1B, as described in this application. For exemplification, these regions were designed to be 8-17 nt

(priming) and 1-50 nt extended beyond the location of the edit (RT). Without wishing to be limited by example, given variability of length, sequences are provided that use the maximum length parameters and comprise all templates of shorter length within the given parameters. Sequences are shown with uppercase letters indicating core sequence and lowercase letters indicating flanking sequence that may be truncated within the described length parameters.

ID	RT Template Sequence	SEQ ID NO	PBS Sequence	SEQ ID NO
1	tatacatgggcttggatccatgtctgatgtactgtgtgcagtggaagacTC	25193	GGAAGGCCaggccaccc	25370
2	tatacatgggcttggatccatgtctgatgtactgtgtgcagtggaagacTC	25194	GGAAGGCCaggccaccc	25371
3	tatacatgggcttggatccatgtctgatgtactgtgtgcagtggaagacTC	25195	GGAAGGCCaggccaccc	25372
4	tgtggctggcctgctttcctctcgggatttcttgggtggcctggccttcCGA	25196	GTCTTCCActgcacaca	25373
5	tgtggctggcctgctttcctctcgggatttcttgggtggcctggccttcCGA	25197	GTCTTCCActgcacaca	25374
8	tgtggctggcctgctttcctctcgggatttcttgggtggcctggccttcCGA	25198	GTCTTCCActgcacaca	25375
10	tatacatgggcttggatccatgtctgatgtactgtgtgcagtggaagacTCG	25199	GAAGGCCAggccaccca	25376
13	tgtggctggcctgctttcctctcgggatttcttgggtggcctggccttcCGAG	25200	TCTTCCACtgcacacag	25377
14	tatacatgggcttggatccatgtctgatgtactgtgtgcagtggaagacTCGG	25201	AAGGCCAGgccacccaa	25378
17	tgtggctggcctgctttcctctcgggatttcttgggtggcctggccttcCGAG	25202	TCTTCCACtgcacacag	25379
21	tatacatgggcttggatccatgtctgatgtactgtgtgcagtggaagacTCGG	25203	AAGGCCAGgccacccaa	25380
23	tgtggctggcctgctttcctctcgggatttcttgggtggcctggccttcCGAG	25204	TCTTCCACtgcacacag	25381
29	tgtggctggcctgctttcctctcgggatttcttgggtggcctggccttcCGAGT	25205	CTTCCACTgcacacagt	25382
30	tgtggctggcctgctttcctctcgggatttcttgggtggcctggccttcCGAGT	25206	CTTCCACTgcacacagt	25383
33	tatacatgggcttggatccatgtctgatgtactgtgtgcagtggaagacTCGGA	25207	AGGCCAGGccacccaag	25384
34	tatacatgggcttggatccatgtctgatgtactgtgtgcagtggaagacTCGGA	25208	AGGCCAGGccacccaag	25385
37	tgtggctggcctgctttcctctcgggatttcttgggtggcctggccttcCGAGT	25209	CTTCCACTgcacacagt	25386
38	tgtggctggcctgctttcctctcgggatttcttgggtggcctggccttcCGAGT	25210	CTTCCACTgcacacagt	25387
41	tgtggctggcctgctttcctctcgggatttcttgggtggcctggccttcCGAGT	25211	CTTCCACTgcacacagt	25388
42	tgtggctggcctgctttcctctcgggatttcttgggtggcctggccttcCGAGT	25212	CTTCCACTgcacacagt	25389
45	tatacatgggcttggatccatgtctgatgtactgtgtgcagtggaagacTCGGA	25213	AGGCCAGGccacccaag	25390

51	tgtggctggcctgctttcctctcgggatttcttgggtggcctggccttcCGAGTC	25214	TTCCACTGcacacagta	25391
52	tgtggctggcctgctttcctctcgggatttcttgggtggcctggccttcCGAGTC	25215	TTCCACTGcacacagta	25392
53	tgtggctggcctgctttcctctcgggatttcttgggtggcctggccttcCGAGTC	25216	TTCCACTGcacacagta	25393
54	tgtggctggcctgctttcctctcgggatttcttgggtggcctggccttcCGAGTC	25217	TTCCACTGcacacagta	25394
55	tatacatgggcttggatccatgtctgatgtactgtgtgcagtggaagacTCGGAA	25218	GGCCAGGCcacccaaga	25395
60	tgtggctggcctgctttcctctcgggatttcttgggtggcctggccttcCGAGTC	25219	TTCCACTGcacacagta	25396
61	tgtggctggcctgctttcctctcgggatttcttgggtggcctggccttcCGAGTC	25220	TTCCACTGcacacagta	25397
62	tatacatgggcttggatccatgtctgatgtactgtgtgcagtggaagacTCGGAA	25221	GGCCAGGCcacccaaga	25398
65	tatacatgggcttggatccatgtctgatgtactgtgtgcagtggaagacTCGGAAG	25222	GCCAGGCCaccaagaa	25399
66	tgtggctggcctgctttcctctcgggatttcttgggtggcctggccttcCGAGTCT	25223	TCCACTGCacacagtac	25400
67	tatacatgggcttggatccatgtctgatgtactgtgtgcagtggaagacTCGGAAG	25224	GCCAGGCCaccaagaa	25401
70	tgtggctggcctgctttcctctcgggatttcttgggtggcctggccttcCGAGTCT	25225	TCCACTGCacacagtac	25402
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137	tgtggctggcctgctttcctctcgggatttcttgggtggcctggccttcCGAGTCTTCCACTG	25258	CACACAGTacatcagac	25435
140	tgtggctggcctgctttcctctcgggatttcttgggtggcctggccttcCGAGTCTTCCACTG	25259	CACACAGTacatcagac	25436
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259	tatacatgggcttggatccatgtctgatgtactgtgtgcagtggaagacTCGGAAGGCCAGGCCACCCAAG	25320	AAATCCCGaggaggaaag	25497
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263	tatacatgggcttggatccatgtctgatgtactgtgtgcagtggaagacTCGGAAGGCCAGGCCACCCAAG	25322	AAATCCCGaggaggaaag	25499
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287	tatacatgggcttggatccatgtctgatgtactgtgtgcagtggaagacTCGGAAGGCCAGGCCACCCAAGAA	25332	ATCCCGAGaggaaagca	25509
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309	tatacatgggcttggatccatgtctgatgtactgtgtgcagtggaagacTCGGAAGGCCAGGCCACCCAAGAAATC	25347	CCGAGAGGaaagcaggc	25524
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314	tgtggctggcctgctttcctctcgggatttcttgggtggcctggccttcCGAGTCTTCCACTGCACACAGTACATCA	25349	GACATGGAtccaagccc	25526
315	tatacatgggcttggatccatgtctgatgtactgtgtgcagtggaagacTCGGAAGGCCAGGCCACCCAAGAAATCC	25350	CGAGAGGAaagcaggcc	25527
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358	tatacatgggcttggatccatgtctgatgtactgtgtgcagtggaagacTCGGAAGGCCAGGCCACCCAAGAAATCCCGAG	25368	AGGAAAGCaggccagcc	25545
359	tatacatgggcttggatccatgtctgatgtactgtgtgcagtggaagacTCGGAAGGCCAGGCCACCCAAGAAATCCCGAG	25369	AGGAAAGCaggccagcc	25546

Table 3C: Exemplary RT sequence (heterologous object sequence) and PBS sequence pairs

Table 3C provides exemplified PBS sequences and heterologous object sequences (reverse transcription template regions) of a template RNA for correcting the pathogenic R243Q mutation in PAH. The gRNA spacers from Table 1C were filtered, e.g., filtered by occurrence within 15 nt of the desired editing location and use of a Tier 1 Cas enzyme. PBS sequences and heterologous object sequences (reverse transcription template regions) were designed relative to the nick site directed by the cognate gRNA from

Table 1C, as described in this application. For exemplification, these regions were designed to be 8-17 nt (priming) and 1-50 nt extended beyond the location of the edit (RT). Without wishing to be limited by example, given variability of length, sequences are provided that use the maximum length parameters and comprise all templates of shorter length within the given parameters. Sequences are shown with uppercase letters indicating core sequence and lowercase letters indicating flanking sequence that may be truncated within the described length parameters.

ID	RT Template Sequence	SEQ ID NO	PBS Sequence	SEQ ID NO
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303	ttgagttttctttcttctttttcatcccagcttgcactggtttccgcctcCGACCTGTGGCTGG CCTGCTTTCCTCTCG	25703	GGATTTCTtg ggtggcc	25888
304	ttgagttttctttcttctttttcatcccagcttgcactggtttccgcctcCGACCTGTGGCTGG CCTGCTTTCCTCTCG	25704	GGATTTCTtg ggtggcc	25889
305	ttgagttttctttcttctttttcatcccagcttgcactggtttccgcctcCGACCTGTGGCTGG CCTGCTTTCCTCTCG	25705	GGATTTCTtg ggtggcc	25890
306	ttgagttttctttcttctttttcatcccagcttgcactggtttccgcctcCGACCTGTGGCTGG CCTGCTTTCCTCTCG	25706	GGATTTCTtg ggtggcc	25891
309	ttgagttttctttcttctttttcatcccagcttgcactggtttccgcctcCGACCTGTGGCTGG CCTGCTTTCCTCTCG	25707	GGATTTCTtg ggtggcc	25892
310	ttgagttttctttcttctttttcatcccagcttgcactggtttccgcctcCGACCTGTGGCTGG CCTGCTTTCCTCTCG	25708	GGATTTCTtg ggtggcc	25893
313	aggccaggccacccaagaaatcccgagaggaaagcaggccagccacaggTCGGAGGC GGAAACCAGTGCAAGCTGGGA	25709	TGAAAAGAa gaaagaaa	25894
314	aggccaggccacccaagaaatcccgagaggaaagcaggccagccacaggTCGGAGGC GGAAACCAGTGCAAGCTGGGA	25710	TGAAAAGAa gaaagaaa	25895
315	ttgagttttctttcttctttttcatcccagcttgcactggtttccgcctcCGACCTGTGGCTGG CCTGCTTTCCTCTCG	25711	GGATTTCTtg ggtggcc	25896
319	ttgagttttctttcttctttttcatcccagcttgcactggtttccgcctcCGACCTGTGGCTGG CCTGCTTTCCTCTCGG	25712	GATTTCTTgg gtggcct	25897
320	ttgagttttctttcttctttttcatcccagcttgcactggtttccgcctcCGACCTGTGGCTGG CCTGCTTTCCTCTCGG	25713	GATTTCTTgg gtggcct	25898
322	aggccaggccacccaagaaatcccgagaggaaagcaggccagccacaggTCGGAGGC GGAAACCAGTGCAAGCTGGGAT	25714	GAAAAGAA gaaagaaaa	25899
323	ttgagttttctttcttctttttcatcccagcttgcactggtttccgcctcCGACCTGTGGCTGG CCTGCTTTCCTCTCGG	25715	GATTTCTTgg gtggcct	25900
327	ttgagttttctttcttctttttcatcccagcttgcactggtttccgcctcCGACCTGTGGCTGG CCTGCTTTCCTCTCGG	25716	GATTTCTTgg gtggcct	25901
328	aggccaggccacccaagaaatcccgagaggaaagcaggccagccacaggTCGGAGGC GGAAACCAGTGCAAGCTGGGAT	25717	GAAAAGAA gaaagaaaa	25902
329	ttgagttttctttcttctttttcatcccagcttgcactggtttccgcctcCGACCTGTGGCTGG CCTGCTTTCCTCTCGG	25718	GATTTCTTgg gtggcct	25903
330	aggccaggccacccaagaaatcccgagaggaaagcaggccagccacaggTCGGAGGC GGAAACCAGTGCAAGCTGGGAT	25719	GAAAAGAA gaaagaaaa	25904
331	aggccaggccacccaagaaatcccgagaggaaagcaggccagccacaggTCGGAGGC GGAAACCAGTGCAAGCTGGGAT	25720	GAAAAGAA gaaagaaaa	25905
336	ttgagttttctttcttctttttcatcccagcttgcactggtttccgcctcCGACCTGTGGCTGG CCTGCTTTCCTCTCGGG	25721	ATTTCTTGgg tggcctg	25906
337	ttgagttttctttcttctttttcatcccagcttgcactggtttccgcctcCGACCTGTGGCTGG CCTGCTTTCCTCTCGGG	25722	ATTTCTTGgg tggcctg	25907
338	aggccaggccacccaagaaatcccgagaggaaagcaggccagccacaggTCGGAGGC GGAAACCAGTGCAAGCTGGGATG	25723	AAAAGAAG aaagaaaac	25908
341	ttgagttttctttcttctttttcatcccagcttgcactggtttccgcctcCGACCTGTGGCTGG CCTGCTTTCCTCTCGGG	25724	ATTTCTTGgg tggcctg	25909
342	ttgagttttctttcttctttttcatcccagcttgcactggtttccgcctcCGACCTGTGGCTGG CCTGCTTTCCTCTCGGG	25725	ATTTCTTGgg tggcctg	25910
343	aggccaggccacccaagaaatcccgagaggaaagcaggccagccacaggTCGGAGGC GGAAACCAGTGCAAGCTGGGATG	25726	AAAAGAAG aaagaaaac	25911
350	ttgagttttctttcttctttttcatcccagcttgcactggtttccgcctcCGACCTGTGGCTGG CCTGCTTTCCTCTCGGGA	25727	TTTCTTGGgt ggcctgg	25912
351	ttgagttttctttcttctttttcatcccagcttgcactggtttccgcctcCGACCTGTGGCTGG CCTGCTTTCCTCTCGGGA	25728	TTTCTTGGgt ggcctgg	25913

353	ttgagttttctttcttcttttcatcccagcttgcactggtttccgcctcCGACCTGTGGCTGG CCTGCTTTCCTCTCGGGA	25729	TTTCTTGGgtggcctgg	25914
357	ttgagttttctttcttcttttcatcccagcttgcactggtttccgcctcCGACCTGTGGCTGG CCTGCTTTCCTCTCGGGA	25730	TTTCTTGGgtggcctgg	25915
358	aggccaggccacccaagaaatcccgagaggaaagcaggccagccacaggTCGGAGGC GGAAACCAGTGCAAGCTGGGATGA	25731	AAAGAAGAaagaaaact	25916

Table 3D: Exemplary RT sequence (heterologous object sequence) and PBS sequence pairs

Table 3D provides exemplified PBS sequences and heterologous object sequences (reverse transcription template regions) of a template RNA for correcting the pathogenic IVS10-11G>A mutation in PAH. The gRNA spacers from Table 1D were filtered, e.g., filtered by occurrence within 15 nt of the desired editing location and use of a Tier 1 Cas enzyme. PBS sequences and heterologous object sequences (reverse transcription template regions) were designed relative to the nick site directed by the cognate gRNA from Table 1D, as described in this application. For exemplification, these regions were designed to be 8-17 nt (priming) and 1-50 nt extended beyond the location of the edit (RT). Without wishing to be limited by example, given variability of length, sequences are provided that use the maximum length parameters and comprise all templates of shorter length within the given parameters. Sequences are shown with uppercase letters indicating core sequence and lowercase letters indicating flanking sequence that may be truncated within the described length parameters.

ID	RT Template Sequence	SEQ ID NO	PBS Sequence	SEQ ID NO
1	gctccaggggagaagctttggcttctctgataagcagtactgtaggccCC	25917	AAGTGAAAAagttattat	26066
2	gcagcagggaatactgatcctgatttaacagtgataataacttttcactTGG	25918	GGCCTACAgtactgctt	26067
3	gctccaggggagaagctttggcttctctgataagcagtactgtaggccCCA	25919	AGTGAAAAgttattatc	26068
6	gcagcagggaatactgatcctgatttaacagtgataataacttttcactTGG	25920	GGCCTACAgtactgctt	26069
10	gctccaggggagaagctttggcttctctgataagcagtactgtaggccCCA	25921	AGTGAAAAgttattatc	26070
12	gcagcagggaatactgatcctgatttaacagtgataataacttttcactTGG	25922	GGCCTACAgtactgctt	26071
16	gctccaggggagaagctttggcttctctgataagcagtactgtaggccCCAA	25923	GTGAAAAGttattatca	26072
17	gctccaggggagaagctttggcttctctgataagcagtactgtaggccCCAA	25924	GTGAAAAGttattatca	26073
20	gctccaggggagaagctttggcttctctgataagcagtactgtaggccCCAA	25925	GTGAAAAGttattatca	26074
23	gcagcagggaatactgatcctgatttaacagtgataataacttttcactTGGG	25926	GCCTACAGtactgctta	26075
24	gcagcagggaatactgatcctgatttaacagtgataataacttttcactTGGG	25927	GCCTACAGtactgctta	26076

25	gctccaggggagaagctttggcttctctgataagcagtactgtaggccCCAA	25928	GTGAAAAGttattatca	26077
28	gctccaggggagaagctttggcttctctgataagcagtactgtaggccCCAA	25929	GTGAAAAGttattatca	26078
31	gctccaggggagaagctttggcttctctgataagcagtactgtaggccCCAAG	25930	TGAAAAGTattatcac	26079
32	gctccaggggagaagctttggcttctctgataagcagtactgtaggccCCAAG	25931	TGAAAAGTattatcac	26080
33	gctccaggggagaagctttggcttctctgataagcagtactgtaggccCCAAG	25932	TGAAAAGTattatcac	26081
34	gcagcagggaatactgatcctgatttaacagtgataataacttttcactTGGGG	25933	CCTACAGTactgcttat	26082
39	gctccaggggagaagctttggcttctctgataagcagtactgtaggccCCAAG	25934	TGAAAAGTattatcac	26083
40	gctccaggggagaagctttggcttctctgataagcagtactgtaggccCCAAG	25935	TGAAAAGTattatcac	26084
43	gctccaggggagaagctttggcttctctgataagcagtactgtaggccCCAAG	25936	TGAAAAGTattatcac	26085
44	gctccaggggagaagctttggcttctctgataagcagtactgtaggccCCAAG	25937	TGAAAAGTattatcac	26086
47	gcagcagggaatactgatcctgatttaacagtgataataacttttcactTGGGG	25938	CCTACAGTactgcttat	26087
48	gctccaggggagaagctttggcttctctgataagcagtactgtaggccCCAAG	25939	TGAAAAGTattatcac	26088
49	gctccaggggagaagctttggcttctctgataagcagtactgtaggccCCAAG	25940	TGAAAAGTattatcac	26089
52	gctccaggggagaagctttggcttctctgataagcagtactgtaggccCCAAGT	25941	GAAAAGTTatatcact	26090
53	gctccaggggagaagctttggcttctctgataagcagtactgtaggccCCAAGT	25942	GAAAAGTTatatcact	26091
54	gcagcagggaatactgatcctgatttaacagtgataataacttttcactTGGGGC	25943	CTACAGTActgcttatc	26092
55	gcagcagggaatactgatcctgatttaacagtgataataacttttcactTGGGGC	25944	CTACAGTActgcttatc	26093
58	gctccaggggagaagctttggcttctctgataagcagtactgtaggccCCAAGT	25945	GAAAAGTTatatcact	26094
59	gctccaggggagaagctttggcttctctgataagcagtactgtaggccCCAAGT	25946	GAAAAGTTatatcact	26095
62	gctccaggggagaagctttggcttctctgataagcagtactgtaggccCCAAGT	25947	GAAAAGTTatatcact	26096
63	gctccaggggagaagctttggcttctctgataagcagtactgtaggccCCAAGT	25948	GAAAAGTTatatcact	26097
64	gcagcagggaatactgatcctgatttaacagtgataataacttttcactTGGGGC	25949	CTACAGTActgcttatc	26098
67	gcagcagggaatactgatcctgatttaacagtgataataacttttcactTGGGGCC	25950	TACAGTACtgcttatca	26099
68	gctccaggggagaagctttggcttctctgataagcagtactgtaggccCCAAGTG	25951	AAAAGTTAttatcactg	26100
69	gctccaggggagaagctttggcttctctgataagcagtactgtaggccCCAAGTG	25952	AAAAGTTAttatcactg	26101
70	gcagcagggaatactgatcctgatttaacagtgataataacttttcactTGGGGCC	25953	TACAGTACtgcttatca	26102
71	gctccaggggagaagctttggcttctctgataagcagtactgtaggccCCAAGTG	25954	AAAAGTTAttatcactg	26103

74	gctccaggggagaagctttggcttctctgataagcagtactgtaggccCCAAGTGA	25955	AAAGTTATtatcactgt	26104
75	gcagcagggaatactgatcctgatttaacagtgataataacttttcactTGGGGCCT	25956	ACAGTACTgcttatcag	26105
76	gctccaggggagaagctttggcttctctgataagcagtactgtaggccCCAAGTGA	25957	AAAGTTATtatcactgt	26106
77	gcagcagggaatactgatcctgatttaacagtgataataacttttcactTGGGGCCTA	25958	CAGTACTGctatcaga	26107
78	gctccaggggagaagctttggcttctctgataagcagtactgtaggccCCAAGTGAA	25959	AAGTTATTatcactgtt	26108
79	gcagcagggaatactgatcctgatttaacagtgataataacttttcactTGGGGCCTAC	25960	AGTACTGCttatcagag	26109
83	gcagcagggaatactgatcctgatttaacagtgataataacttttcactTGGGGCCTAC	25961	AGTACTGCttatcagag	26110
84	gctccaggggagaagctttggcttctctgataagcagtactgtaggccCCAAGTGAAA	25962	AGTTATTAtcactgtta	26111
85	gcagcagggaatactgatcctgatttaacagtgataataacttttcactTGGGGCCTAC	25963	AGTACTGCttatcagag	26112
86	gcagcagggaatactgatcctgatttaacagtgataataacttttcactTGGGGCCTAC	25964	AGTACTGCttatcagag	26113
87	gcagcagggaatactgatcctgatttaacagtgataataacttttcactTGGGGCCTAC	25965	AGTACTGCttatcagag	26114
90	gcagcagggaatactgatcctgatttaacagtgataataacttttcactTGGGGCCTACA	25966	GTACTGCTtatcagaga	26115
93	gcagcagggaatactgatcctgatttaacagtgataataacttttcactTGGGGCCTACA	25967	GTACTGCTtatcagaga	26116
94	gcagcagggaatactgatcctgatttaacagtgataataacttttcactTGGGGCCTACA	25968	GTACTGCTtatcagaga	26117
97	gcagcagggaatactgatcctgatttaacagtgataataacttttcactTGGGGCCTACA	25969	GTACTGCTtatcagaga	26118
98	gcagcagggaatactgatcctgatttaacagtgataataacttttcactTGGGGCCTACA	25970	GTACTGCTtatcagaga	26119
101	gctccaggggagaagctttggcttctctgataagcagtactgtaggccCCAAGTGAAAA	25971	GTTATTATcactgttaa	26120
102	gcagcagggaatactgatcctgatttaacagtgataataacttttcactTGGGGCCTACA	25972	GTACTGCTtatcagaga	26121
103	gcagcagggaatactgatcctgatttaacagtgataataacttttcactTGGGGCCTACA	25973	GTACTGCTtatcagaga	26122
106	gcagcagggaatactgatcctgatttaacagtgataataacttttcactTGGGGCCTACAG	25974	TACTGCTTatcagagaa	26123
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112	gcagcagggaatactgatcctgatttaacagtgataataacttttcactTGGGGCCTACAG	25978	TACTGCTTatcagagaa	26127
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116	gctccaggggagaagctttggcttctctgataagcagtactgtaggccCCAAGTGAAAAG	25982	TTATTATCactgttaaa	26131
119	gcagcagggaatactgatcctgatttaacagtgataataacttttcactTGGGGCCTACAGT	25983	ACTGCTTAtcagagaag	26132
120	gcagcagggaatactgatcctgatttaacagtgataataacttttcactTGGGGCCTACAGT	25984	ACTGCTTAtcagagaag	26133
121	gcagcagggaatactgatcctgatttaacagtgataataacttttcactTGGGGCCTACAGT	25985	ACTGCTTAtcagagaag	26134
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126	gcagcagggaatactgatcctgatttaacagtgataataacttttcactTGGGGCCTACAGTA	25988	CTGCTTATcagagaagc	26137
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136	gcagcagggaatactgatcctgatttaacagtgataataacttttcactTGGGGCCTACAGTAC	25992	TGCTTATCagagaagcc	26141
137	gcagcagggaatactgatcctgatttaacagtgataataacttttcactTGGGGCCTACAGTAC	25993	TGCTTATCagagaagcc	26142
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139	gcagcagggaatactgatcctgatttaacagtgataataacttttcactTGGGGCCTACAGTACT	25995	GCTTATCAgagaagcca	26144
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145	gctccaggggagaagctttggcttctctgataagcagtactgtaggccCCAAGTGAAAAGTTATTA	25999	TCACTGTTaaatcagga	26148
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154	gcagcagggaatactgatcctgatttaacagtgataataacttttcactTGGGGCCTACAGTACTGCT	26002	TATCAGAGaagccaaag	26151
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156	gcagcagggaatactgatcctgatttaacagtgataataacttttcactTGGGGCCTACAGTACTGCT	26004	TATCAGAGaagccaaag	26153
157	gctccaggggagaagctttggcttctctgataagcagtactgtaggccCCAAGTGAAAAGTTATTAT	26005	CACTGTTAaatcaggat	26154
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159	gctccaggggagaagctttggcttctctgataagcagtactgtaggccCCAAGTGAAAAGTTATTAT	26007	CACTGTTAaatcaggat	26156
164	gctccaggggagaagctttggcttctctgataagcagtactgtaggccCCAAGTGAAAAGTTATTATC	26008	ACTGTTAAatcaggatc	26157

167	gcagcagggaatactgatcctgatttaacagtgataataacttttcactTGGGGCCTACAGTACTGCTT	26009	ATCAGAGAAagccaaagc	26158
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187	gcagcagggaatactgatcctgatttaacagtgataataacttttcactTGGGGCCTACAGTACTGCTTAT	26018	CAGAGAAGccaaagctt	26167
188	gctccaggggagaagctttggcttctctgataagcagtactgtaggccCCAAGTGAAAAGTTATTATCAC	26019	TGTTAAATcaggatcag	26168
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196	gcagcagggaatactgatcctgatttaacagtgataataacttttcactTGGGGCCTACAGTACTGCTTATC	26023	AGAGAAGCcaaagcttc	26172
197	gctccaggggagaagctttggcttctctgataagcagtactgtaggccCCAAGTGAAAAGTTATTATCACT	26024	GTTAAATCaggatcagt	26173
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204	gctccaggggagaagctttggcttctctgataagcagtactgtaggccCCAAGTGAAAAGTTATTATCACTG	26026	TTAAATCAggatcagta	26175
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209	gctccaggggagaagctttggcttctctgataagcagtactgtaggccCCAAGTGAAAAGTTATTATCACTG	26028	TTAAATCAggatcagta	26177
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211	gcagcagggaatactgatcctgatttaacagtgataataacttttcactTGGGGCCTACAGTACTGCTTATCA	26030	GAGAAGCCaaagcttct	26179
215	gcagcagggaatactgatcctgatttaacagtgataataacttttcactTGGGGCCTACAGTACTGCTTATCAG	26031	AGAAGCCAaagcttctc	26180
218	gctccaggggagaagctttggcttctctgataagcagtactgtaggccCCAAGTGAAAAGTTATTATCACTGT	26032	TAAATCAGgatcagtat	26181
219	gctccaggggagaagctttggcttctctgataagcagtactgtaggccCCAAGTGAAAAGTTATTATCACTGT	26033	TAAATCAGgatcagtat	26182
220	gcagcagggaatactgatcctgatttaacagtgataataacttttcactTGGGGCCTACAGTACTGCTTATCAG	26034	AGAAGCCAaagcttctc	26183
223	gcagcagggaatactgatcctgatttaacagtgataataacttttcactTGGGGCCTACAGTACTGCTTATCAGA	26035	GAAGCCAAagcttctcc	26184

224	gctccaggggagaagctttggcttctctgataagcagtactgtaggccCCAAGTGAAAAGTTATTATCACTGTT	26036	AAATCAGGatcagtatt	26185
225	gctccaggggagaagctttggcttctctgataagcagtactgtaggccCCAAGTGAAAAGTTATTATCACTGTT	26037	AAATCAGGatcagtatt	26186
226	gctccaggggagaagctttggcttctctgataagcagtactgtaggccCCAAGTGAAAAGTTATTATCACTGTT	26038	AAATCAGGatcagtatt	26187
229	gcagcagggaatactgatcctgatttaacagtgataataacttttcactTGGGGCCTACAGTACTGCTTATCAGA	26039	GAAGCCAAagcttctcc	26188
232	gctccaggggagaagctttggcttctctgataagcagtactgtaggccCCAAGTGAAAAGTTATTATCACTGTT	26040	AAATCAGGatcagtatt	26189
236	gctccaggggagaagctttggcttctctgataagcagtactgtaggccCCAAGTGAAAAGTTATTATCACTGTTA	26041	AATCAGGAtcagtattc	26190
237	gctccaggggagaagctttggcttctctgataagcagtactgtaggccCCAAGTGAAAAGTTATTATCACTGTTA	26042	AATCAGGAtcagtattc	26191
238	gcagcagggaatactgatcctgatttaacagtgataataacttttcactTGGGGCCTACAGTACTGCTTATCAGAG	26043	AAGCCAAAgcttctccc	26192
242	gcagcagggaatactgatcctgatttaacagtgataataacttttcactTGGGGCCTACAGTACTGCTTATCAGAG	26044	AAGCCAAAgcttctccc	26193
247	gctccaggggagaagctttggcttctctgataagcagtactgtaggccCCAAGTGAAAAGTTATTATCACTGTTAA	26045	ATCAGGATcagtattcc	26194
250	gcagcagggaatactgatcctgatttaacagtgataataacttttcactTGGGGCCTACAGTACTGCTTATCAGAGA	26046	AGCCAAAGcttctcccc	26195
251	gcagcagggaatactgatcctgatttaacagtgataataacttttcactTGGGGCCTACAGTACTGCTTATCAGAGA	26047	AGCCAAAGcttctcccc	26196
252	gctccaggggagaagctttggcttctctgataagcagtactgtaggccCCAAGTGAAAAGTTATTATCACTGTTAA	26048	ATCAGGATcagtattcc	26197
255	gcagcagggaatactgatcctgatttaacagtgataataacttttcactTGGGGCCTACAGTACTGCTTATCAGAGAA	26049	GCCAAAGCttctccccc	26198
256	gctccaggggagaagctttggcttctctgataagcagtactgtaggccCCAAGTGAAAAGTTATTATCACTGTTAAA	26050	TCAGGATCagtattccc	26199
257	gcagcagggaatactgatcctgatttaacagtgataataacttttcactTGGGGCCTACAGTACTGCTTATCAGAGAA	26051	GCCAAAGCttctccccc	26200
258	gctccaggggagaagctttggcttctctgataagcagtactgtaggccCCAAGTGAAAAGTTATTATCACTGTTAAA	26052	TCAGGATCagtattccc	26201
261	gctccaggggagaagctttggcttctctgataagcagtactgtaggccCCAAGTGAAAAGTTATTATCACTGTTAAA	26053	TCAGGATCagtattccc	26202
262	gcagcagggaatactgatcctgatttaacagtgataataacttttcactTGGGGCCTACAGTACTGCTTATCAGAGAA	26054	GCCAAAGCttctccccc	26203
264	gctccaggggagaagctttggcttctctgataagcagtactgtaggccCCAAGTGAAAAGTTATTATCACTGTTAAAT	26055	CAGGATCAgtattccct	26204
265	gcagcagggaatactgatcctgatttaacagtgataataacttttcactTGGGGCCTACAGTACTGCTTATCAGAGAAG	26056	CCAAAGCTtctccccct	26205
269	gcagcagggaatactgatcctgatttaacagtgataataacttttcactTGGGGCCTACAGTACTGCTTATCAGAGAAGC	26057	CAAAGCTTctcccccctg	26206
270	gctccaggggagaagctttggcttctctgataagcagtactgtaggccCCAAGTGAAAAGTTATTATCACTGTTAAATC	26058	AGGATCAGtattccctg	26207
271	gctccaggggagaagctttggcttctctgataagcagtactgtaggccCCAAGTGAAAAGTTATTATCACTGTTAAATC	26059	AGGATCAGtattccctg	26208
272	gctccaggggagaagctttggcttctctgataagcagtactgtaggccCCAAGTGAAAAGTTATTATCACTGTTAAATC	26060	AGGATCAGtattccctg	26209
273	gctccaggggagaagctttggcttctctgataagcagtactgtaggccCCAAGTGAAAAGTTATTATCACTGTTAAATCA	26061	GGATCAGTattccctgc	26210
274	gcagcagggaatactgatcctgatttaacagtgataataacttttcactTGGGGCCTACAGTACTGCTTATCAGAGAAGCC	26062	AAAGCTTCtcccctgg	26211

275	gctccaggggagaagctttggcttctctgataagcagtactgtaggccCCAAGTGAAAAGTTATTATCACTGTTAAATCA	26063	GGATCAGTattccctgc	26212
276	gcagcagggaatactgatcctgatttaacagtgataataacttttcactTGGGGCCTACAGTACTGCTTATCAGAGAAGCC	26064	AAAGCTTCtcccctgg	26213
277	gcagcagggaatactgatcctgatttaacagtgataataacttttcactTGGGGCCTACAGTACTGCTTATCAGAGAAGCC	26065	AAAGCTTCtcccctgg	26214

Capital letters indicate “core nucleotides” while lower case letters indicate “flanking nucleotides.” Herein, when an RNA sequence (e.g., a template RNA sequence) is said to comprise a particular sequence (e.g., a sequence of Table 3A, Table 3B, Table 3C, or Table 3D or a portion thereof) that comprises thymine (T), it is of course understood that the RNA sequence may (and frequently does) comprise uracil (U) in place of T. For instance, the RNA sequence may comprise U at every position shown as T in the sequence in Table 3A, Table 3B, Table 3C, or Table 3D. More specifically, the present disclosure provides an RNA sequence according to every heterologous object sequence and PBS sequence shown in Table 3A, Table 3B, Table 3C, or Table 3D, wherein the RNA sequence has a U in place of each T in the sequence of Table 3A, Table 3B, Table 3C, or Table 3D.

In some embodiments of the systems and methods herein, the template RNA comprises a gRNA scaffold (e.g., that binds a gene modifying polypeptide, e.g., a Cas polypeptide) that comprises a sequence of a gRNA scaffold of Table 12. In some embodiments, the gRNA scaffold comprises a sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, or 99% identity to a gRNA scaffold of Table 12. In some embodiments, the gRNA scaffold comprises a sequence of a scaffold region of Table 12 that corresponds to the RT template sequence, the spacer sequence, or both, or a sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, or 99% identity thereto.

In some embodiments of the systems and methods herein, the system further comprises a second strand-targeting gRNA that directs a nick to the second strand of the human PAH gene. In some embodiments, the second strand-targeting gRNA comprises a left gRNA spacer sequence or a right gRNA spacer sequence from Table 2A, Table 2B, Table 2C, or Table 2D. In some embodiments, the gRNA spacer additionally comprises one or more (e.g., 2, 3, or all) consecutive nucleotides starting with the 3’ end of the flanking nucleotides of the left gRNA spacer sequence or right gRNA spacer sequence. In some embodiments, the second strand-

targeting gRNA comprises a sequence comprising the core nucleotides of a second nick gRNA sequence from Table 4A, Table 4B, Table 4C, or Table 4D, or a sequence having at least 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, or 99% identity thereto. In some embodiments, the second nick gRNA sequence additionally comprises one or more consecutive nucleotides starting with the 3' end of the flanking nucleotides of the second nick gRNA sequence. In some embodiments, the second nick gRNA comprises a gRNA scaffold sequence that is orthogonal to the Cas domain of the gene modifying polypeptide. In some embodiments, the second nick gRNA comprises a gRNA scaffold sequence of Table 12.

Table 2A: Exemplary left gRNA spacer and right gRNA spacer pairs

Table 2A provides exemplified second-nick gRNA species for optional use for correcting the pathogenic R408W mutation in PAH. The gRNA spacers from Table 1A were filtered, e.g., filtered by occurrence within 15 nt of the desired editing location and use of a Tier 1 Cas enzyme. Second-nick gRNAs were generated by searching the opposite strand of DNA in the regions -40 to -140 ("left") and +40 to +140 ("right"), relative to the first nick site defined by the first gRNA, for the PAM utilized by the corresponding Cas variant. One exemplary spacer is shown for each side of the target nick site.

ID	Left gRNA spacer	SEQ ID NO	Left PAM	Right gRNA spacer	SEQ ID NO	Right PAM
1	CTCGTAAGGTGTAAATTACT	26215	TAC	AGTTCTCAGTGGCATTTTAC	26595	TTC
2	GGCTGATTCCATTAACAGTA	26216	AG	TTCCTAAAAAAGAAGTAAAA	26596	TG
6	CCATTAACAGTAAGTAATTT	26217	ACA	CCTAAAAAAGAAGTAAAATG	26597	CCA
7	TCGTAAGGTGTAAATTACTT	26218	ACT	GTTCTCAGTGGCATTTTACT	26598	TCT
10	tttTGGCTGATTCCATTAACAGTA	26219	AGTAATT	gaaGACCCTGCTCTAGGGAGGTGT	26599	CCGTGTT
13	CAGTAAGTAATTTACACCTT	26220	ACG	AAAAAAGAAGTAAAATGCCA	26600	CTG
14	TAAGTAATTTACACCTTACG	26221	AGG	TTGAAGACCCTGCTCTAGGG	26601	AGG
17	CATTAACAGTAAGTAATTTA	26222	CAC	CTAAAAAAGAAGTAAAATGC	26602	CAC
18	GTAAGGTGTAAATTACTTAC	26223	TG	TGGCATTTTACTTCTTTTTT	26603	AG
21	AGTAAGTAATTTACACCTTA	26224	CG	AAAAAGAAGTAAAATGCCAC	26604	TG
25	CGTAAGGTGTAAATTACTTA	26225	CTG	TTCTCAGTGGCATTTTACTT	26605	CTT

26	gtggCCTCGTAAGGTGTAAATTA	26226	CTTACTGT	aagaGAGTTCTCAGTGGCATTTT	26606	ACTTC
29	gtAAATTACTTACTGTTAATGGAA	26227	TCAGCC	ttTTACTTCTTTTTTAGGAACACG	26607	GACACC
30	AGTAAGTAATTTACACCTTAC	26228	GAGG	CTTAAGACTACCTTTCTCCAA	26608	ATGG
31	CAGTAAGTAATTTACACCTTA	26229	CGAG	AAAAAAGAAGTAAAATGCCAC	26609	TGAG
34	CGTAAGGTGTAAATTACTTA	26230	CTG	GTGGCATTTTACTTCTTTTT	26610	TAG
35	TGTAAATTACTTACTGTTAA	26231	TGG	TGGCATTTTACTTCTTTTTT	26611	AGG
38	GTAAGGTGTAAATTACTTAC	26232	TGT	TCTCAGTGGCATTTTACTTC	26612	TTT
41	CAGTAAGTAATTTACACCTT	26233	ACG	AAAAAAGAAGTAAAATGCCA	26613	CTG
42	ATTAACAGTAAGTAATTTAC	26234	ACC	TAAAAAAGAAGTAAAATGCC	26614	ACT
43	GTAAGGTGTAAATTACTTAC	26235	TG	TGGCATTTTACTTCTTTTTT	26615	AG
46	gtggCCTCGTAAGGTGTAAATTA	26236	CTTACTGT	aagaGAGTTCTCAGTGGCATTTT	26616	ACTTC
47	gtggCCTCGTAAGGTGTAAATTA	26237	CTTACTGT	aagaGAGTTCTCAGTGGCATTTT	26617	ACTTC
50	gtAAATTACTTACTGTTAATGGAA	26238	TCAGCC	ttTTACTTCTTTTTTAGGAACACG	26618	GACACC
51	AACAGTAAGTAATTTACACCT	26239	TACGA	TAAAAAAGAAGTAAAATGCCA	26619	CTGAG
52	AACAGTAAGTAATTTACACCT	26240	TACGA	TAAAAAAGAAGTAAAATGCCA	26620	CTGAG
55	GGTGTAAATTACTTACTGTTA	26241	ATGG	AGTGGCATTTTACTTCTTTTT	26621	TAGG
56	GGTGTAAATTACTTACTGTTA	26242	ATGG	CAGTGGCATTTTACTTCTTTT	26622	TTAG
57	CAGTAAGTAATTTACACCTTA	26243	CGAG	AAAAAAGAAGTAAAATGCCAC	26623	TGAG
62	CGTAAGGTGTAAATTACTTA	26244	CTG	GTGGCATTTTACTTCTTTTT	26624	TAG
63	TAAGGTGTAAATTACTTACT	26245	GTT	CTCAGTGGCATTTTACTTCT	26625	TTT
64	TTAACAGTAAGTAATTTACA	26246	CCT	AAAAAAGAAGTAAAATGCCA	26626	CTG
65	gtggCCTCGTAAGGTGTAAATTA	26247	CTTACTGT	agtgGCATTTTACTTCTTTTTTA	26627	GGAAC
66	AACAGTAAGTAATTTACACCT	26248	TACGA	AAAAAAGAAGTAAAATGCCAC	26628	TGAGA
67	GTAAGGTGTAAATTACTTACT	26249	GTTAAT	TCAGTGGCATTTTACTTCTTT	26629	TTTAG
68	TAACAGTAAGTAATTTACAC	26250	CTT	AAAAAGAAGTAAAATGCCAC	26630	TGA
69	AAGGTGTAAATTACTTACTG	26251	TTA	TCAGTGGCATTTTACTTCTT	26631	TTT
72	AACAGTAAGTAATTTACACCT	26252	TACGA	AAAAAGAAGTAAAATGCCACT	26632	GAGAA

73	AACAGTAAGTAATTTACACC	26253	TTA	AAAAGAAGTAAAATGCCACT	26633	GAG
74	AGGTGTAAATTACTTACTGT	26254	TAA	CAGTGGCATTTTACTTCTTT	26634	TTT
77	AGTAAGTAATTTACACCTTA	26255	CG	AAAGAAGTAAAATGCCACTG	26635	AG
81	ACAGTAAGTAATTTACACCT	26256	TAC	AAAGAAGTAAAATGCCACTG	26636	AGA
82	GGTGTAAATTACTTACTGTT	26257	AAT	AGTGGCATTTTACTTCTTTT	26637	TTA
86	CAGTAAGTAATTTACACCTT	26258	ACG	AAAAGAAGTAAAATGCCACT	26638	GAG
87	TAAGTAATTTACACCTTACG	26259	AGG	TAAGACTACCTTTCTCCAAA	26639	TGG
90	CAGTAAGTAATTTACACCTT	26260	ACG	AAGAAGTAAAATGCCACTGA	26640	GAA
91	AGTAAGTAATTTACACCTTA	26261	CG	AAAGAAGTAAAATGCCACTG	26641	AG
94	GTGTAAATTACTTACTGTTA	26262	ATG	GTGGCATTTTACTTCTTTTT	26642	TAG
95	acagTAAGTAATTTACACCTTAC	26263	GAGGC	aaaaAAGAAGTAAAATGCCACTG	26643	AGAAC
96	acagTAAGTAATTTACACCTTAC	26264	GAGGC	aaaaAAGAAGTAAAATGCCACTG	26644	AGAAC
99	aaCAGTAAGTAATTTACACCTTAC	26265	GAGGCC	tcCGTGTTCCTAAAAAAGAAGTAA	26645	AATGCC
100	AGTAAGTAATTTACACCTTAC	26266	GAGG	CTTAAGACTACCTTTCTCCAA	26646	ATGG
101	CAGTAAGTAATTTACACCTTA	26267	CGAG	AAAAAAGAAGTAAAATGCCAC	26647	TGAG
104	GTAAGTAATTTACACCTTAC	26268	GAG	AAAAGAAGTAAAATGCCACT	26648	GAG
105	TAAGTAATTTACACCTTACG	26269	AGG	TAAGACTACCTTTCTCCAAA	26649	TGG
108	AGTAAGTAATTTACACCTTA	26270	CGA	AGAAGTAAAATGCCACTGAG	26650	AAC
109	AGTAAGTAATTTACACCTTA	26271	CG	AAAGAAGTAAAATGCCACTG	26651	AG
112	TGTAAATTACTTACTGTTAA	26272	TGG	TGGCATTTTACTTCTTTTTT	26652	AGG
113	acagTAAGTAATTTACACCTTAC	26273	GAGGC	aaaaGAAGTAAAATGCCACTGAG	26653	AACTC
114	acagTAAGTAATTTACACCTTAC	26274	GAGGC	aaaaGAAGTAAAATGCCACTGAG	26654	AACTC
115	gtgtAAATTACTTACTGTTAATG	26275	GAATC	agtgGCATTTTACTTCTTTTTTA	26655	GGAAC
116	acagTAAGTAATTTACACCTTAC	26276	GAGGC	aaaaGAAGTAAAATGCCACTGAG	26656	AACTC
117	gtgtAAATTACTTACTGTTAATG	26277	GAATC	agtgGCATTTTACTTCTTTTTTA	26657	GGAAC
119	gtAAATTACTTACTGTTAATGGAA	26278	TCAGCC	ttTTACTTCTTTTTTAGGAACACG	26658	GACACC
120	taACAGTAAGTAATTTACACCTT	26279	ACGAG	taAAAAAGAAGTAAAATGCCACT	26659	GAGAA

121	CAGTAAGTAATTTACACCTTA	26280	CGAGG	AAAAAGAAGTAAAATGCCACT	26660	GAGAA
122	AGTAAGTAATTTACACCTTAC	26281	GAGG	CTTAAGACTACCTTTCTCCAA	26661	ATGG
123	AGTAAGTAATTTACACCTTAC	26282	GAGG	AAAAAAGAAGTAAAATGCCAC	26662	TGAG
126	GTAAGTAATTTACACCTTAC	26283	GAG	AAAAGAAGTAAAATGCCACT	26663	GAG
127	GTAAGTAATTTACACCTTAC	26284	GAG	GAAGTAAAATGCCACTGAGA	26664	ACT
128	GTAAATTACTTACTGTTAAT	26285	GGA	GGCATTTTACTTCTTTTTTA	26665	GGA
129	gtgtAAATTACTTACTGTTAATG	26286	GAATC	agtgGCATTTTACTTCTTTTTTA	26666	GGAAC
130	gtgtAAATTACTTACTGTTAATG	26287	GAATC	agtgGCATTTTACTTCTTTTTTA	26667	GGAAC
134	CAGTAAGTAATTTACACCTTA	26288	CGAGG	TAAAATGCCACTGAGAACTCT	26668	CTTAA
135	AGTAAGTAATTTACACCTTAC	26289	GAGG	AAATGCCACTGAGAACTCTCT	26669	TAAG
138	TAAGTAATTTACACCTTACG	26290	AGG	AAGTAAAATGCCACTGAGAA	26670	CTC
140	TAAATTACTTACTGTTAATG	26291	GAA	GCATTTTACTTCTTTTTTAG	26671	GAA
146	CAGTAAGTAATTTACACCTTA	26292	CGAGG	TAAAATGCCACTGAGAACTCT	26672	CTTAA
147	AAGTAATTTACACCTTACGA	26293	GG	AAAGAAGTAAAATGCCACTG	26673	AG
151	AAGTAATTTACACCTTACGA	26294	GGC	AGTAAAATGCCACTGAGAAC	26674	TCT
152	AAATTACTTACTGTTAATGG	26295	AAT	CATTTTACTTCTTTTTTAGG	26675	AAC
158	taACAGTAAGTAATTTACACCTT	26296	ACGAG	taAAAAAGAAGTAAAATGCCACT	26676	GAGAA
159	CAGTAAGTAATTTACACCTTA	26297	CGAGG	TAAAATGCCACTGAGAACTCT	26677	CTTAA
160	AAATTACTTACTGTTAATGGA	26298	ATCAG	ATTTTACTTCTTTTTTAGGAA	26678	CACGG
161	AAATTACTTACTGTTAATGGA	26299	ATCAG	ATTTTACTTCTTTTTTAGGAA	26679	CACGG
166	TAAGTAATTTACACCTTACG	26300	AGG	ATGCCACTGAGAACTCTCTT	26680	AAG
167	AGTAATTTACACCTTACGAG	26301	GCC	GTAAAATGCCACTGAGAACT	26681	CTC
168	AATTACTTACTGTTAATGGA	26302	ATC	ATTTTACTTCTTTTTTAGGA	26682	ACA
174	AATTTACACCTTACGAGGCCA	26303	CTCGG	TAAAATGCCACTGAGAACTCT	26683	CTTAA
175	ATTTACACCTTACGAGGCCAC	26304	TCGG	AAATGCCACTGAGAACTCTCT	26684	TAAG
177	AAGTAATTTACACCTTACGA	26305	GG	TGCCACTGAGAACTCTCTTA	26685	AG
181	GTAATTTACACCTTACGAGG	26306	CCA	TAAAATGCCACTGAGAACTC	26686	TCT

182	ATTACTTACTGTTAATGGAA	26307	TCA	TTTTACTTCTTTTTTAGGAA	26687	CAC
187	taACAGTAAGTAATTTACACCTT	26308	ACGAG	taAAAAAGAAGTAAAATGCCACT	26688	GAGAA
188	AATTTACACCTTACGAGGCCA	26309	CTCGG	TAAAATGCCACTGAGAACTCT	26689	CTTAA
191	TTTACACCTTACGAGGCCAC	26310	TCG	ATGCCACTGAGAACTCTCTT	26690	AAG
192	TAATTTACACCTTACGAGGC	26311	CAC	AAAATGCCACTGAGAACTCT	26691	CTT
193	TTACTTACTGTTAATGGAAT	26312	CAG	TTTACTTCTTTTTTAGGAAC	26692	ACG
194	aaatTACTTACTGTTAATGGAAT	26313	CAGCC	atttTACTTCTTTTTTAGGAACA	26693	CGGAC
195	aaatTACTTACTGTTAATGGAAT	26314	CAGCC	atttTACTTCTTTTTTAGGAACA	26694	CGGAC
198	AATTTACACCTTACGAGGCCA	26315	CTCGG	AAAATGCCACTGAGAACTCTC	26695	TTAAG
199	TACTTACTGTTAATGGAATC	26316	AG	TTACTTCTTTTTTAGGAACA	26696	CG
203	TACTTACTGTTAATGGAATC	26317	AGC	TTACTTCTTTTTTAGGAACA	26697	CGG
204	AATTTACACCTTACGAGGCC	26318	ACT	AAATGCCACTGAGAACTCTC	26698	TTA
208	TTACTTACTGTTAATGGAAT	26319	CAG	TTACTTCTTTTTTAGGAACA	26699	CGG
209	ACTTACTGTTAATGGAATCA	26320	GCC	TACTTCTTTTTTAGGAACAC	26700	GGA
210	ATTTACACCTTACGAGGCCA	26321	CTC	AATGCCACTGAGAACTCTCT	26701	TAA
211	aaatTACTTACTGTTAATGGAAT	26322	CAGCC	atttTACTTCTTTTTTAGGAACA	26702	CGGAC
214	gtAAATTACTTACTGTTAATGGAA	26323	TCAGCC	ttTTACTTCTTTTTTAGGAACACG	26703	GACACC
215	TTTACACCTTACGAGGCCAC	26324	TCG	ATGCCACTGAGAACTCTCTT	26704	AAG
217	CTTACTGTTAATGGAATCAG	26325	CCA	ACTTCTTTTTTAGGAACACG	26705	GAC
218	cttaCTGTTAATGGAATCAGCCA	26326	AAATCTTA	tttaCTTCTTTTTTAGGAACACG	26706	GACAC
221	TTACACCTTACGAGGCCACT	26327	CG	TGCCACTGAGAACTCTCTTA	26707	AG
224	TACTTACTGTTAATGGAATC	26328	AG	TACTTCTTTTTTAGGAACAC	26708	GG
228	TTACACCTTACGAGGCCACT	26329	CGG	TGCCACTGAGAACTCTCTTA	26709	AGA
230	TTACTGTTAATGGAATCAGC	26330	CAA	CTTCTTTTTTAGGAACACGG	26710	ACA
231	tttaCACCTTACGAGGCCACTCG	26331	GTTTC	aaaaTGCCACTGAGAACTCTCTT	26711	AAGAC
232	tttaCACCTTACGAGGCCACTCG	26332	GTTTC	aaaaTGCCACTGAGAACTCTCTT	26712	AAGAC
238	taACAGTAAGTAATTTACACCTT	26333	ACGAG	taAAAAAGAAGTAAAATGCCACT	26713	GAGAA

239	AATTTACACCTTACGAGGCCA	26334	CTCGGT	AAATGCCACTGAGAACTCTCT	26714	TAAGA
242	TTACACCTTACGAGGCCACT	26335	CGG	ATGCCACTGAGAACTCTCTT	26715	AAG
243	TACACCTTACGAGGCCACTC	26336	GGT	GCCACTGAGAACTCTCTTAA	26716	GAC
246	TTACTTACTGTTAATGGAAT	26337	CAG	TTACTTCTTTTTTAGGAACA	26717	CGG
247	TACTGTTAATGGAATCAGCC	26338	AAA	TTCTTTTTTAGGAACACGGA	26718	CAC
251	AATTTACACCTTACGAGGCCA	26339	CTCGGT	AAATGCCACTGAGAACTCTCT	26719	TAAGA
252	TACACCTTACGAGGCCACTC	26340	GG	TGCCACTGAGAACTCTCTTA	26720	AG
256	ACACCTTACGAGGCCACTCG	26341	GTT	CCACTGAGAACTCTCTTAAG	26721	ACT
257	ACTGTTAATGGAATCAGCCA	26342	AAA	TCTTTTTTAGGAACACGGAC	26722	ACC
258	cttaCTGTTAATGGAATCAGCCA	26343	AAATC	acttCTTTTTTAGGAACACGGAC	26723	ACCTC
264	TTACACCTTACGAGGCCACT	26344	CGG	ATGCCACTGAGAACTCTCTT	26724	AAG
265	CACCTTACGAGGCCACTCGG	26345	TTT	CACTGAGAACTCTCTTAAGA	26725	CTA
266	CTGTTAATGGAATCAGCCAA	26346	AAT	CTTTTTTAGGAACACGGACA	26726	CCT
268	CTTACGAGGCCACTCGGTTTC	26347	TCAG	AAATGCCACTGAGAACTCTCT	26727	TAAG
269	ACCTTACGAGGCCACTCGGT	26348	TTC	ACTGAGAACTCTCTTAAGAC	26728	TAC
270	TGTTAATGGAATCAGCCAAA	26349	ATC	TTTTTTAGGAACACGGACAC	26729	CTC
271	tacaCCTTACGAGGCCACTCGGT	26350	TTCTCAGT	tgccACTGAGAACTCTCTTAAGA	26730	CTACCTTT
272	tacaCCTTACGAGGCCACTCGGT	26351	TTCTCAGT	tgccACTGAGAACTCTCTTAAGA	26731	CTACCTTT
274	tacaCCTTACGAGGCCACTCGGT	26352	TTCTCAGT	tgccACTGAGAACTCTCTTAAGA	26732	CTACCTTT
275	CCTTACGAGGCCACTCGGTTT	26353	CTCAG	ACTCTCTTAAGACTACCTTTC	26733	TCCAA
276	ACGAGGCCACTCGGTTTCTC	26354	AG	TGCCACTGAGAACTCTCTTA	26734	AG
280	CCTTACGAGGCCACTCGGTT	26355	TCT	CTGAGAACTCTCTTAAGACT	26735	ACC
281	GTTAATGGAATCAGCCAAAA	26356	TCT	TTTTTAGGAACACGGACACC	26736	TCC
286	TACGAGGCCACTCGGTTTCT	26357	CAG	ATGCCACTGAGAACTCTCTT	26737	AAG
287	CTTACGAGGCCACTCGGTTT	26358	CTC	TGAGAACTCTCTTAAGACTA	26738	CCT
288	TTAATGGAATCAGCCAAAAT	26359	CTT	TTTTAGGAACACGGACACCT	26739	CCC
293	TGGAATCAGCCAAAATCTTA	26360	AG	AGGAACACGGACACCTCCCT	26740	AG

297	TAATGGAATCAGCCAAAATC	26361	TTA	TTTAGGAACACGGACACCTC	26741	CCT
298	TTACGAGGCCACTCGGTTTC	26362	TCA	GAGAACTCTCTTAAGACTAC	26742	CTT
299	gttaATGGAATCAGCCAAAATCT	26363	TAAGC	ttctTTTTTAGGAACACGGACAC	26743	CTCCCTAG
300	gttaATGGAATCAGCCAAAATCT	26364	TAAGC	ttctTTTTTAGGAACACGGACAC	26744	CTCCCTAG
306	gaATCAGCCAAAATCTTAAGCTG	26365	CTGGG	ttTTAGGAACACGGACACCTCCC	26745	TAGAG
307	TTAATGGAATCAGCCAAAATC	26366	TTAAG	TTTAGGAACACGGACACCTCC	26746	CTAGA
310	ATGGAATCAGCCAAAATCTT	26367	AAG	TAGGAACACGGACACCTCCC	26747	TAG
311	CAGCCAAAATCTTAAGCTGC	26368	TGG	CACGGACACCTCCCTAGAGC	26748	AGG
314	AATGGAATCAGCCAAAATCT	26369	TAA	TTAGGAACACGGACACCTCC	26749	CTA
315	ACGAGGCCACTCGGTTTCTC	26370	AG	TGCCACTGAGAACTCTCTTA	26750	AG
318	TGGAATCAGCCAAAATCTTA	26371	AG	AGGAACACGGACACCTCCCT	26751	AG
322	TACGAGGCCACTCGGTTTCT	26372	CAG	AGAACTCTCTTAAGACTACC	26752	TTT
328	gaATCAGCCAAAATCTTAAGCTG	26373	CTGGG	ttTTAGGAACACGGACACCTCCC	26753	TAGAG
329	TTAATGGAATCAGCCAAAATC	26374	TTAAG	TTAGGAACACGGACACCTCCC	26754	TAGAG
330	ATCAGCCAAAATCTTAAGCTG	26375	CTGG	AACACGGACACCTCCCTAGAG	26755	CAGG
331	TAATGGAATCAGCCAAAATCT	26376	TAAG	TAGGAACACGGACACCTCCCT	26756	AGAG
334	TACGAGGCCACTCGGTTTCT	26377	CAG	TTAAGACTACCTTTCTCCAA	26757	ATG
335	TTACACCTTACGAGGCCACT	26378	CGG	TAAGACTACCTTTCTCCAAA	26758	TGG
338	ACGAGGCCACTCGGTTTCTC	26379	AGT	GAACTCTCTTAAGACTACCT	26759	TTC
341	ATGGAATCAGCCAAAATCTT	26380	AAG	TAGGAACACGGACACCTCCC	26760	TAG
342	ATGGAATCAGCCAAAATCTT	26381	AAG	TAGGAACACGGACACCTCCC	26761	TAG
343	ACGAGGCCACTCGGTTTCTC	26382	AG	TGCCACTGAGAACTCTCTTA	26762	AG
346	tacgAGGCCACTCGGTTTCTCAG	26383	TAATCGAA	tgagAACTCTCTTAAGACTACCT	26763	TTCTC
347	tacgAGGCCACTCGGTTTCTCAG	26384	TAATCGAA	tgagAACTCTCTTAAGACTACCT	26764	TTCTC
351	TTAATGGAATCAGCCAAAATC	26385	TTAAG	TTAGGAACACGGACACCTCCC	26765	TAGAG
352	ATTTACACCTTACGAGGCCAC	26386	TCGG	CTTAAGACTACCTTTCTCCAA	26766	ATGG
353	CTTACGAGGCCACTCGGTTTC	26387	TCAG	CTTAAGACTACCTTTCTCCAA	26767	ATGG

354	TAATGGAATCAGCCAAAATCT	26388	TAAG	TAGGAACACGGACACCTCCCT	26768	AGAG
357	TACGAGGCCACTCGGTTTCT	26389	CAG	TTAAGACTACCTTTCTCCAA	26769	ATG
358	TTACACCTTACGAGGCCACT	26390	CGG	TAAGACTACCTTTCTCCAAA	26770	TGG
361	CGAGGCCACTCGGTTTCTCA	26391	GTA	AACTCTCTTAAGACTACCTT	26771	TCT
362	ACGAGGCCACTCGGTTTCTC	26392	AG	TAAGACTACCTTTCTCCAAA	26772	TG
365	TGGAATCAGCCAAAATCTTA	26393	AGC	AGGAACACGGACACCTCCCT	26773	AGA
366	GTGTAAATTACTTACTGTTA	26394	ATGGAAT	AGTGGCATTTTACTTCTTTT	26774	TTAGGAA
369	gaGGCCACTCGGTTTCTCAGTAA	26395	TCGAA	taAAAAAGAAGTAAAATGCCACT	26775	GAGAA
370	TACGAGGCCACTCGGTTTCTC	26396	AGTAAT	ACTCTCTTAAGACTACCTTTC	26776	TCCAA
371	gaGGCCACTCGGTTTCTCAGTAA	26397	TCGAA	taAAAAAGAAGTAAAATGCCACT	26777	GAGAA
372	TACGAGGCCACTCGGTTTCTC	26398	AGTAAT	ACTCTCTTAAGACTACCTTTC	26778	TCCAA
375	AATCAGCCAAAATCTTAAGCT	26399	GCTGG	GGAACACGGACACCTCCCTAG	26779	AGCAG
376	ATTTACACCTTACGAGGCCAC	26400	TCGG	CTTAAGACTACCTTTCTCCAA	26780	ATGG
377	CTTACGAGGCCACTCGGTTTC	26401	TCAG	CTTAAGACTACCTTTCTCCAA	26781	ATGG
380	TACGAGGCCACTCGGTTTCT	26402	CAG	TTAAGACTACCTTTCTCCAA	26782	ATG
381	GAGGCCACTCGGTTTCTCAG	26403	TAA	ACTCTCTTAAGACTACCTTT	26783	CTC
382	GGAATCAGCCAAAATCTTAA	26404	GCT	GGAACACGGACACCTCCCTA	26784	GAG

Table 2B: Exemplary left gRNA spacer and right gRNA spacer pairs

Table 2B provides exemplified second-nick gRNA species for optional use for correcting the pathogenic R261Q mutation in PAH. The gRNA spacers from Table 1B were filtered, e.g., filtered by occurrence within 15 nt of the desired editing location and use of a Tier 1 Cas enzyme. Second-nick gRNAs were generated by searching the opposite strand of DNA in the regions -40 to -140 (“left”) and +40 to +140 (“right”), relative to the first nick site defined by the first gRNA, for the PAM utilized by the corresponding Cas variant. One exemplary spacer is shown for each side of the target nick site.

ID	Left gRNA spacer	SEQ ID NO	Left PAM	Right gRNA spacer	SEQ ID NO	Right PAM
1	gcAGCAGGAAAAGATGGCGCTCAT	26975	TGTGCC	aaGAAGAAAGAAAACTCAAAGCTC	27329	ATCACC

2	AGGAAAAGATGGCGCTCATT	26976	GTG	AAAAGAAGAAAGAAAACTCA	27330	AAG
3	agcaGGAAAAGATGGCGCTCATT	26977	GTGCCTGG	gatgAAAAGAAGAAAGAAAACTC	27331	AAAGC
4	AGCTACCAGTTGCCAGGCACA	26978	ATGAG	CTGACTCAGTGGTGATGAGCT	27332	TTGAGT
5	GCTACCAGTTGCCAGGCACAA	26979	TGAG	TGACTCAGTGGTGATGAGCTT	27333	TGAG
8	GTTGCCAGGCACAATGAGCG	26980	CCA	GGTGATGAGCTTTGAGTTTT	27334	CTT
10	GGAAAAGATGGCGCTCATTG	26981	TGC	AAAGAAGAAAGAAAACTCAA	27335	AGC
13	AGCTACCAGTTGCCAGGCACA	26982	ATGAG	CTGACTCAGTGGTGATGAGCT	27336	TTGAGT
14	GGAAAAGATGGCGCTCATTG	26983	TG	AAAGAAGAAAGAAAACTCAA	27337	AG
17	CAGTTGCCAGGCACAATGAG	26984	CG	CTCAGTGGTGATGAGCTTTG	27338	AG
21	GAAAAGATGGCGCTCATTGT	26985	GCC	AAGAAGAAAGAAAACTCAAA	27339	GCT
23	TTGCCAGGCACAATGAGCGC	26986	CAT	GTGATGAGCTTTGAGTTTTC	27340	TTT
29	ccAGCTACCAGTTGCCAGGCACA	26987	ATGAG	ctCTGACTCAGTGGTGATGAGCT	27341	TTGAG
30	AGCTACCAGTTGCCAGGCACA	26988	ATGAG	CTGACTCAGTGGTGATGAGCT	27342	TTGAGT
33	AAAGATGGCGCTCATTGTGC	26989	CTG	AAAAGAAGAAAGAAAACTCA	27343	AAG
34	AAAAGATGGCGCTCATTGTG	26990	CCT	AGAAGAAAGAAAACTCAAAG	27344	CTC
37	CCAGTTGCCAGGCACAATGA	26991	GCG	ACTCAGTGGTGATGAGCTTT	27345	GAG
38	TCCTCCAGCTACCAGTTGCC	26992	AGG	TCCTAGTGCCTCTGACTCAG	27346	TGG
41	TGCCAGGCACAATGAGCGCC	26993	ATC	TGATGAGCTTTGAGTTTTCT	27347	TTC
42	CAGTTGCCAGGCACAATGAG	26994	CG	CTCAGTGGTGATGAGCTTTG	27348	AG
45	ggaaAAGATGGCGCTCATTGTGC	26995	CTGGC	aaagAAGAAAGAAAACTCAAAGC	27349	TCATC
51	ccAGCTACCAGTTGCCAGGCACA	26996	ATGAG	ctCTGACTCAGTGGTGATGAGCT	27350	TTGAG
52	AGCTACCAGTTGCCAGGCACA	26997	ATGAG	AGTTTTCTTTCTTCTTTTCAT	27351	CCCAG
53	TGTCCTCCAGCTACCAGTTGC	26998	CAGG	TTCTTTTCATCCCAGCTTGCA	27352	CTGG
54	GCTACCAGTTGCCAGGCACAA	26999	TGAG	TGACTCAGTGGTGATGAGCTT	27353	TGAG
55	AAAAGATGGCGCTCATTGTGC	27000	CTGG	TGAAAAGAAGAAAGAAAACTC	27354	AAAG
60	CCAGTTGCCAGGCACAATGA	27001	GCG	ACTCAGTGGTGATGAGCTTT	27355	GAG
61	GCCAGGCACAATGAGCGCCA	27002	TCT	GATGAGCTTTGAGTTTTCTT	27356	TCT

62	AAAGATGGCGCTCATTGTGC	27003	CTG	GAAGAAAGAAAACTCAAAGC	27357	TCA
65	AAGATGGCGCTCATTGTGCCT	27004	GGCAA	GAAAACTCAAAGCTCATCACC	27358	ACTGA
66	ATGAGCGCCATCTTTTCCTGC	27005	TGCAA	AGTTTTCTTTCTTCTTTTCAT	27359	CCCAG
67	AAGATGGCGCTCATTGTGCCT	27006	GGCAA	GAAAACTCAAAGCTCATCACC	27360	ACTGA
70	CCAGGCACAATGAGCGCCAT	27007	CTT	ATGAGCTTTGAGTTTTCTTT	27361	CTT
71	AAGATGGCGCTCATTGTGCC	27008	TGG	AAGAAAGAAAACTCAAAGCT	27362	CAT
73	AAGATGGCGCTCATTGTGCCT	27009	GGCAA	GAAAACTCAAAGCTCATCACC	27363	ACTGA
74	CAGGCACAATGAGCGCCATC	27010	TTT	TGAGCTTTGAGTTTTCTTTC	27364	TTC
75	AGATGGCGCTCATTGTGCCT	27011	GGC	AGAAAGAAAACTCAAAGCTC	27365	ATC
78	AGGCACAATGAGCGCCATCT	27012	TTT	GAGCTTTGAGTTTTCTTTCT	27366	TCT
79	GATGGCGCTCATTGTGCCTG	27013	GCA	GAAAGAAAACTCAAAGCTCA	27367	TCA
81	CAATGAGCGCCATCTTTTCC	27014	TG	TTCTTTCTTCTTTTCATCCC	27368	AG
85	GGCACAATGAGCGCCATCTT	27015	TTC	AGCTTTGAGTTTTCTTTCTT	27369	CTT
86	ATGGCGCTCATTGTGCCTGG	27016	CAA	AAAGAAAACTCAAAGCTCAT	27370	CAC
87	aaagATGGCGCTCATTGTGCCTG	27017	GCAACTGG	gaagAAAGAAAACTCAAAGCTCA	27371	TCACC
88	aaagATGGCGCTCATTGTGCCTG	27018	GCAACTGG	gaagAAAGAAAACTCAAAGCTCA	27372	TCACC
91	gcAGCAGGAAAAGATGGCGCTCAT	27019	TGTGCC	aaGAAGAAAGAAAACTCAAAGCTC	27373	ATCACC
94	ACAATGAGCGCCATCTTTTC	27020	CTG	TTTCTTTCTTCTTTTCATCC	27374	CAG
95	GCACAATGAGCGCCATCTTT	27021	TCC	GCTTTGAGTTTTCTTTCTTC	27375	TTT
96	TGGCGCTCATTGTGCCTGGC	27022	AAC	AAGAAAACTCAAAGCTCATC	27376	ACC
97	aggcACAATGAGCGCCATCTTTT	27023	CCTGC	tgagCTTTGAGTTTTCTTTCTTC	27377	TTTTC
98	aaagATGGCGCTCATTGTGCCTG	27024	GCAACTGG	agaaAGAAAACTCAAAGCTCATC	27378	ACCAC
99	aaagATGGCGCTCATTGTGCCTG	27025	GCAACTGG	agaaAGAAAACTCAAAGCTCATC	27379	ACCAC
100	aggcACAATGAGCGCCATCTTTT	27026	CCTGC	tgagCTTTGAGTTTTCTTTCTTC	27380	TTTTC
101	aaagATGGCGCTCATTGTGCCTG	27027	GCAACTGG	agaaAGAAAACTCAAAGCTCATC	27381	ACCAC
106	ATGAGCGCCATCTTTTCCTGC	27028	TGCAA	AGTTTTCTTTCTTCTTTTCAT	27382	CCCAG
107	GAGCGCCATCTTTTCCTGCTG	27029	CAAG	GTTTTCTTTCTTCTTTTCATC	27383	CCAG

110	CACAATGAGCGCCATCTTTT	27030	CCT	CTTTGAGTTTTCTTTCTTCT	27384	TTT
112	GGCGCTCATTGTGCCTGGCA	27031	ACT	AGAAAACTCAAAGCTCATCA	27385	CCA
115	ATGAGCGCCATCTTTTCCTGC	27032	TGCAA	AGTTTTCTTTCTTCTTTTCAT	27386	CCCAG
116	CAATGAGCGCCATCTTTTCC	27033	TG	TTCTTTCTTCTTTTCATCCC	27387	AG
119	CGCTCATTGTGCCTGGCAAC	27034	TG	AACTCAAAGCTCATCACCAC	27388	TG
123	ACAATGAGCGCCATCTTTTC	27035	CTG	TTTGAGTTTTCTTTCTTCTT	27389	TTC
125	GCGCTCATTGTGCCTGGCAA	27036	CTG	GAAAACTCAAAGCTCATCAC	27390	CAC
132	tgAGCGCCATCTTTTCCTGCTGC	27037	AAGAA	ctCTGACTCAGTGGTGATGAGCT	27391	TTGAGT
133	ATGAGCGCCATCTTTTCCTGC	27038	TGCAA	AGTTTTCTTTCTTCTTTTCAT	27392	CCCAG
136	ACAATGAGCGCCATCTTTTC	27039	CTG	TTTCTTTCTTCTTTTCATCC	27393	CAG
137	CTTTTCCTGCTGCAAGAATG	27040	AGG	CTTTTCATCCCAGCTTGCAC	27394	TGG
140	CAATGAGCGCCATCTTTTCC	27041	TGC	TTGAGTTTTCTTTCTTCTTT	27395	TCA
143	CGCTCATTGTGCCTGGCAAC	27042	TGG	AAACTCAAAGCTCATCACCA	27396	CTG
144	CGCTCATTGTGCCTGGCAAC	27043	TGG	GCTCATCACCACTGAGTCAG	27397	AGG
147	CGCTCATTGTGCCTGGCAAC	27044	TGG	AAAACTCAAAGCTCATCACC	27398	ACT
148	CAATGAGCGCCATCTTTTCC	27045	TG	TTCTTTCTTCTTTTCATCCC	27399	AG
151	CGCTCATTGTGCCTGGCAAC	27046	TG	AACTCAAAGCTCATCACCAC	27400	TG
154	gcgcTCATTGTGCCTGGCAACTG	27047	GTAGCTGG	aaaaCTCAAAGCTCATCACCACT	27401	GAGTCAGA
160	gcAGCAGGAAAAGATGGCGCTCAT	27048	TGTGCC	aaGAAGAAAGAAAACTCAAAGCTC	27402	ATCACC
161	tgAGCGCCATCTTTTCCTGCTGC	27049	AAGAA	ctCTGACTCAGTGGTGATGAGCT	27403	TTGAGT
162	ATGAGCGCCATCTTTTCCTGC	27050	TGCAA	AGTTTTCTTTCTTCTTTTCAT	27404	CCCAG
163	ATCTTTTCCTGCTGCAAGAAT	27051	GAGG	TTCTTTTCATCCCAGCTTGCA	27405	CTGG
164	GAGCGCCATCTTTTCCTGCTG	27052	CAAG	GTTTTCTTTCTTCTTTTCATC	27406	CCAG
165	GGCGCTCATTGTGCCTGGCAA	27053	CTGG	AAGCTCATCACCACTGAGTCA	27407	GAGG
166	GCTCATTGTGCCTGGCAACTG	27054	GTAG	AAACTCAAAGCTCATCACCAC	27408	TGAG
169	ATGAGCGCCATCTTTTCCTG	27055	CTG	TTTCTTTCTTCTTTTCATCC	27409	CAG
170	AATGAGCGCCATCTTTTCCT	27056	GCT	TGAGTTTTCTTTCTTCTTTT	27410	CAT

173	CGCTCATTGTGCCTGGCAAC	27057	TGG	AAACTCAAAGCTCATCACCA	27411	CTG
174	GCTCATTGTGCCTGGCAACT	27058	GGT	AAACTCAAAGCTCATCACCA	27412	CTG
175	gcgcTCATTGTGCCTGGCAACTG	27059	GTAGCTGG	aaaaCTCAAAGCTCATCACCACT	27413	GAGTCAGA
176	gcgcTCATTGTGCCTGGCAACTG	27060	GTAGCTGG	aaaaCTCAAAGCTCATCACCACT	27414	GAGTCAGA
179	ATGAGCGCCATCTTTTCCTGC	27061	TGCAA	AGTTTTCTTTCTTCTTTTCAT	27415	CCCAG
180	CGCTCATTGTGCCTGGCAACT	27062	GGTAG	AAAACTCAAAGCTCATCACCA	27416	CTGAGT
181	TGAGCGCCATCTTTTCCTGC	27063	TG	TTCTTTCTTCTTTTCATCCC	27417	AG
185	ATGAGCGCCATCTTTTCCTG	27064	CTG	GAGTTTTCTTTCTTCTTTTC	27418	ATC
186	CTCATTGTGCCTGGCAACTG	27065	GTA	AACTCAAAGCTCATCACCAC	27419	TGA
189	ATGAGCGCCATCTTTTCCTG	27066	CTG	TTTCTTTCTTCTTTTCATCC	27420	CAG
190	TGAGCGCCATCTTTTCCTGC	27067	TGC	AGTTTTCTTTCTTCTTTTCA	27421	TCC
191	TCATTGTGCCTGGCAACTGG	27068	TAG	ACTCAAAGCTCATCACCACT	27422	GAG
193	GAGCGCCATCTTTTCCTGCTG	27069	CAAG	GTTTTCTTTCTTCTTTTCATC	27423	CCAG
194	CATTGTGCCTGGCAACTGGT	27070	AG	CTCAAAGCTCATCACCACTG	27424	AG
198	CATTGTGCCTGGCAACTGGT	27071	AGC	CTCAAAGCTCATCACCACTG	27425	AGT
199	GAGCGCCATCTTTTCCTGCT	27072	GCA	GTTTTCTTTCTTCTTTTCAT	27426	CCC
203	GAGCGCCATCTTTTCCTGCTG	27073	CAAGA	AGTTTTCTTTCTTCTTTTCAT	27427	CCCAG
204	GAGCGCCATCTTTTCCTGCTG	27074	CAAGA	AGTTTTCTTTCTTCTTTTCAT	27428	CCCAG
209	TTGTGCCTGGCAACTGGTAG	27075	CTG	ACTCAAAGCTCATCACCACT	27429	GAG
210	TGTGCCTGGCAACTGGTAGC	27076	TGG	GCTCATCACCACTGAGTCAG	27430	AGG
213	ATTGTGCCTGGCAACTGGTA	27077	GCT	TCAAAGCTCATCACCACTGA	27431	GTC
214	TGAGCGCCATCTTTTCCTGC	27078	TG	TTCTTTCTTCTTTTCATCCC	27432	AG
217	CATTGTGCCTGGCAACTGGT	27079	AG	CTCAAAGCTCATCACCACTG	27433	AG
221	AGCGCCATCTTTTCCTGCTG	27080	CAA	TTTTCTTTCTTCTTTTCATC	27434	CCA
222	gcgcTCATTGTGCCTGGCAACTG	27081	GTAGCTGG	aaaaCTCAAAGCTCATCACCACT	27435	GAGTCAGA
223	gcgcTCATTGTGCCTGGCAACTG	27082	GTAGCTGG	aaaaCTCAAAGCTCATCACCACT	27436	GAGTCAGA
226	gcAGCAGGAAAAGATGGCGCTCAT	27083	TGTGCC	aaGAAGAAAGAAAACTCAAAGCTC	27437	ATCACC

227	ATTGTGCCTGGCAACTGGTAG	27084	CTGG	AAGCTCATCACCACTGAGTCA	27438	GAGG
228	ATTGTGCCTGGCAACTGGTAG	27085	CTGG	TCAAAGCTCATCACCACTGAG	27439	TCAG
231	GCGCCATCTTTTCCTGCTGC	27086	AAG	TTTCTTTCTTCTTTTCATCC	27440	CAG
232	GCGCCATCTTTTCCTGCTGC	27087	AAG	TTTCTTTCTTCTTTTCATCC	27441	CAG
235	TTGTGCCTGGCAACTGGTAG	27088	CTG	AAAGCTCATCACCACTGAGT	27442	CAG
236	TTGTGCCTGGCAACTGGTAG	27089	CTG	CAAAGCTCATCACCACTGAG	27443	TCA
237	gcgcTCATTGTGCCTGGCAACTG	27090	GTAGCTGG	aaaaCTCAAAGCTCATCACCACT	27444	GAGTCAGA
238	gcgcTCATTGTGCCTGGCAACTG	27091	GTAGCTGG	aaaaCTCAAAGCTCATCACCACT	27445	GAGTCAGA
239	TTGTGCCTGGCAACTGGTAGC	27092	TGGAG	CAAAGCTCATCACCACTGAGT	27446	CAGAG
240	CGCCATCTTTTCCTGCTGCA	27093	AG	TTCTTTCTTCTTTTCATCCC	27447	AG
243	TGTGCCTGGCAACTGGTAGC	27094	TG	AAGCTCATCACCACTGAGTC	27448	AG
247	CGCCATCTTTTCCTGCTGCA	27095	AGA	TTCTTTCTTCTTTTCATCCC	27449	AGC
249	TGTGCCTGGCAACTGGTAGC	27096	TGG	AAAGCTCATCACCACTGAGT	27450	CAG
250	cacaATGAGCGCCATCTTTTCCT	27097	GCTGC	gagtTTTCTTTCTTCTTTTCATC	27451	CCAGCTTG
251	cacaATGAGCGCCATCTTTTCCT	27098	GCTGC	gagtTTTCTTTCTTCTTTTCATC	27452	CCAGCTTG
254	GCGCCATCTTTTCCTGCTGC	27099	AAG	TTTCTTTCTTCTTTTCATCC	27453	CAG
255	GCCATCTTTTCCTGCTGCAA	27100	GAA	TCTTTCTTCTTTTCATCCCA	27454	GCT
258	TGTGCCTGGCAACTGGTAGC	27101	TGG	AGCTCATCACCACTGAGTCA	27455	GAG
259	TGTGCCTGGCAACTGGTAGC	27102	TGG	GCTCATCACCACTGAGTCAG	27456	AGG
262	GTGCCTGGCAACTGGTAGCT	27103	GGA	AAGCTCATCACCACTGAGTC	27457	AGA
263	GTGCCTGGCAACTGGTAGCT	27104	GG	AAGCTCATCACCACTGAGTC	27458	AG
267	GTGCCTGGCAACTGGTAGCTG	27105	GAGG	AAGCTCATCACCACTGAGTCA	27459	GAGG
268	GTGCCTGGCAACTGGTAGCTG	27106	GAGG	AAGCTCATCACCACTGAGTCA	27460	GAGG
271	TGCCTGGCAACTGGTAGCTG	27107	GAG	AGCTCATCACCACTGAGTCA	27461	GAG
272	GCCTGGCAACTGGTAGCTGG	27108	AGG	GCTCATCACCACTGAGTCAG	27462	AGG
275	TGCCTGGCAACTGGTAGCTG	27109	GAG	AGCTCATCACCACTGAGTCA	27463	GAG
276	CGCCATCTTTTCCTGCTGCA	27110	AG	TTCTTTCTTCTTTTCATCCC	27464	AG

279	GTGCCTGGCAACTGGTAGCT	27111	GG	AAGCTCATCACCACTGAGTC	27465	AG
283	CCATCTTTTCCTGCTGCAAG	27112	AAT	CTTTCTTCTTTTCATCCCAG	27466	CTT
286	ttGTGCCTGGCAACTGGTAGCTG	27113	GAGGA	ctCAAAGCTCATCACCACTGAGT	27467	CAGAG
287	GTGCCTGGCAACTGGTAGCTG	27114	GAGGA	AAAGCTCATCACCACTGAGTC	27468	AGAGG
288	ttGTGCCTGGCAACTGGTAGCTG	27115	GAGGA	ctCAAAGCTCATCACCACTGAGT	27469	CAGAG
289	GTGCCTGGCAACTGGTAGCTG	27116	GAGGA	AAAGCTCATCACCACTGAGTC	27470	AGAGG
292	GTGCCTGGCAACTGGTAGCTG	27117	GAGG	AAGCTCATCACCACTGAGTCA	27471	GAGG
293	GTGCCTGGCAACTGGTAGCTG	27118	GAGG	AAGCTCATCACCACTGAGTCA	27472	GAGG
296	CATCTTTTCCTGCTGCAAGA	27119	ATG	TTTCTTCTTTTCATCCCAGC	27473	TTG
297	CATCTTTTCCTGCTGCAAGA	27120	ATG	TTTCTTCTTTTCATCCCAGC	27474	TTG
300	GCCTGGCAACTGGTAGCTGG	27121	AGG	GCTCATCACCACTGAGTCAG	27475	AGG
301	GCCTGGCAACTGGTAGCTGG	27122	AGG	GCTCATCACCACTGAGTCAG	27476	AGG
302	CCTGGCAACTGGTAGCTGGAG	27123	GACAGT	CATCACCACTGAGTCAGAGGC	27477	ACTAG
303	ATCTTTTCCTGCTGCAAGAA	27124	TGA	TTCTTCTTTTCATCCCAGCT	27478	TGC
304	CCTGGCAACTGGTAGCTGGA	27125	GGA	CTCATCACCACTGAGTCAGA	27479	GGC
305	TCTTTTCCTGCTGCAAGAAT	27126	GAG	TCTTCTTTTCATCCCAGCTT	27480	GCA
306	CTGGCAACTGGTAGCTGGAG	27127	GAC	TCATCACCACTGAGTCAGAG	27481	GCA
308	CTTTTCCTGCTGCAAGAATG	27128	AGG	CTTCTTTTCATCCCAGCTTG	27482	CAC
309	TGGCAACTGGTAGCTGGAGG	27129	ACA	CATCACCACTGAGTCAGAGG	27483	CAC
310	TTTTCCTGCTGCAAGAATGA	27130	GG	CTTTTCATCCCAGCTTGCAC	27484	TG
314	TTTTCCTGCTGCAAGAATGA	27131	GGT	TTCTTTTCATCCCAGCTTGC	27485	ACT
315	GGCAACTGGTAGCTGGAGGA	27132	CAG	ATCACCACTGAGTCAGAGGC	27486	ACT
316	tcctGCTGCAAGAATGAGGTTTG	27133	GGTTCATT	tcttTCTTCTTTTCATCCCAGCT	27487	TGCACTGG
317	tcctGCTGCAAGAATGAGGTTTG	27134	GGTTCATT	tcttTCTTCTTTTCATCCCAGCT	27488	TGCACTGG
321	CTTTTCCTGCTGCAAGAATG	27135	AGG	TCTTTTCATCCCAGCTTGCA	27489	CTG
322	TTTCCTGCTGCAAGAATGAG	27136	GTT	TCTTTTCATCCCAGCTTGCA	27490	CTG
323	GCAACTGGTAGCTGGAGGAC	27137	AGT	TCACCACTGAGTCAGAGGCA	27491	CTA

324	ctggCAACTGGTAGCTGGAGGAC	27138	AGTAC	caccACTGAGTCAGAGGCACTAG	27492	GAGAC
325	ctggCAACTGGTAGCTGGAGGAC	27139	AGTAC	caccACTGAGTCAGAGGCACTAG	27493	GAGAC
327	TTCCTGCTGCAAGAATGAGG	27140	TTT	CTTTTCATCCCAGCTTGCAC	27494	TGG
329	CAACTGGTAGCTGGAGGACA	27141	GTA	CACCACTGAGTCAGAGGCAC	27495	TAG
332	CCTGCTGCAAGAATGAGGTT	27142	TG	TTTTCATCCCAGCTTGCACT	27496	GG
335	GCAACTGGTAGCTGGAGGAC	27143	AG	ACCACTGAGTCAGAGGCACT	27497	AG
339	TCCTGCTGCAAGAATGAGGT	27144	TTG	TTTTCATCCCAGCTTGCACT	27498	GGT
341	AACTGGTAGCTGGAGGACAG	27145	TAC	ACCACTGAGTCAGAGGCACT	27499	AGG
350	CCTGCTGCAAGAATGAGGTT	27146	TGG	CTTTTCATCCCAGCTTGCAC	27500	TGG
351	CCTGCTGCAAGAATGAGGTT	27147	TGG	TTTCATCCCAGCTTGCACTG	27501	GTT
354	GTAGCTGGAGGACAGTACTC	27148	ACG	ACCACTGAGTCAGAGGCACT	27502	AGG
355	TAGCTGGAGGACAGTACTCA	27149	CGG	ACCACTGAGTCAGAGGCACT	27503	AGG
358	ACTGGTAGCTGGAGGACAGT	27150	ACT	CCACTGAGTCAGAGGCACTA	27504	GGA
359	GCAACTGGTAGCTGGAGGAC	27151	AG	CCACTGAGTCAGAGGCACTA	27505	GG

Table 2C: Exemplary left gRNA spacer and right gRNA spacer pairs

Table 2C provides exemplified second-nick gRNA species for optional use for correcting the pathogenic R243Q mutation in PAH. The gRNA spacers from Table 1C were filtered, e.g., filtered by occurrence within 15 nt of the desired editing location and use of a Tier 1 Cas enzyme. Second-nick gRNAs were generated by searching the opposite strand of DNA in the regions -40 to -140 (“left”) and +40 to +140 (“right”), relative to the first nick site defined by the first gRNA, for the PAM utilized by the corresponding Cas variant. One exemplary spacer is shown for each side of the target nick site.

ID	Left gRNA spacer	SEQ ID NO	Left PAM	Right gRNA spacer	SEQ ID NO	Right PAM
3	CACGGTTCGGGGGTATACAT	27683	GGG	GAGACCTTTAGGTAGTGGAG	28053	TAG
4	ACGGTTCGGGGGTATACATG	27684	GGC	ACCTTTAGGTAGTGGAGTAG	28054	TAC
5	ACTGCACACAGTACATCAGAC	27685	ATGG	TGTGTACTACTCCACTACCTA	28055	AAGG
6	CCCATGTATACCCCCGAACCG	27686	TGAG	ATGTGTACTACTCCACTACCT	28056	AAAG

9	ATCCAAGCCCATGTATACCC	27687	CCG	GTGTACTACTCCACTACCTA	28057	AAG
10	TGGATCCAAGCCCATGTATA	27688	CCC	CAGTTATGTGTACTACTCCA	28058	CTA
11	CGGTTCGGGGGTATACATGG	27689	GCT	CCTTTAGGTAGTGGAGTAGT	28059	ACA
12	acatGGATCCAAGCCCATGTATA	27690	CCCCCGAA	gggcAGTTATGTGTACTACTCCA	28060	CTACCTAA
13	acatGGATCCAAGCCCATGTATA	27691	CCCCCGAA	gggcAGTTATGTGTACTACTCCA	28061	CTACCTAA
14	GGATCCAAGCCCATGTATACC	27692	CCCGA	GTTATGTGTACTACTCCACTA	28062	CCTAA
15	CCCATGTATACCCCCGAACCG	27693	TGAG	ATGTGTACTACTCCACTACCT	28063	AAAG
17	TCCAAGCCCATGTATACCCC	27694	CG	TGTACTACTCCACTACCTAA	28064	AG
21	GGATCCAAGCCCATGTATAC	27695	CCC	AGTTATGTGTACTACTCCAC	28065	TAC
22	GGTTCGGGGGTATACATGGG	27696	CTT	CTTTAGGTAGTGGAGTAGTA	28066	CAC
25	tgGATCCAAGCCCATGTATACCC	27697	CCGAA	gcCTAGCGTCAAAGCCTATGTCC	28067	CTGGG
26	GGATCCAAGCCCATGTATACC	27698	CCCGA	GTTATGTGTACTACTCCACTA	28068	CCTAA
29	ATCCAAGCCCATGTATACCC	27699	CCG	GTGTACTACTCCACTACCTA	28069	AAG
30	TGCACACAGTACATCAGACA	27700	TGG	TGTACTACTCCACTACCTAA	28070	AGG
33	GATCCAAGCCCATGTATACC	27701	CCC	GTTATGTGTACTACTCCACT	28071	ACC
34	TCCAAGCCCATGTATACCCC	27702	CG	TGTACTACTCCACTACCTAA	28072	AG
37	GTTCGGGGGTATACATGGGC	27703	TTG	TTTAGGTAGTGGAGTAGTAC	28073	ACA
42	tgGATCCAAGCCCATGTATACCC	27704	CCGAA	gcCTAGCGTCAAAGCCTATGTCC	28074	CTGGG
43	GATCCAAGCCCATGTATACCC	27705	CCGAA	GTTATGTGTACTACTCCACTA	28075	CCTAA
44	ACTGCACACAGTACATCAGAC	27706	ATGG	TGTGTACTACTCCACTACCTA	28076	AAGG
45	CCCATGTATACCCCCGAACCG	27707	TGAG	ATGTGTACTACTCCACTACCT	28077	AAAG
48	ATCCAAGCCCATGTATACCC	27708	CCG	GTGTACTACTCCACTACCTA	28078	AAG
49	ATCCAAGCCCATGTATACCC	27709	CCG	TTATGTGTACTACTCCACTA	28079	CCT
50	TTCGGGGGTATACATGGGCT	27710	TGG	TTAGGTAGTGGAGTAGTACA	28080	CAT
51	ggttCGGGGGTATACATGGGCTT	27711	GGATC	ctttAGGTAGTGGAGTAGTACAC	28081	ATAAC
52	ggttCGGGGGTATACATGGGCTT	27712	GGATC	ctttAGGTAGTGGAGTAGTACAC	28082	ATAAC
57	cgGTTCGGGGGTATACATGGGCTT	27713	GGATCC	ttAGGTAGTGGAGTAGTACACATA	28083	ACTGCC

58	GATCCAAGCCCATGTATACCC	27714	CCGAA	TTATGTGTACTACTCCACTAC	28084	CTAAA
59	TCCAAGCCCATGTATACCCC	27715	CGA	TATGTGTACTACTCCACTAC	28085	CTA
60	TCGGGGGTATACATGGGCTT	27716	GGA	TAGGTAGTGGAGTAGTACAC	28086	ATA
61	ggttCGGGGGTATACATGGGCTT	27717	GGATC	ctttAGGTAGTGGAGTAGTACAC	28087	ATAAC
62	ggttCGGGGGTATACATGGGCTT	27718	GGATC	ctttAGGTAGTGGAGTAGTACAC	28088	ATAAC
64	GGTTCGGGGGTATACATGGGC	27719	TTGGAT	TTTAGGTAGTGGAGTAGTACA	28089	CATAA
65	TCCAAGCCCATGTATACCCC	27720	CG	TGTACTACTCCACTACCTAA	28090	AG
69	CCAAGCCCATGTATACCCCC	27721	GAA	ATGTGTACTACTCCACTACC	28091	TAA
70	CGGGGGTATACATGGGCTTG	27722	GAT	AGGTAGTGGAGTAGTACACA	28092	TAA
76	AGCCCATGTATACCCCCGAA	27723	CCG	GTGTACTACTCCACTACCTA	28093	AAG
77	TGCACACAGTACATCAGACA	27724	TGG	TGTACTACTCCACTACCTAA	28094	AGG
80	CAAGCCCATGTATACCCCCG	27725	AAC	TGTGTACTACTCCACTACCT	28095	AAA
81	TCCAAGCCCATGTATACCCC	27726	CG	TGTACTACTCCACTACCTAA	28096	AG
84	GGGGGTATACATGGGCTTGG	27727	ATC	GGTAGTGGAGTAGTACACAT	28097	AAC
86	ACTGCACACAGTACATCAGAC	27728	ATGG	TGTGTACTACTCCACTACCTA	28098	AAGG
87	CCCATGTATACCCCCGAACCG	27729	TGAG	TGTGTACTACTCCACTACCTA	28099	AAGG
90	AGCCCATGTATACCCCCGAA	27730	CCG	GTGTACTACTCCACTACCTA	28100	AAG
91	AAGCCCATGTATACCCCCGA	27731	ACC	GTGTACTACTCCACTACCTA	28101	AAG
92	GGGGTATACATGGGCTTGGA	27732	TCC	GTAGTGGAGTAGTACACATA	28102	ACT
93	gttcGGGGGTATACATGGGCTTG	27733	GATCCATG	taggTAGTGGAGTAGTACACATA	28103	ACTGC
96	cgGTTCGGGGGTATACATGGGCTT	27734	GGATCC	taGGTAGTGGAGTAGTACACATAA	28104	CTGCCC
97	aacCGTGAGTACTGTCCTCCAGCT	27735	ACCAGTT	ctaGCGTCAAAGCCTATGTCCCTG	28105	GGCAGTT
98	AGCCCATGTATACCCCCGAAC	27736	CGTGA	ATGTGTACTACTCCACTACCT	28106	AAAGGT
99	AGCCCATGTATACCCCCGAAC	27737	CGTGA	ATGTGTACTACTCCACTACCT	28107	AAAGGT
102	CCCATGTATACCCCCGAACCG	27738	TGAG	TGTGTACTACTCCACTACCTA	28108	AAGG
103	AGCCCATGTATACCCCCGAA	27739	CCG	TGTACTACTCCACTACCTAA	28109	AGG
104	GGGTATACATGGGCTTGGAT	27740	CCA	TAGTGGAGTAGTACACATAA	28110	CTG

105	ggggTATACATGGGCTTGGATCC	27741	ATGTCTGA	aggtAGTGGAGTAGTACACATAA	28111	CTGCCCAG
106	ggggTATACATGGGCTTGGATCC	27742	ATGTCTGA	aggtAGTGGAGTAGTACACATAA	28112	CTGCCCAG
107	ggggTATACATGGGCTTGGATCC	27743	ATGTCTGA	aggtAGTGGAGTAGTACACATAA	28113	CTGCCCAG
108	AGCCCATGTATACCCCCGAAC	27744	CGTGA	ATGTGTACTACTCCACTACCT	28114	AAAGGT
109	TATACATGGGCTTGGATCCA	27745	TG	AGTGGAGTAGTACACATAAC	28115	TG
112	GCCCATGTATACCCCCGAAC	27746	CGT	GTACTACTCCACTACCTAAA	28116	GGT
114	GGTATACATGGGCTTGGATC	27747	CAT	AGTGGAGTAGTACACATAAC	28117	TGC
121	GTATACATGGGCTTGGATCC	27748	ATG	TAGTGGAGTAGTACACATAA	28118	CTG
122	GTATACATGGGCTTGGATCC	27749	ATG	GTGGAGTAGTACACATAACT	28119	GCC
123	CCCATGTATACCCCCGAACC	27750	GTG	TACTACTCCACTACCTAAAG	28120	GTC
124	ggggTATACATGGGCTTGGATCC	27751	ATGTC	ggtaGTGGAGTAGTACACATAAC	28121	TGCCC
126	cgGTTCGGGGGTATACATGGGCTT	27752	GGATCC	taGGTAGTGGAGTAGTACACATAA	28122	CTGCCC
127	CCATGTATACCCCCGAACCG	27753	TGA	ACTACTCCACTACCTAAAGG	28123	TCT
128	TATACATGGGCTTGGATCCA	27754	TGT	TGGAGTAGTACACATAACTG	28124	CCC
129	cccaTGTATACCCCCGAACCGTG	27755	AGTAC	tgtaCTACTCCACTACCTAAAGG	28125	TCTCCTAG
130	cccaTGTATACCCCCGAACCGTG	27756	AGTAC	tgtaCTACTCCACTACCTAAAGG	28126	TCTCCTAG
131	ggggTATACATGGGCTTGGATCC	27757	ATGTC	ggtaGTGGAGTAGTACACATAAC	28127	TGCCC
132	ATGTATACCCCCGAACCGTG	27758	AG	GTACTACTCCACTACCTAAA	28128	GG
136	CATGTATACCCCCGAACCGT	27759	GAG	CTACTCCACTACCTAAAGGT	28129	CTC
137	ATACATGGGCTTGGATCCAT	27760	GTC	GGAGTAGTACACATAACTGC	28130	CCA
141	CATGTATACCCCCGAACCGT	27761	GAG	TCCACTACCTAAAGGTCTCC	28131	TAG
142	ATGTATACCCCCGAACCGTG	27762	AGT	TACTCCACTACCTAAAGGTC	28132	TCC
143	TACATGGGCTTGGATCCATG	27763	TCT	GAGTAGTACACATAACTGCC	28133	CAG
144	cccaTGTATACCCCCGAACCGTG	27764	AGTAC	tgtaCTACTCCACTACCTAAAGG	28134	TCTCCTAG
145	ggggTATACATGGGCTTGGATCC	27765	ATGTC	ggagTAGTACACATAACTGCCCA	28135	GGGAC
148	atGTATACCCCCGAACCGTGAGTA	27766	CTGTCC	taCTCCACTACCTAAAGGTCTCCT	28136	AGTGCC
149	cgGTTCGGGGGTATACATGGGCTT	27767	GGATCC	taGGTAGTGGAGTAGTACACATAA	28137	CTGCCC

150	CCCATGTATACCCCCGAACCG	27768	TGAG	ACTCCACTACCTAAAGGTCTC	28138	CTAG
151	TGTATACCCCCGAACCGTGA	27769	GTA	ACTCCACTACCTAAAGGTCT	28139	CCT
152	ACATGGGCTTGGATCCATGT	27770	CTG	AGTAGTACACATAACTGCCC	28140	AGG
153	cccaTGTATACCCCCGAACCGTG	27771	AGTAC	actcCACTACCTAAAGGTCTCCT	28141	AGTGC
154	catgGGCTTGGATCCATGTCTGA	27772	TGTACTGT	ggagTAGTACACATAACTGCCCA	28142	GGGAC
155	GCCCATGTATACCCCCGAACC	27773	GTGAGT	TACTCCACTACCTAAAGGTCT	28143	CCTAGT
156	CATGGGCTTGGATCCATGTC	27774	TG	GTAGTACACATAACTGCCCA	28144	GG
160	CATGGGCTTGGATCCATGTC	27775	TGA	GTAGTACACATAACTGCCCA	28145	GGG
161	GTATACCCCCGAACCGTGAG	27776	TAC	CTCCACTACCTAAAGGTCTC	28146	CTA
167	TGGGCTTGGATCCATGTCTG	27777	ATG	GTAGTACACATAACTGCCCA	28147	GGG
168	TTCGGGGGTATACATGGGCT	27778	TGG	GTAGTACACATAACTGCCCA	28148	GGG
171	ATGGGCTTGGATCCATGTCT	27779	GAT	TAGTACACATAACTGCCCAG	28149	GGA
172	TACCCCCGAACCGTGAGTAC	27780	TG	CCACTACCTAAAGGTCTCCT	28150	AG
175	CATGGGCTTGGATCCATGTC	27781	TG	TAGTACACATAACTGCCCAG	28151	GG
179	TATACCCCCGAACCGTGAGT	27782	ACT	TCCACTACCTAAAGGTCTCC	28152	TAG
183	ATGTCTGATGTACTGTGTGCA	27783	GTGG	GAGTAGTACACATAACTGCCC	28153	AGGG
184	TCCATGTCTGATGTACTGTGT	27784	GCAG	GAGTAGTACACATAACTGCCC	28154	AGGG
187	ATACCCCCGAACCGTGAGTA	27785	CTG	CACTACCTAAAGGTCTCCTA	28155	GTG
188	TCCTCCAGCTACCAGTTGCC	27786	AGG	TGTACTACTCCACTACCTAA	28156	AGG
191	ATACCCCCGAACCGTGAGTA	27787	CTG	CCACTACCTAAAGGTCTCCT	28157	AGT
194	TGGGCTTGGATCCATGTCTG	27788	ATG	GTAGTACACATAACTGCCCA	28158	GGG
195	TGGGCTTGGATCCATGTCTG	27789	ATG	AGTACACATAACTGCCCAGG	28159	GAC
196	TACCCCCGAACCGTGAGTAC	27790	TG	CCACTACCTAAAGGTCTCCT	28160	AG
199	tgtaTACCCCCGAACCGTGAGTA	27791	CTGTC	actcCACTACCTAAAGGTCTCCT	28161	AGTGC
203	atGTATACCCCCGAACCGTGAGTA	27792	CTGTCC	taCTCCACTACCTAAAGGTCTCCT	28162	AGTGCC
204	aacTGGTAGCTGGAGGACAGTACT	27793	CACGGTT		28163	
205	ATACATGGGCTTGGATCCATG	27794	TCTGAT	GTACACATAACTGCCCAGGGA	28164	CATAG

206	ATACATGGGCTTGGATCCATG	27795	TCTGAT	GTACACATAACTGCCCAGGGA	28165	CATAG
207	TGTCCTCCAGCTACCAGTTGC	27796	CAGG	TGTGTACTACTCCACTACCTA	28166	AAGG
208	CCGAACCGTGAGTACTGTCCT	27797	CCAG	ACTCCACTACCTAAAGGTCTC	28167	CTAG
211	ATACCCCCGAACCGTGAGTA	27798	CTG	CACTACCTAAAGGTCTCCTA	28168	GTG
212	TACCCCCGAACCGTGAGTAC	27799	TGT	CACTACCTAAAGGTCTCCTA	28169	GTG
213	GGGCTTGGATCCATGTCTGA	27800	TGT	GTACACATAACTGCCCAGGG	28170	ACA
214	gtatACCCCCGAACCGTGAGTAC	27801	TGTCC	ctccACTACCTAAAGGTCTCCTA	28171	GTGCC
215	gtatACCCCCGAACCGTGAGTAC	27802	TGTCC	ctccACTACCTAAAGGTCTCCTA	28172	GTGCC
217	CCCGAACCGTGAGTACTGTCC	27803	TCCAG	ACCTAAAGGTCTCCTAGTGCC	28173	TCTGA
218	CCGAACCGTGAGTACTGTCCT	27804	CCAG	ACTCCACTACCTAAAGGTCTC	28174	CTAG
219	GGCTTGGATCCATGTCTGAT	27805	GTA	TACACATAACTGCCCAGGGA	28175	CAT
220	ACCCCCGAACCGTGAGTACT	27806	GTC	ACTACCTAAAGGTCTCCTAG	28176	TGC
224	CCCGAACCGTGAGTACTGTCC	27807	TCCAG	ACCTAAAGGTCTCCTAGTGCC	28177	TCTGA
225	TACCCCCGAACCGTGAGTAC	27808	TG	ACTACCTAAAGGTCTCCTAG	28178	TG
229	CCCCCGAACCGTGAGTACTG	27809	TCC	CTACCTAAAGGTCTCCTAGT	28179	GCC
230	GCTTGGATCCATGTCTGATG	27810	TAC	ACACATAACTGCCCAGGGAC	28180	ATA
236	GAACCGTGAGTACTGTCCTC	27811	CAG	CACTACCTAAAGGTCTCCTA	28181	GTG
237	CCCCGAACCGTGAGTACTGT	27812	CCT	TACCTAAAGGTCTCCTAGTG	28182	CCT
238	TGGATCCATGTCTGATGTAC	27813	TG	ACATAACTGCCCAGGGACAT	28183	AG
242	CTTGGATCCATGTCTGATGT	27814	ACT	CACATAACTGCCCAGGGACA	28184	TAG
243	catgGGCTTGGATCCATGTCTGA	27815	TGTACTGT	gtacACATAACTGCCCAGGGACA	28185	TAGGCTTT
244	catgGGCTTGGATCCATGTCTGA	27816	TGTACTGT	gtacACATAACTGCCCAGGGACA	28186	TAGGCTTT
249	CCGAACCGTGAGTACTGTCCT	27817	CCAG	ACTCCACTACCTAAAGGTCTC	28187	CTAG
254	TTGGATCCATGTCTGATGTA	27818	CTG	ACATAACTGCCCAGGGACAT	28188	AGG
255	TTGGATCCATGTCTGATGTA	27819	CTG	ACATAACTGCCCAGGGACAT	28189	AGG
256	CCCGAACCGTGAGTACTGTC	27820	CTC	ACCTAAAGGTCTCCTAGTGC	28190	CTC
257	taccCCCGAACCGTGAGTACTGT	27821	CCTCC	ccacTACCTAAAGGTCTCCTAGT	28191	GCCTC

258	taccCCCGAACCGTGAGTACTGT	27822	CCTCC	ccacTACCTAAAGGTCTCCTAGT	28192	GCCTC
260	CCCGAACCGTGAGTACTGTCC	27823	TCCAG	ACCTAAAGGTCTCCTAGTGCC	28193	TCTGA
261	CCGAACCGTGAGTACTGTCC	27824	TCC	CCTAAAGGTCTCCTAGTGCC	28194	TCT
263	TGGATCCATGTCTGATGTAC	27825	TGT	CATAACTGCCCAGGGACATA	28195	GGC
264	ttggATCCATGTCTGATGTACTG	27826	TGTGCAGT	gtacACATAACTGCCCAGGGACA	28196	TAGGCTTT
269	CCCGAACCGTGAGTACTGTCC	27827	TCCAG	ACCTAAAGGTCTCCTAGTGCC	28197	TCTGA
270	AACCGTGAGTACTGTCCTCC	27828	AG	TAAAGGTCTCCTAGTGCCTC	28198	TG
274	CGAACCGTGAGTACTGTCCT	27829	CCA	CTAAAGGTCTCCTAGTGCCT	28199	CTG
275	GGATCCATGTCTGATGTACT	27830	GTG	ATAACTGCCCAGGGACATAG	28200	GCT
281	aaGCCCATGTATACCCCCGAACC	27831	GTGAGT	ctAGTGCCTCTGACTCAGTGGTG	28201	ATGAG
282	CCCGAACCGTGAGTACTGTCC	27832	TCCAG	ACCTAAAGGTCTCCTAGTGCC	28202	TCTGA
285	GAACCGTGAGTACTGTCCTC	27833	CAG	CTAAAGGTCTCCTAGTGCCT	28203	CTG
286	TCCTCCAGCTACCAGTTGCC	27834	AGG	TCCTAGTGCCTCTGACTCAG	28204	TGG
289	GAACCGTGAGTACTGTCCTC	27835	CAG	TAAAGGTCTCCTAGTGCCTC	28205	TGA
290	AACCGTGAGTACTGTCCTCC	27836	AG	TAAAGGTCTCCTAGTGCCTC	28206	TG
293	GATCCATGTCTGATGTACTG	27837	TG	CATAACTGCCCAGGGACATA	28207	GG
297	GATCCATGTCTGATGTACTG	27838	TGT	TAACTGCCCAGGGACATAGG	28208	CTT
303	aaGCCCATGTATACCCCCGAACC	27839	GTGAGT	ctAGTGCCTCTGACTCAGTGGTG	28209	ATGAG
304	CCCGAACCGTGAGTACTGTCC	27840	TCCAG	AAGGTCTCCTAGTGCCTCTGA	28210	CTCAG
305	TGTCCTCCAGCTACCAGTTGC	27841	CAGG	TCTCCTAGTGCCTCTGACTCA	28211	GTGG
306	CCGAACCGTGAGTACTGTCCT	27842	CCAG	AGGTCTCCTAGTGCCTCTGAC	28212	TCAG
309	GAACCGTGAGTACTGTCCTC	27843	CAG	CTAAAGGTCTCCTAGTGCCT	28213	CTG
310	AACCGTGAGTACTGTCCTCC	27844	AGC	AAAGGTCTCCTAGTGCCTCT	28214	GAC
313	ATCCATGTCTGATGTACTGT	27845	GTG	ACTGCCCAGGGACATAGGCT	28215	TTG
314	ATCCATGTCTGATGTACTGT	27846	GTG	AACTGCCCAGGGACATAGGC	28216	TTT
315	AGCGCCATCTTTTCCTGCTG	27847	CAAGAAT		28217	
319	CGTGAGTACTGTCCTCCAGCT	27848	ACCAGT	AAGGTCTCCTAGTGCCTCTGA	28218	CTCAG

320	CCGAACCGTGAGTACTGTCCT	27849	CCAG	AGGTCTCCTAGTGCCTCTGAC	28219	TCAG
322	TCCATGTCTGATGTACTGTGT	27850	GCAG	ACACATAACTGCCCAGGGACA	28220	TAGG
323	AACCGTGAGTACTGTCCTCC	27851	AG	TAAAGGTCTCCTAGTGCCTC	28221	TG
327	ACCGTGAGTACTGTCCTCCA	27852	GCT	AAGGTCTCCTAGTGCCTCTG	28222	ACT
328	TCCATGTCTGATGTACTGTG	27853	TGC	ACTGCCCAGGGACATAGGCT	28223	TTG
329	AGCGCCATCTTTTCCTGCTG	27854	CAAGAAT		28224	
330	ttggATCCATGTCTGATGTACTG	27855	TGTGCAGT	ataaCTGCCCAGGGACATAGGCT	28225	TTGAC
331	ttggATCCATGTCTGATGTACTG	27856	TGTGCAGT	ataaCTGCCCAGGGACATAGGCT	28226	TTGAC
336	aaGCCCATGTATACCCCCGAACC	27857	GTGAGT	ctAGTGCCTCTGACTCAGTGGTG	28227	ATGAG
337	CGTGAGTACTGTCCTCCAGCT	27858	ACCAGT	AAGGTCTCCTAGTGCCTCTGA	28228	CTCAG
338	ATCCATGTCTGATGTACTGTG	27859	TGCAGT	TAACTGCCCAGGGACATAGGC	28229	TTTGA
341	GAACCGTGAGTACTGTCCTC	27860	CAG	GTCTCCTAGTGCCTCTGACT	28230	CAG
342	CCGTGAGTACTGTCCTCCAG	27861	CTA	AGGTCTCCTAGTGCCTCTGA	28231	CTC
343	CCATGTCTGATGTACTGTGT	27862	GCA	CTGCCCAGGGACATAGGCTT	28232	TGA
350	CGTGAGTACTGTCCTCCAGCT	27863	ACCAGT	AAGGTCTCCTAGTGCCTCTGA	28233	CTCAG
351	GTGAGTACTGTCCTCCAGCTA	27864	CCAG	AGGTCTCCTAGTGCCTCTGAC	28234	TCAG
353	AACCGTGAGTACTGTCCTCC	27865	AG	TCTCCTAGTGCCTCTGACTC	28235	AG
357	CGTGAGTACTGTCCTCCAGC	27866	TAC	GGTCTCCTAGTGCCTCTGAC	28236	TCA
358	CATGTCTGATGTACTGTGTG	27867	CAG	TGCCCAGGGACATAGGCTTT	28237	GAC

Table 2D: Exemplary left gRNA spacer and right gRNA spacer pairs

Table 2D provides exemplified second-nick gRNA species for optional use for correcting the pathogenic IVS10-11G>A mutation in PAH. The gRNA spacers from Table 1D were filtered, e.g., filtered by occurrence within 15 nt of the desired editing location and use of a Tier 1 Cas enzyme. Second-nick gRNAs were generated by searching the opposite strand of DNA in the regions -40 to -140 (“left”) and +40 to +140 (“right”), relative to the first nick site defined by the first gRNA, for the PAM utilized by the corresponding Cas variant. One exemplary spacer is shown for each side of the target nick site.

ID	Left gRNA spacer	SEQ ID NO	Left PAM	Right gRNA spacer	SEQ ID NO	Right PAM
1	TCTCTGCCACGTAATAGAGG	28423	GGC	TCACCCCGATTCCTTCTACA	28721	TCA
2	GGAGTTCCAGCCCCTCTATTA	28424	CGTGG	GCATTTGGGCTGTGATGTAGA	28722	AGGAAT
3	TCTCTGCCACGTAATAGAGG	28425	GG	CCCGATTCCTTCTACATCAC	28723	AG
6	GAGTTCCAGCCCCTCTATTA	28426	CG	ATTTGGGCTGTGATGTAGAA	28724	GG
10	CTCTGCCACGTAATAGAGGG	28427	GCT	CACCCCGATTCCTTCTACAT	28725	CAC
12	GGAGTTCCAGCCCCTCTATT	28428	ACG	TTTGGGCTGTGATGTAGAAG	28726	GAA
16	TCTGCCACGTAATAGAGGGG	28429	CTG	CCCCGATTCCTTCTACATCA	28727	CAG
17	CTGCCACGTAATAGAGGGGC	28430	TGG	CAAATTACTTTGCACATACT	28728	AGG
20	TCTGCCACGTAATAGAGGGG	28431	CTG	ACCCCGATTCCTTCTACATC	28729	ACA
23	GGAGTTCCAGCCCCTCTATT	28432	ACG	GGGCTGTGATGTAGAAGGAA	28730	TCG
24	GAGTTCCAGCCCCTCTATTA	28433	CGT	TTGGGCTGTGATGTAGAAGG	28731	AAT
25	CTGCCACGTAATAGAGGGGC	28434	TG	CCCGATTCCTTCTACATCAC	28732	AG
28	ctctGCCACGTAATAGAGGGGCT	28435	GGAAC	ctcaCCCCGATTCCTTCTACATC	28733	ACAGC
31	tcTGCCACGTAATAGAGGGGCTGG	28436	AACTCC	ctCACCCCGATTCCTTCTACATCA	28734	CAGCCC
32	CTCTGCCACGTAATAGAGGGG	28437	CTGG	GCCAAATTACTTTGCACATAC	28735	TAGG
33	CTCTGCCACGTAATAGAGGGG	28438	CTGG	CACCCCGATTCCTTCTACATC	28736	ACAG
34	GAGTTCCAGCCCCTCTATTAC	28439	GTGG	TGGGCTGTGATGTAGAAGGAA	28737	TCGG
39	CTGCCACGTAATAGAGGGGC	28440	TGG	CCCCGATTCCTTCTACATCA	28738	CAG
40	CTGCCACGTAATAGAGGGGC	28441	TGG	CAAATTACTTTGCACATACT	28739	AGG
43	CTGCCACGTAATAGAGGGGC	28442	TGG	CCCCGATTCCTTCTACATCA	28740	CAG
44	CTGCCACGTAATAGAGGGGC	28443	TG	CCCGATTCCTTCTACATCAC	28741	AG
47	AGTTCCAGCCCCTCTATTAC	28444	GTG	TGGGCTGTGATGTAGAAGGA	28742	ATC
48	ctctGCCACGTAATAGAGGGGCT	28445	GGAAC	tcacCCCGATTCCTTCTACATCA	28743	CAGCCCAA
49	ctctGCCACGTAATAGAGGGGCT	28446	GGAAC	tcacCCCGATTCCTTCTACATCA	28744	CAGCCCAA
52	tcTCTGCCACGTAATAGAGGGGC	28447	TGGAA	ttCTACATCACAGCCCAAATGCT	28745	GTGAG

53	TCTGCCACGTAATAGAGGGGC	28448	TGGAA	CCGATTCCTTCTACATCACAG	28746	CCCAA
54	GTTCCAGCCCCTCTATTACGT	28449	GGCAG	TGGGCTGTGATGTAGAAGGAA	28747	TCGGG
55	GTTCCAGCCCCTCTATTACGT	28450	GGCAG	TGGGCTGTGATGTAGAAGGAA	28748	TCGGG
58	CTCTGCCACGTAATAGAGGGG	28451	CTGG	GCCAAATTACTTTGCACATAC	28749	TAGG
59	CTCTGCCACGTAATAGAGGGG	28452	CTGG	CACCCCGATTCCTTCTACATC	28750	ACAG
62	CTGCCACGTAATAGAGGGGC	28453	TGG	CCCCGATTCCTTCTACATCA	28751	CAG
63	TGCCACGTAATAGAGGGGCT	28454	GGA	CCCGATTCCTTCTACATCAC	28752	AGC
64	GTTCCAGCCCCTCTATTACG	28455	TGG	GGGCTGTGATGTAGAAGGAA	28753	TCG
67	GTTCCAGCCCCTCTATTACGT	28456	GGCAG	GGGCTGTGATGTAGAAGGAAT	28754	CGGGG
68	TCTGCCACGTAATAGAGGGGC	28457	TGGAA	CCGATTCCTTCTACATCACAG	28755	CCCAA
69	CTCTGCCACGTAATAGAGGGG	28458	CTGG	CACCCCGATTCCTTCTACATC	28756	ACAG
70	TTCCAGCCCCTCTATTACGT	28459	GGC	GGCTGTGATGTAGAAGGAAT	28757	CGG
71	GCCACGTAATAGAGGGGCTG	28460	GAA	CCGATTCCTTCTACATCACA	28758	GCC
74	TCTGCCACGTAATAGAGGGGC	28461	TGGAA	CCGATTCCTTCTACATCACAG	28759	CCCAA
75	TCCAGCCCCTCTATTACGTG	28462	GCA	GCTGTGATGTAGAAGGAATC	28760	GGG
76	CCACGTAATAGAGGGGCTGG	28463	AAC	CGATTCCTTCTACATCACAG	28761	CCC
77	CCAGCCCCTCTATTACGTGG	28464	CAG	CTGTGATGTAGAAGGAATCG	28762	GGG
78	CACGTAATAGAGGGGCTGGA	28465	ACT	GATTCCTTCTACATCACAGC	28763	CCA
79	CAGCCCCTCTATTACGTGGC	28466	AG	TGTGATGTAGAAGGAATCGG	28764	GG
83	CAGCCCCTCTATTACGTGGC	28467	AGA	TGTGATGTAGAAGGAATCGG	28765	GGT
84	ACGTAATAGAGGGGCTGGAA	28468	CTC	ATTCCTTCTACATCACAGCC	28766	CAA
85	cggaGTTCCAGCCCCTCTATTAC	28469	GTGGC	gcatTTGGGCTGTGATGTAGAAG	28767	GAATCGGG
86	cggaGTTCCAGCCCCTCTATTAC	28470	GTGGC	gcatTTGGGCTGTGATGTAGAAG	28768	GAATCGGG
87	cggaGTTCCAGCCCCTCTATTAC	28471	GTGGC	gcatTTGGGCTGTGATGTAGAAG	28769	GAATCGGG
90	taTTACGTGGCAGAGAGTTTTAAT	28472	GATGCC	ggTGAGATGAGAGAAGGGGCACAA	28770	ATGGCC
93	AGCCCCTCTATTACGTGGCA	28473	GAG	GTGATGTAGAAGGAATCGGG	28771	GTG
94	GTTCCAGCCCCTCTATTACG	28474	TGG	CTGTGATGTAGAAGGAATCG	28772	GGG

97	AGCCCCTCTATTACGTGGCA	28475	GAG	GTGATGTAGAAGGAATCGGG	28773	GTG
98	GCCCCTCTATTACGTGGCAG	28476	AG	TGTGATGTAGAAGGAATCGG	28774	GG
101	CGTAATAGAGGGGCTGGAAC	28477	TCC	TTCCTTCTACATCACAGCCC	28775	AAA
102	cggaGTTCCAGCCCCTCTATTAC	28478	GTGGCAGA	gcatTTGGGCTGTGATGTAGAAG	28776	GAATCGGG
103	cggaGTTCCAGCCCCTCTATTAC	28479	GTGGCAGA	gcatTTGGGCTGTGATGTAGAAG	28777	GAATCGGG
106	taTTACGTGGCAGAGAGTTTTAAT	28480	GATGCC	ggTGAGATGAGAGAAGGGGCACAA	28778	ATGGCC
107	GAGTTCCAGCCCCTCTATTAC	28481	GTGG	GGCTGTGATGTAGAAGGAATC	28779	GGGG
108	AGCCCCTCTATTACGTGGCAG	28482	AGAG	GTGATGTAGAAGGAATCGGGG	28780	TGAG
111	CCCCTCTATTACGTGGCAGA	28483	GAG	GTGATGTAGAAGGAATCGGG	28781	GTG
112	GCCCCTCTATTACGTGGCAG	28484	AGA	TGATGTAGAAGGAATCGGGG	28782	TGA
113	GTAATAGAGGGGCTGGAACT	28485	CCG	TCCTTCTACATCACAGCCCA	28783	AAT
114	cgtaATAGAGGGGCTGGAACTCC	28486	GTGAC	gattCCTTCTACATCACAGCCCA	28784	AATGCTGT
115	cggaGTTCCAGCCCCTCTATTAC	28487	GTGGCAGA	gcatTTGGGCTGTGATGTAGAAG	28785	GAATCGGG
116	cgtaATAGAGGGGCTGGAACTCC	28488	GTGAC	gattCCTTCTACATCACAGCCCA	28786	AATGCTGT
119	CAGCCCCTCTATTACGTGGCA	28489	GAGAGT	GTGATGTAGAAGGAATCGGGG	28787	TGAGAT
120	AGCCCCTCTATTACGTGGCAG	28490	AGAG	GTGATGTAGAAGGAATCGGGG	28788	TGAG
121	CCCCTCTATTACGTGGCAGA	28491	GAG	GATGTAGAAGGAATCGGGGT	28789	GAG
122	TAATAGAGGGGCTGGAACTC	28492	CGT	CCTTCTACATCACAGCCCAA	28790	ATG
125	CTCTATTACGTGGCAGAGAGT	28493	TTTAA	ATGTAGAAGGAATCGGGGTGA	28791	GATGA
126	CCCTCTATTACGTGGCAGAG	28494	AG	ATGTAGAAGGAATCGGGGTG	28792	AG
130	CCCTCTATTACGTGGCAGAG	28495	AGT	ATGTAGAAGGAATCGGGGTG	28793	AGA
131	AATAGAGGGGCTGGAACTCC	28496	GTG	CTTCTACATCACAGCCCAAA	28794	TGC
132	cgtaATAGAGGGGCTGGAACTCC	28497	GTGAC	gattCCTTCTACATCACAGCCCA	28795	AATGCTGT
136	CCCCTCTATTACGTGGCAGA	28498	GAG	GTAGAAGGAATCGGGGTGAG	28796	ATG
137	CCTCTATTACGTGGCAGAGA	28499	GTT	TGTAGAAGGAATCGGGGTGA	28797	GAT
138	ATAGAGGGGCTGGAACTCCG	28500	TGA	TTCTACATCACAGCCCAAAT	28798	GCT
139	CTCTATTACGTGGCAGAGAG	28501	TTT	GTAGAAGGAATCGGGGTGAG	28799	ATG

140	TAGAGGGGCTGGAACTCCGT	28502	GAC	TCTACATCACAGCCCAAATG	28800	CTG
141	TCTATTACGTGGCAGAGAGT	28503	TTT	TAGAAGGAATCGGGGTGAGA	28801	TGA
142	AGAGGGGCTGGAACTCCGTG	28504	ACA	CTACATCACAGCCCAAATGC	28802	TGT
145	GAGGGGCTGGAACTCCGTGA	28505	CAG	TACATCACAGCCCAAATGCT	28803	GTG
146	CTATTACGTGGCAGAGAGTT	28506	TTA	AGAAGGAATCGGGGTGAGAT	28804	GAG
150	TACGTGGCAGAGAGTTTTAA	28507	TG	GAAGGAATCGGGGTGAGATG	28805	AG
154	TATTACGTGGCAGAGAGTTT	28508	TAA	GAAGGAATCGGGGTGAGATG	28806	AGA
155	AGGGGCTGGAACTCCGTGAC	28509	AGT	ACATCACAGCCCAAATGCTG	28807	TGA
156	attaCGTGGCAGAGAGTTTTAAT	28510	GATGCCAA	ggaaTCGGGGTGAGATGAGAGAA	28808	GGGGC
157	cgtaATAGAGGGGCTGGAACTCC	28511	GTGAC	tctaCATCACAGCCCAAATGCTG	28809	TGAGCCAA
158	attaCGTGGCAGAGAGTTTTAAT	28512	GATGCCAA	ggaaTCGGGGTGAGATGAGAGAA	28810	GGGGC
159	cgtaATAGAGGGGCTGGAACTCC	28513	GTGAC	tctaCATCACAGCCCAAATGCTG	28811	TGAGCCAA
164	GGGGCTGGAACTCCGTGACAG	28514	TGTAA	ATCACAGCCCAAATGCTGTGA	28812	GCCAA
167	TTACGTGGCAGAGAGTTTTA	28515	ATG	AAGGAATCGGGGTGAGATGA	28813	GAG
168	ATTACGTGGCAGAGAGTTTT	28516	AAT	AAGGAATCGGGGTGAGATGA	28814	GAG
169	GGGGCTGGAACTCCGTGACA	28517	GTG	CATCACAGCCCAAATGCTGT	28815	GAG
173	GGCAGAGAGTTTTAATGATGC	28518	CAAG	AGGAATCGGGGTGAGATGAGA	28816	GAAG
174	GGGCTGGAACTCCGTGACAG	28519	TGT	ATCACAGCCCAAATGCTGTG	28817	AGC
175	TTACGTGGCAGAGAGTTTTA	28520	ATG	AGGAATCGGGGTGAGATGAG	28818	AGA
179	TATTACGTGGCAGAGAGTTTT	28521	AATGA	AGGAATCGGGGTGAGATGAGA	28819	GAAGG
180	TATTACGTGGCAGAGAGTTTT	28522	AATGA	AGGAATCGGGGTGAGATGAGA	28820	GAAGG
183	TACGTGGCAGAGAGTTTTAA	28523	TG	AGGAATCGGGGTGAGATGAG	28821	AG
187	TACGTGGCAGAGAGTTTTAA	28524	TGA	GGAATCGGGGTGAGATGAGA	28822	GAA
188	GGCTGGAACTCCGTGACAGT	28525	GTA	TCACAGCCCAAATGCTGTGA	28823	GCC
191	GGGGCTGGAACTCCGTGACAG	28526	TGTAA	TCACAGCCCAAATGCTGTGAG	28824	CCAAA
192	GGGGCTGGAACTCCGTGACAG	28527	TGTAA	TCACAGCCCAAATGCTGTGAG	28825	CCAAA
195	CGTGGCAGAGAGTTTTAATG	28528	ATG	GAATCGGGGTGAGATGAGAG	28826	AAG

196	ACGTGGCAGAGAGTTTTAAT	28529	GAT	GAATCGGGGTGAGATGAGAG	28827	AAG
197	GCTGGAACTCCGTGACAGTG	28530	TAA	CACAGCCCAAATGCTGTGAG	28828	CCA
201	GGCAGAGAGTTTTAATGATGC	28531	CAAG	GAATCGGGGTGAGATGAGAGA	28829	AGGG
204	GGGCTGGAACTCCGTGACAG	28532	TG	ATCACAGCCCAAATGCTGTG	28830	AG
207	CGTGGCAGAGAGTTTTAATG	28533	ATG	AATCGGGGTGAGATGAGAGA	28831	AGG
209	CTGGAACTCCGTGACAGTGT	28534	AAT	ACAGCCCAAATGCTGTGAGC	28832	CAA
210	ttacGTGGCAGAGAGTTTTAATG	28535	ATGCCAAG	ggaaTCGGGGTGAGATGAGAGAA	28833	GGGGC
211	ttacGTGGCAGAGAGTTTTAATG	28536	ATGCCAAG	ggaaTCGGGGTGAGATGAGAGAA	28834	GGGGC
215	GTGGCAGAGAGTTTTAATGAT	28537	GCCAA	GAATCGGGGTGAGATGAGAGA	28835	AGGGG
218	AACTCCGTGACAGTGTAATT	28538	TTG	CATCACAGCCCAAATGCTGT	28836	GAG
219	TGGAACTCCGTGACAGTGTA	28539	ATT	CAGCCCAAATGCTGTGAGCC	28837	AAA
220	GTGGCAGAGAGTTTTAATGA	28540	TGC	ATCGGGGTGAGATGAGAGAA	28838	GGG
223	GTGGCAGAGAGTTTTAATGAT	28541	GCCAA	GAATCGGGGTGAGATGAGAGA	28839	AGGGG
224	GGAACTCCGTGACAGTGTAAT	28542	TTTGG	TCACAGCCCAAATGCTGTGAG	28840	CCAAAT
225	GGAACTCCGTGACAGTGTAAT	28543	TTTGG	TCACAGCCCAAATGCTGTGAG	28841	CCAAAT
226	ACTCCGTGACAGTGTAATTT	28544	TG	ATCACAGCCCAAATGCTGTG	28842	AG
229	TGGCAGAGAGTTTTAATGAT	28545	GCC	TCGGGGTGAGATGAGAGAAG	28843	GGG
232	GGAACTCCGTGACAGTGTAA	28546	TTT	AGCCCAAATGCTGTGAGCCA	28844	AAT
236	AACTCCGTGACAGTGTAATT	28547	TTG	ATGCTGTGAGCCAAATTACT	28845	TTG
237	GAACTCCGTGACAGTGTAAT	28548	TTT	GCCCAAATGCTGTGAGCCAA	28846	ATT
238	GTGGCAGAGAGTTTTAATGA	28549	TG	CGGGGTGAGATGAGAGAAGG	28847	GG
242	GGCAGAGAGTTTTAATGATG	28550	CCA	CGGGGTGAGATGAGAGAAGG	28848	GGC
247	GAACTCCGTGACAGTGTAATT	28551	TTGG	TACATCACAGCCCAAATGCTG	28849	TGAG
250	CAGAGAGTTTTAATGATGCC	28552	AAG	TCGGGGTGAGATGAGAGAAG	28850	GGG
251	GCAGAGAGTTTTAATGATGC	28553	CAA	GGGGTGAGATGAGAGAAGGG	28851	GCA
252	AACTCCGTGACAGTGTAATT	28554	TTG	CCCAAATGCTGTGAGCCAAA	28852	TTA
255	GCAGAGAGTTTTAATGATGCC	28555	AAGGA	GGGGTGAGATGAGAGAAGGGG	28853	CACAA

256	GAACTCCGTGACAGTGTAATT	28556	TTGGA	TCACAGCCCAAATGCTGTGAG	28854	CCAAAT
257	GCAGAGAGTTTTAATGATGCC	28557	AAGGA	GGGGTGAGATGAGAGAAGGGG	28855	CACAA
258	GAACTCCGTGACAGTGTAATT	28558	TTGGA	TCACAGCCCAAATGCTGTGAG	28856	CCAAAT
261	ACTCCGTGACAGTGTAATTT	28559	TGG	CCAAATGCTGTGAGCCAAAT	28857	TAC
262	CAGAGAGTTTTAATGATGCC	28560	AAG	GGGTGAGATGAGAGAAGGGG	28858	CAC
264	CTCCGTGACAGTGTAATTTT	28561	GGA	CAAATGCTGTGAGCCAAATT	28859	ACT
265	AGAGAGTTTTAATGATGCCA	28562	AGG	GGTGAGATGAGAGAAGGGGC	28860	ACA
269	GAGAGTTTTAATGATGCCAA	28563	GGA	GTGAGATGAGAGAAGGGGCA	28861	CAA
270	TCCGTGACAGTGTAATTTTG	28564	GAT	AAATGCTGTGAGCCAAATTA	28862	CTT
271	actcCGTGACAGTGTAATTTTGG	28565	ATGGC	ccaaATGCTGTGAGCCAAATTAC	28863	TTTGC
272	actcCGTGACAGTGTAATTTTGG	28566	ATGGC	ccaaATGCTGTGAGCCAAATTAC	28864	TTTGC
273	CTCCGTGACAGTGTAATTTTG	28567	GATGG	TCACAGCCCAAATGCTGTGAG	28865	CCAAAT
274	AGAGTTTTAATGATGCCAAG	28568	GAG	TGAGATGAGAGAAGGGGCAC	28866	AAA
275	CCGTGACAGTGTAATTTTGG	28569	ATG	AATGCTGTGAGCCAAATTAC	28867	TTT
276	ttacGTGGCAGAGAGTTTTAATG	28570	ATGCCAAG	gtgaGATGAGAGAAGGGGCACAA	28868	ATGGCCTA
277	ttacGTGGCAGAGAGTTTTAATG	28571	ATGCCAAG	gtgaGATGAGAGAAGGGGCACAA	28869	ATGGCCTA

Capital letters indicate “core nucleotides” while lower case letters indicate “flanking nucleotides.” Herein, when an RNA sequence (e.g., a gRNA to produce a second nick) is said to comprise a particular sequence (e.g., a sequence of Table 2A, Table 2B, Table 2C, or Table 2D or a portion thereof) that comprises thymine (T), it is of course understood that the RNA sequence may (and frequently does) comprise uracil (U) in place of T. For instance, the RNA sequence may comprise U at every position shown as T in the sequence in Table 2A, Table 2B, Table 2C, or Table 2D. More specifically, the present disclosure provides an RNA sequence according to every gRNA spacer sequence shown in Table 2A, Table 2B, Table 2C, or Table 2D, wherein the RNA sequence has a U in place of each T in the sequence in Table 2A, Table 2B, Table 2C, or Table 2D.

In some embodiments, the systems and methods provided herein may comprise a template sequence listed in **Table** 4A, Table 4B, Table 4C, or Table 4D. Table 4A, Table 4B, Table 4C, or Table 4D provides exemplary template RNA sequences (column 4) and optional second-nick gRNA spacer sequences (column 5) designed to be paired with a gene modifying polypeptide to correct a mutation in the PAH gene. The templates in Table 4A, Table 4B, Table 4C, or Table 4D are meant to exemplify the total sequence of: (1) gRNA spacer (e.g., for targeting for first strand nick), (2) gRNA scaffold, (3) heterologous object sequence, and (4) PBS sequence (e.g., for initiating TPRT at first strand nick).

Table 4A. Exemplary template RNA sequences and second nick gRNA spacer sequences

Table 4A provides design of RNA components of gene modifying systems for correcting the pathogenic R408W, mutation in PAH. The gRNA spacers from Table 1A were filtered, e.g., filtered by occurrence within 15 nt of the desired editing location and use of a Tier 1 Cas enzyme. For each gRNA ID, this table details the sequence of a complete template RNA, optional second-nick gRNA, and Cas variant for use in a Cas-RT fusion gene modifying polypeptide. For exemplification, PBS sequences and post-edit homology regions (after the location of the edit) are set to 12 nt and 30 nt, respectively. Additionally, a second-nick gRNA is selected with preference for a distance near 100 nt from the first nick and a first preference for a design resulting in a PAM-in system, as described elsewhere in this application.

ID	Cas species	strand	Template RNA	SEQ ID NO	second-nick gRNA	SEQ ID NO
1	SpyCas9-SpRY	-	TTGCTGCCACAATACCTTGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCgtatgggtcgtagcgaactgagaagggcCGAGGTATTGtggc	29019	CTCGTAAGGTGTAAATTACTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGC	29209
2	SpyCas9-NG	+	AGCGAACTGAGAAGGGCCAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCtcttaggaactttgctgccacaataccTCGGCCCTTCTcagt	29020	TTCCTAAAAAAGAAGTAAAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGC	29210
6	SpyCas9-SpRY	+	AGCGAACTGAGAAGGGCCAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCtcttaggaactttgctgccacaataccTCGGCCCTTCTcagt	29021	CCTAAAAAAGAAGTAAAATGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGC	29211
7	SpyCas9-SpRY	-	TTTGCTGCCACAATACCTTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCtatgggtcgtagcgaactgagaagggcCGAGGTATTGTggca	29022	TCGTAAGGTGTAAATTACTTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGC	29212
10	PpnCas9	+	gtcGTAGCGAACTGAGAAGGGCCAGTTGTAGCTCCCTTTTTCATTTCGCGAAAGCGAAATGAAAAACGTTGTTACAATAAGAGATGAATTTCTCGCAAAGCTCTGCCTCTTGAAATTTCGGTTTCAAGAGGCATCcttaggaactttgctgccacaataccTCGGCCCTTCTCagtt	29023	gaaGACCCTGCTCTAGGGAGGTGTGTTGTAGCTCCCTTTTTCATTTCGCGAAAGCGAAATGAAAAACGTTGTTACAATAAGAGATGAATTTCTCGCAAAGCTCTGCCTCTTGAAATTTCGGTTTCAAGAGGCATC	29213
13	ScaCas9-Sc++	+	TAGCGAACTGAGAAGGGCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAA	29024	AAAAAAGAAGTAAAATGCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCT	29214

			GTGGCACCGAGTCGGTGCcttaggaactttgctgccacaataccTCGGCCCTTCTCagtt		AGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGC	
14	SpyCas9	+	TAGCGAACTGAGAAGGGCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCcttaggaactttgctgccacaataccTCGGCCCTTCTCagtt	29025	TTGAAGACCCTGCTCTAGGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGC	29215
17	SpyCas9-SpRY	+	TAGCGAACTGAGAAGGGCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCcttaggaactttgctgccacaataccTCGGCCCTTCTCagtt	29026	CTAAAAAAGAAGTAAAATGCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGC	29216
18	SpyCas9-NG	-	CTTTGCTGCCACAATACCTTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCatgggtcgtagcgaactgagaagggcCGAGGTATTGTGgcag	29027	GTAAGGTGTAAATTACTTACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGC	29217
21	SpyCas9-NG	+	TAGCGAACTGAGAAGGGCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCcttaggaactttgctgccacaataccTCGGCCCTTCTCagtt	29028	AAAAAGAAGTAAAATGCCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGC	29218
25	SpyCas9-SpRY	-	CTTTGCTGCCACAATACCTTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCatgggtcgtagcgaactgagaagggcCGAGGTATTGTGgcag	29029	CGTAAGGTGTAAATTACTTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGC	29219
26	BlatCas9	-	gaacTTTGCTGCCACAATACCTTGCTATAGTTCCTTACTGAAAGGTAAGTTGCTATAGTAAGGGCAACAGACCCGAGGCGTTGGGGATCGCCTAGCCCGTGTTTACGGGCTCTCCCCATATTCAAAATAATGACAGACGAGCACCTTGGAGCATTTATCTCCGAGGTGCTatgggtcgtagcgaactgagaagggcCGAGGTATTGTGgcag	29030	gtggCCTCGTAAGGTGTAAATTAGCTATAGTTCCTTACTGAAAGGTAAGTTGCTATAGTAAGGGCAACAGACCCGAGGCGTTGGGGATCGCCTAGCCCGTGTTTACGGGCTCTCCCCATATTCAAAATAATGACAGACGAGCACCTTGGAGCATTTATCTCCGAGGTGCT	29220
29	Nme2Cas9	-	agGAACTTTGCTGCCACAATACCTGTTGTAGCTCCCTTTCTCATTTCGGAAACGAAATGAGAACCGTTGCTACAATAAGGCCGTCTGAAAAGATGTGCCGCAACGCTCTGCCCCTTAAAGCTTCTGCTTTAAGGGGCATCGTTTAtgggtcgtagcgaactgagaaggcCGAGGTATTGTGGcagc	29031	gtAAATTACTTACTGTTAATGGAAGTTGTAGCTCCCTTTCTCATTTCGGAAACGAAATGAGAACCGTTGCTACAATAAGGCCGTCTGAAAAGATGTGCCGCAACGCTCTGCCCCTTAAAGCTTCTGCTTTAAGGGGCATCGTTTA	29221
30	SauriCas9	+	CGTAGCGAACTGAGAAGGGCCGTTTTAGTACTCTGGAAACAGAATCTACTAAAACAAGGCAAAATGCCGTGTTTATCTCGTCAACTTGTTGGCGAGAttaggaactttgctgccacaataccTCGGCCCTTCTCAgttc	29032	CTTAAGACTACCTTTCTCCAAGTTTTAGTACTCTGGAAACAGAATCTACTAAAACAAGGCAAAATGCCGTGTTTATCTCGTCAACTTGTTGGCGAGA	29222

31	SauriCas9-KKH	+	CGTAGCGAACTGAGAAGGGCCGTTTTAGTACTCTGGAAACAGAATCTACTAAAACAAGGCAAAATGCCGTGTTTATCTCGTCAACTTGTTGGCGAGAttaggaactttgctgccacaataccTCGGCCCTTCTCAgttc	29033	AAAAAAGAAGTAAAATGCCACGTTTTAGTACTCTGGAAACAGAATCTACTAAAACAAGGCAAAATGCCGTGTTTATCTCGTCAACTTGTTGGCGAGA	29223
34	ScaCas9-Sc++	-	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCtgggtcgtagcgaactgagaagggcCGAGGTATTGTGGcagc	29034	CGTAAGGTGTAAATTACTTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGC	29224
35	SpyCas9	-	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCtgggtcgtagcgaactgagaagggcCGAGGTATTGTGGcagc	29035	TGTAAATTACTTACTGTTAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGC	29225
38	SpyCas9-SpRY	-	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCtgggtcgtagcgaactgagaagggcCGAGGTATTGTGGcagc	29036	GTAAGGTGTAAATTACTTACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGC	29226
41	ScaCas9-Sc++	+	GTAGCGAACTGAGAAGGGCCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCttaggaactttgctgccacaataccTCGGCCCTTCTCAgttc	29037	AAAAAAGAAGTAAAATGCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGC	29227
42	SpyCas9-SpRY	+	GTAGCGAACTGAGAAGGGCCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCttaggaactttgctgccacaataccTCGGCCCTTCTCAgttc	29038	TAAAAAAGAAGTAAAATGCCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGC	29228
43	SpyCas9-NG	-	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCtgggtcgtagcgaactgagaagggcCGAGGTATTGTGGcagc	29039	GTAAGGTGTAAATTACTTACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGC	29229
46	BlatCas9	-	ggaaCTTTGCTGCCACAATACCTGCTATAGTTCCTTACTGAAAGGTAAGTTGCTATAGTAAGGGCAACAGACCCGAGGCGTTGGGGATCGCCTAGCCCGTGTTTACGGGCTCTCCCCATATTCAAAATAATGACAGACGAGCACCTTGGAGCATTTATCTCCGAGGTGCTtgggtcgtagcgaactgagaagggcCGAGGTATTGTGGcagc	29040	gtggCCTCGTAAGGTGTAAATTAGCTATAGTTCCTTACTGAAAGGTAAGTTGCTATAGTAAGGGCAACAGACCCGAGGCGTTGGGGATCGCCTAGCCCGTGTTTACGGGCTCTCCCCATATTCAAAATAATGACAGACGAGCACCTTGGAGCATTTATCTCCGAGGTGCT	29230
47	BlatCas9	-	ggaaCTTTGCTGCCACAATACCTGCTATAGTTCCTTACTGAAAGGTAAGTTGCTATAGTAAGGGCAACAGACCCGAGGCGTTGGGGATCGCCTAGCCCGTGTTTACGGGCTCTCCCCATATTCAAAATAATGACAGACGAGCACCTTGGAGCATTTATC	29041	gtggCCTCGTAAGGTGTAAATTAGCTATAGTTCCTTACTGAAAGGTAAGTTGCTATAGTAAGGGCAACAGACCCGAGGCGTTGGGGATCGCCTAGCCCGTGTTTACGGGCTCTCCCC	29231

			TCCGAGGTGCTtgggtcgtagcgaactgagaagggcCGAGGTATTGTGGcagc		ATATTCAAAATAATGACAGACGAGCACCTTGGAGCATTTATCTCCGAGGTGCT	
50	Nme2Cas9	-	taGGAACTTTGCTGCCACAATACCGTTGTAGCTCCCTTTCTCATTTCGGAAACGAAATGAGAACCGTTGCTACAATAAGGCCGTCTGAAAAGATGTGCCGCAACGCTCTGCCCCTTAAAGCTTCTGCTTTAAGGGGCATCGTTTAgggtcgtagcgaactgagaaggcCGAGGTATTGTGGCagca	29042	gtAAATTACTTACTGTTAATGGAAGTTGTAGCTCCCTTTCTCATTTCGGAAACGAAATGAGAACCGTTGCTACAATAAGGCCGTCTGAAAAGATGTGCCGCAACGCTCTGCCCCTTAAAGCTTCTGCTTTAAGGGGCATCGTTTA	29232
51	SauCas9KKH	+	TCGTAGCGAACTGAGAAGGGCGTTTTAGTACTCTGGAAACAGAATCTACTAAAACAAGGCAAAATGCCGTGTTTATCTCGTCAACTTGTTGGCGAGAtaggaactttgctgccacaataccTCGGCCCTTCTCAGttcg	29043	TAAAAAAGAAGTAAAATGCCAGTTTTAGTACTCTGGAAACAGAATCTACTAAAACAAGGCAAAATGCCGTGTTTATCTCGTCAACTTGTTGGCGAGA	29233
52	SauCas9KKH	+	TCGTAGCGAACTGAGAAGGGCGTTTTAGTACTCTGGAAACAGAATCTACTAAAACAAGGCAAAATGCCGTGTTTATCTCGTCAACTTGTTGGCGAGAtaggaactttgctgccacaataccTCGGCCCTTCTCAGttcg	29044	TAAAAAAGAAGTAAAATGCCAGTTTTAGTACTCTGGAAACAGAATCTACTAAAACAAGGCAAAATGCCGTGTTTATCTCGTCAACTTGTTGGCGAGA	29234
55	SauriCas9	-	GAACTTTGCTGCCACAATACCGTTTTAGTACTCTGGAAACAGAATCTACTAAAACAAGGCAAAATGCCGTGTTTATCTCGTCAACTTGTTGGCGAGAgggtcgtagcgaactgagaagggcCGAGGTATTGTGGCagca	29045	GGTGTAAATTACTTACTGTTAGTTTTAGTACTCTGGAAACAGAATCTACTAAAACAAGGCAAAATGCCGTGTTTATCTCGTCAACTTGTTGGCGAGA	29235
56	SauriCas9-KKH	-	GAACTTTGCTGCCACAATACCGTTTTAGTACTCTGGAAACAGAATCTACTAAAACAAGGCAAAATGCCGTGTTTATCTCGTCAACTTGTTGGCGAGAgggtcgtagcgaactgagaagggcCGAGGTATTGTGGCagca	29046	GGTGTAAATTACTTACTGTTAGTTTTAGTACTCTGGAAACAGAATCTACTAAAACAAGGCAAAATGCCGTGTTTATCTCGTCAACTTGTTGGCGAGA	29236
57	SauriCas9-KKH	+	TCGTAGCGAACTGAGAAGGGCGTTTTAGTACTCTGGAAACAGAATCTACTAAAACAAGGCAAAATGCCGTGTTTATCTCGTCAACTTGTTGGCGAGAtaggaactttgctgccacaataccTCGGCCCTTCTCAGttcg	29047	AAAAAAGAAGTAAAATGCCACGTTTTAGTACTCTGGAAACAGAATCTACTAAAACAAGGCAAAATGCCGTGTTTATCTCGTCAACTTGTTGGCGAGA	29237
62	ScaCas9-Sc++	-	AACTTTGCTGCCACAATACCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCgggtcgtagcgaactgagaagggcCGAGGTATTGTGGCagca	29048	CGTAAGGTGTAAATTACTTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGC	29238
63	SpyCas9-SpRY	-	AACTTTGCTGCCACAATACCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCgggtcgtagcgaactgagaagggcCGAGGTATTGTGGCagca	29049	TAAGGTGTAAATTACTTACTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGC	29239
64	SpyCas9-SpRY	+	CGTAGCGAACTGAGAAGGGCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCtaggaactttgctgccacaataccTCGGCCCTTCTCAGttcg	29050	AAAAAAGAAGTAAAATGCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGC	29240

65	BlatCas9	-	aggaACTTTGCTGCCACAATACCGCTATAGTTCCTTACTGAAAGGTAAGTTGCTATAGTAAGGGCAACAGACCCGAGGCGTTGGGGATCGCCTAGCCCGTGTTTACGGGCTCTCCCCATATTCAAAATAATGACAGACGAGCACCTTGGAGCATTTATCTCCGAGGTGCTgggtcgtagcgaactgagaagggcCGAGGTATTGTGGCagca	29051	gtggCCTCGTAAGGTGTAAATTAGCTATAGTTCCTTACTGAAAGGTAAGTTGCTATAGTAAGGGCAACAGACCCGAGGCGTTGGGGATCGCCTAGCCCGTGTTTACGGGCTCTCCCCATATTCAAAATAATGACAGACGAGCACCTTGGAGCATTTATCTCCGAGGTGCT	29241
66	SauCas9KKH	+	GTCGTAGCGAACTGAGAAGGGGTTTTAGTACTCTGGAAACAGAATCTACTAAAACAAGGCAAAATGCCGTGTTTATCTCGTCAACTTGTTGGCGAGAaggaactttgctgccacaataccTCGGCCCTTCTCAGTtcgc	29052	AAAAAAGAAGTAAAATGCCACGTTTTAGTACTCTGGAAACAGAATCTACTAAAACAAGGCAAAATGCCGTGTTTATCTCGTCAACTTGTTGGCGAGA	29242
67	SauCas9KKH	-	GGAACTTTGCTGCCACAATACGTTTTAGTACTCTGGAAACAGAATCTACTAAAACAAGGCAAAATGCCGTGTTTATCTCGTCAACTTGTTGGCGAGAggtcgtagcgaactgagaagggcCGAGGTATTGTGGCAgcaa	29053	GTAAGGTGTAAATTACTTACTGTTTTAGTACTCTGGAAACAGAATCTACTAAAACAAGGCAAAATGCCGTGTTTATCTCGTCAACTTGTTGGCGAGA	29243
68	SpyCas9-SpRY	+	TCGTAGCGAACTGAGAAGGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCaggaactttgctgccacaataccTCGGCCCTTCTCAGTtcgc	29054	AAAAAGAAGTAAAATGCCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGC	29244
69	SpyCas9-SpRY	-	GAACTTTGCTGCCACAATACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCggtcgtagcgaactgagaagggcCGAGGTATTGTGGCAgcaa	29055	AAGGTGTAAATTACTTACTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGC	29245
72	SauCas9KKH	+	GGTCGTAGCGAACTGAGAAGGGTTTTAGTACTCTGGAAACAGAATCTACTAAAACAAGGCAAAATGCCGTGTTTATCTCGTCAACTTGTTGGCGAGAggaactttgctgccacaataccTCGGCCCTTCTCAGTTcgct	29056	AAAAAGAAGTAAAATGCCACTGTTTTAGTACTCTGGAAACAGAATCTACTAAAACAAGGCAAAATGCCGTGTTTATCTCGTCAACTTGTTGGCGAGA	29246
73	SpyCas9-SpRY	+	GTCGTAGCGAACTGAGAAGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCggaactttgctgccacaataccTCGGCCCTTCTCAGTTcgct	29057	AAAAGAAGTAAAATGCCACTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGC	29247
74	SpyCas9-SpRY	-	GGAACTTTGCTGCCACAATAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCgtcgtagcgaactgagaagggcCGAGGTATTGTGGCAGcaaa	29058	AGGTGTAAATTACTTACTGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGC	29248
77	SpyCas9-NG	+	GGTCGTAGCGAACTGAGAAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCgaactttgctgccacaataccTCGGCCCTTCTCAGTTCgcta	29059	AAAGAAGTAAAATGCCACTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGC	29249

81	SpyCas9-SpRY	+	GGTCGTAGCGAACTGAGAAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCgaactttgctgccacaataccTCGGCCCTTCTCAGTTCgcta	29060	AAAGAAGTAAAATGCCACTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGC	29250
82	SpyCas9-SpRY	-	AGGAACTTTGCTGCCACAATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCtcgtagcgaactgagaagggcCGAGGTATTGTGGCAGCaaag	29061	GGTGTAAATTACTTACTGTTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGC	29251
86	ScaCas9-Sc++	+	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCaactttgctgccacaataccTCGGCCCTTCTCAGTTCGctac	29062	AAAAGAAGTAAAATGCCACTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGC	29252
87	SpyCas9	+	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCaactttgctgccacaataccTCGGCCCTTCTCAGTTCGctac	29063	TAAGACTACCTTTCTCCAAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGC	29253
90	SpyCas9-SpRY	+	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCaactttgctgccacaataccTCGGCCCTTCTCAGTTCGctac	29064	AAGAAGTAAAATGCCACTGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGC	29254
91	SpyCas9-NG	+	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCaactttgctgccacaataccTCGGCCCTTCTCAGTTCGctac	29065	AAAGAAGTAAAATGCCACTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGC	29255
94	SpyCas9-SpRY	-	TAGGAACTTTGCTGCCACAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCcgtagcgaactgagaagggcCGAGGTATTGTGGCAGCAaagt	29066	GTGTAAATTACTTACTGTTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGC	29256
95	BlatCas9	+	tatgGGTCGTAGCGAACTGAGAAGCTATAGTTCCTTACTGAAAGGTAAGTTGCTATAGTAAGGGCAACAGACCCGAGGCGTTGGGGATCGCCTAGCCCGTGTTTACGGGCTCTCCCCATATTCAAAATAATGACAGACGAGCACCTTGGAGCATTTATCTCCGAGGTGCTaactttgctgccacaataccTCGGCCCTTCTCAGTTCGctac	29067	aaaaAAGAAGTAAAATGCCACTGGCTATAGTTCCTTACTGAAAGGTAAGTTGCTATAGTAAGGGCAACAGACCCGAGGCGTTGGGGATCGCCTAGCCCGTGTTTACGGGCTCTCCCCATATTCAAAATAATGACAGACGAGCACCTTGGAGCATTTATCTCCGAGGTGCT	29257
96	BlatCas9	+	tatgGGTCGTAGCGAACTGAGAAGCTATAGTTCCTTACTGAAAGGTAAGTTGCTATAGTAAGGGCAACAGACCCGAGGCGTTGGGGATCGCCTAGCCCGTGTTTACGGGCTCTCCCCATATTCAAAATAATGACAGACGAGCACCTTGGAGCATTTATC	29068	aaaaAAGAAGTAAAATGCCACTGGCTATAGTTCCTTACTGAAAGGTAAGTTGCTATAGTAAGGGCAACAGACCCGAGGCGTTGGGGATCGCCTAGCCCGTGTTTACGGGCTCTCCCC	29258

			TCCGAGGTGCTaactttgctgccacaataccTCGGCCCTTCTCAGTTCGctac		ATATTCAAAATAATGACAGACGAGCACCTTGGAGCATTTATCTCCGAGGTGCT	
99	Nme2Cas9	+	tgTATGGGTCGTAGCGAACTGAGAGTTGTAGCTCCCTTTCTCATTTCGGAAACGAAATGAGAACCGTTGCTACAATAAGGCCGTCTGAAAAGATGTGCCGCAACGCTCTGCCCCTTAAAGCTTCTGCTTTAAGGGGCATCGTTTAactttgctgccacaataccTCGGCCCTTCTCAGTTCGCtacg	29069	tcCGTGTTCCTAAAAAAGAAGTAAGTTGTAGCTCCCTTTCTCATTTCGGAAACGAAATGAGAACCGTTGCTACAATAAGGCCGTCTGAAAAGATGTGCCGCAACGCTCTGCCCCTTAAAGCTTCTGCTTTAAGGGGCATCGTTTA	29259
100	SauriCas9	+	ATGGGTCGTAGCGAACTGAGAGTTTTAGTACTCTGGAAACAGAATCTACTAAAACAAGGCAAAATGCCGTGTTTATCTCGTCAACTTGTTGGCGAGAactttgctgccacaataccTCGGCCCTTCTCAGTTCGCtacg	29070	CTTAAGACTACCTTTCTCCAAGTTTTAGTACTCTGGAAACAGAATCTACTAAAACAAGGCAAAATGCCGTGTTTATCTCGTCAACTTGTTGGCGAGA	29260
101	SauriCas9-KKH	+	ATGGGTCGTAGCGAACTGAGAGTTTTAGTACTCTGGAAACAGAATCTACTAAAACAAGGCAAAATGCCGTGTTTATCTCGTCAACTTGTTGGCGAGAactttgctgccacaataccTCGGCCCTTCTCAGTTCGCtacg	29071	AAAAAAGAAGTAAAATGCCACGTTTTAGTACTCTGGAAACAGAATCTACTAAAACAAGGCAAAATGCCGTGTTTATCTCGTCAACTTGTTGGCGAGA	29261
104	ScaCas9-Sc++	+	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCactttgctgccacaataccTCGGCCCTTCTCAGTTCGCtacg	29072	AAAAGAAGTAAAATGCCACTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGC	29262
105	SpyCas9	+	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCactttgctgccacaataccTCGGCCCTTCTCAGTTCGCtacg	29073	TAAGACTACCTTTCTCCAAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGC	29263
108	SpyCas9-SpRY	+	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCactttgctgccacaataccTCGGCCCTTCTCAGTTCGCtacg	29074	AGAAGTAAAATGCCACTGAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGC	29264
109	SpyCas9-NG	+	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCactttgctgccacaataccTCGGCCCTTCTCAGTTCGCtacg	29075	AAAGAAGTAAAATGCCACTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGC	29265
112	SpyCas9-SpRY	-	TTAGGAACTTTGCTGCCACAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCgtagcgaactgagaagggcCGAGGTATTGTGGCAGCAAagtt	29076	TGTAAATTACTTACTGTTAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGC	29266
113	BlatCas9	+	gtatGGGTCGTAGCGAACTGAGAGCTATAGTTCCTTACTGAAAGGTAAGTTGCTATAGTAAGGGCAACAGACCCGAGGCGTTGGGGATCGCCTAGCCCGTGTTTACGGGCTCTCCCCATATTCAAAATAATGACAGACGAGCACCTTGGAGCATTTATC	29077	aaaaGAAGTAAAATGCCACTGAGGCTATAGTTCCTTACTGAAAGGTAAGTTGCTATAGTAAGGGCAACAGACCCGAGGCGTTGGGGATCGCCTAGCCCGTGTTTACGGGCTCTCCCC	29267

			TCCGAGGTGCTactttgctgccacaataccTCGGCCCTTCTCAGTTCG Ctacg		ATATTCAAAATAATGACAGACGAGCACCT TGGAGCATTTATCTCCGAGGTGCT	
114	BlatCas9	+	gtatGGGTCGTAGCGAACTGAGAGCTATAGTTCCTTACTGA AAGGTAAGTTGCTATAGTAAGGGCAACAGACCCGAGGCG TTGGGGATCGCCTAGCCCGTGTTTACGGGCTCTCCCCATA TTCAAAATAATGACAGACGAGCACCTTGGAGCATTTATC TCCGAGGTGCTactttgctgccacaataccTCGGCCCTTCTCAGTTCG Ctacg	29078	aaaaGAAGTAAAATGCCACTGAGGCTATAG TTCCTTACTGAAAGGTAAGTTGCTATAGT AAGGGCAACAGACCCGAGGCGTTGGGGA TCGCCTAGCCCGTGTTTACGGGCTCTCCCC ATATTCAAAATAATGACAGACGAGCACCT TGGAGCATTTATCTCCGAGGTGCT	29268
115	BlatCas9	-	gtctTAGGAACTTTGCTGCCACAGCTATAGTTCCTTACTGAA AGGTAAGTTGCTATAGTAAGGGCAACAGACCCGAGGCGT TGGGGATCGCCTAGCCCGTGTTTACGGGCTCTCCCCATAT TCAAAATAATGACAGACGAGCACCTTGGAGCATTTATCT CCGAGGTGCTgtagcgaactgagaagggcCGAGGTATTGTGGCAGC AAagtt	29079	gtgtAAATTACTTACTGTTAATGGCTATAGT TCCTTACTGAAAGGTAAGTTGCTATAGTA AGGGCAACAGACCCGAGGCGTTGGGGAT CGCCTAGCCCGTGTTTACGGGCTCTCCCC ATATTCAAAATAATGACAGACGAGCACCT TGGAGCATTTATCTCCGAGGTGCT	29269
116	BlatCas9	+	gtatGGGTCGTAGCGAACTGAGAGCTATAGTTCCTTACTGA AAGGTAAGTTGCTATAGTAAGGGCAACAGACCCGAGGCG TTGGGGATCGCCTAGCCCGTGTTTACGGGCTCTCCCCATA TTCAAAATAATGACAGACGAGCACCTTGGAGCATTTATC TCCGAGGTGCTactttgctgccacaataccTCGGCCCTTCTCAGTTCG Ctacg	29080	aaaaGAAGTAAAATGCCACTGAGGCTATAG TTCCTTACTGAAAGGTAAGTTGCTATAGT AAGGGCAACAGACCCGAGGCGTTGGGGA TCGCCTAGCCCGTGTTTACGGGCTCTCCCC ATATTCAAAATAATGACAGACGAGCACCT TGGAGCATTTATCTCCGAGGTGCT	29270
117	BlatCas9	-	gtctTAGGAACTTTGCTGCCACAGCTATAGTTCCTTACTGAA AGGTAAGTTGCTATAGTAAGGGCAACAGACCCGAGGCGT TGGGGATCGCCTAGCCCGTGTTTACGGGCTCTCCCCATAT TCAAAATAATGACAGACGAGCACCTTGGAGCATTTATCT CCGAGGTGCTgtagcgaactgagaagggcCGAGGTATTGTGGCAGC AAagtt	29081	gtgtAAATTACTTACTGTTAATGGCTATAGT TCCTTACTGAAAGGTAAGTTGCTATAGTA AGGGCAACAGACCCGAGGCGTTGGGGAT CGCCTAGCCCGTGTTTACGGGCTCTCCCC ATATTCAAAATAATGACAGACGAGCACCT TGGAGCATTTATCTCCGAGGTGCT	29271
119	Nme2Cas9	-	tgGTCTTAGGAACTTTGCTGCCACGTTGTAGCTCCCTTTCT CATTTCGGAAACGAAATGAGAACCGTTGCTACAATAAGG CCGTCTGAAAAGATGTGCCGCAACGCTCTGCCCCTTAAA GCTTCTGCTTTAAGGGGCATCGTTTAtagcgaactgagaagggcCG AGGTATTGTGGCAGCAAAgttc	29082	gtAAATTACTTACTGTTAATGGAAGTTGTA GCTCCCTTTCTCATTTCGGAAACGAAATG AGAACCGTTGCTACAATAAGGCCGTCTGA AAAGATGTGCCGCAACGCTCTGCCCCTTA AAGCTTCTGCTTTAAGGGGCATCGTTTA	29272
120	SauCas9	+	tgTATGGGTCGTAGCGAACTGAGGTTTTAGTACTCTGGAA ACAGAATCTACTAAAACAAGGCAAAATGCCGTGTTTATC TCGTCAACTTGTTGGCGAGActttgctgccacaataccTCGGCCCTT CTCAGTTCGCTacga	29083	taAAAAAGAAGTAAAATGCCACTGTTTTAG TACTCTGGAAACAGAATCTACTAAAACAA GGCAAAATGCCGTGTTTATCTCGTCAACT TGTTGGCGAGA	29273
121	SauCas9KKH	+	TATGGGTCGTAGCGAACTGAGGTTTTAGTACTCTGGAAA CAGAATCTACTAAAACAAGGCAAAATGCCGTGTTTATCT CGTCAACTTGTTGGCGAGActttgctgccacaataccTCGGCCCTTC TCAGTTCGCTacga	29084	AAAAAGAAGTAAAATGCCACTGTTTTAGT ACTCTGGAAACAGAATCTACTAAAACAAG GCAAAATGCCGTGTTTATCTCGTCAACTT GTTGGCGAGA	29274

122	SauriCas9	+	TATGGGTCGTAGCGAACTGAGGTTTTAGTACTCTGGAAACAGAATCTACTAAAACAAGGCAAAATGCCGTGTTTATCTCGTCAACTTGTTGGCGAGActttgctgccacaataccTCGGCCCTTCTCAGTTCGCTacga	29085	CTTAAGACTACCTTTCTCCAAGTTTTAGTACTCTGGAAACAGAATCTACTAAAACAAGGCAAAATGCCGTGTTTATCTCGTCAACTTGTTGGCGAGA	29275
123	SauriCas9-KKH	+	TATGGGTCGTAGCGAACTGAGGTTTTAGTACTCTGGAAACAGAATCTACTAAAACAAGGCAAAATGCCGTGTTTATCTCGTCAACTTGTTGGCGAGActttgctgccacaataccTCGGCCCTTCTCAGTTCGCTacga	29086	AAAAAAGAAGTAAAATGCCACGTTTTAGTACTCTGGAAACAGAATCTACTAAAACAAGGCAAAATGCCGTGTTTATCTCGTCAACTTGTTGGCGAGA	29276
126	ScaCas9-Sc++	+	ATGGGTCGTAGCGAACTGAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCctttgctgccacaataccTCGGCCCTTCTCAGTTCGCTacga	29087	AAAAGAAGTAAAATGCCACTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGC	29277
127	SpyCas9-SpRY	+	ATGGGTCGTAGCGAACTGAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCctttgctgccacaataccTCGGCCCTTCTCAGTTCGCTacga	29088	GAAGTAAAATGCCACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGC	29278
128	SpyCas9-SpRY	-	CTTAGGAACTTTGCTGCCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCtagcgaactgagaagggcCGAGGTATTGTGGCAGCAAAgttc	29089	GTAAATTACTTACTGTTAATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGC	29279
129	BlatCas9	-	ggtcTTAGGAACTTTGCTGCCACGCTATAGTTCCTTACTGAAAGGTAAGTTGCTATAGTAAGGGCAACAGACCCGAGGCGTTGGGGATCGCCTAGCCCGTGTTTACGGGCTCTCCCCATATTCAAAATAATGACAGACGAGCACCTTGGAGCATTTATCTCCGAGGTGCTtagcgaactgagaagggcCGAGGTATTGTGGCAGCAAAgttc	29090	gtgtAAATTACTTACTGTTAATGGCTATAGTTCCTTACTGAAAGGTAAGTTGCTATAGTAAGGGCAACAGACCCGAGGCGTTGGGGATCGCCTAGCCCGTGTTTACGGGCTCTCCCCATATTCAAAATAATGACAGACGAGCACCTTGGAGCATTTATCTCCGAGGTGCT	29280
130	BlatCas9	-	ggtcTTAGGAACTTTGCTGCCACGCTATAGTTCCTTACTGAAAGGTAAGTTGCTATAGTAAGGGCAACAGACCCGAGGCGTTGGGGATCGCCTAGCCCGTGTTTACGGGCTCTCCCCATATTCAAAATAATGACAGACGAGCACCTTGGAGCATTTATCTCCGAGGTGCTtagcgaactgagaagggcCGAGGTATTGTGGCAGCAAAgttc	29091	gtgtAAATTACTTACTGTTAATGGCTATAGTTCCTTACTGAAAGGTAAGTTGCTATAGTAAGGGCAACAGACCCGAGGCGTTGGGGATCGCCTAGCCCGTGTTTACGGGCTCTCCCCATATTCAAAATAATGACAGACGAGCACCTTGGAGCATTTATCTCCGAGGTGCT	29281
134	SauCas9KKH	+	GTATGGGTCGTAGCGAACTGAGTTTTAGTACTCTGGAAACAGAATCTACTAAAACAAGGCAAAATGCCGTGTTTATCTCGTCAACTTGTTGGCGAGAtttgctgccacaataccTCGGCCCTTCTCAGTTCGCTAcgac	29092	TAAAATGCCACTGAGAACTCTGTTTTAGTACTCTGGAAACAGAATCTACTAAAACAAGGCAAAATGCCGTGTTTATCTCGTCAACTTGTTGGCGAGA	29282
135	SauriCas9-KKH	+	GTATGGGTCGTAGCGAACTGAGTTTTAGTACTCTGGAAACAGAATCTACTAAAACAAGGCAAAATGCCGTGTTTATCT	29093	AAATGCCACTGAGAACTCTCTGTTTTAGTACTCTGGAAACAGAATCTACTAAAACAAG	29283

			CGTCAACTTGTTGGCGAGAtttgctgccacaataccTCGGCCCTTCTCAGTTCGCTAcgac		GCAAAATGCCGTGTTTATCTCGTCAACTTGTTGGCGAGA	
138	SpyCas9-SpRY	+	TATGGGTCGTAGCGAACTGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCtttgctgccacaataccTCGGCCCTTCTCAGTTCGCTAcgac	29094	AAGTAAAATGCCACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGC	29284
140	SpyCas9-SpRY	-	TCTTAGGAACTTTGCTGCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCagcgaactgagaagggcCGAGGTATTGTGGCAGCAAAGttcc	29095	TAAATTACTTACTGTTAATGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGC	29285
146	SauCas9KKH	+	TGTATGGGTCGTAGCGAACTGGTTTTAGTACTCTGGAAACAGAATCTACTAAAACAAGGCAAAATGCCGTGTTTATCTCGTCAACTTGTTGGCGAGAttgctgccacaataccTCGGCCCTTCTCAGTTCGCTACgacc	29096	TAAAATGCCACTGAGAACTCTGTTTTAGTACTCTGGAAACAGAATCTACTAAAACAAGGCAAAATGCCGTGTTTATCTCGTCAACTTGTTGGCGAGA	29286
147	SpyCas9-NG	+	GTATGGGTCGTAGCGAACTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCttgctgccacaataccTCGGCCCTTCTCAGTTCGCTACgacc	29097	AAAGAAGTAAAATGCCACTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGC	29287
151	SpyCas9-SpRY	+	GTATGGGTCGTAGCGAACTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCttgctgccacaataccTCGGCCCTTCTCAGTTCGCTACgacc	29098	AGTAAAATGCCACTGAGAACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGC	29288
152	SpyCas9-SpRY	-	GTCTTAGGAACTTTGCTGCCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCgcgaactgagaagggcCGAGGTATTGTGGCAGCAAAGTtcct	29099	AAATTACTTACTGTTAATGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGC	29289
158	SauCas9	+	ggGTGTATGGGTCGTAGCGAACTGTTTTAGTACTCTGGAAACAGAATCTACTAAAACAAGGCAAAATGCCGTGTTTATCTCGTCAACTTGTTGGCGAGAtgctgccacaataccTCGGCCCTTCTCAGTTCGCTACGaccc	29100	taAAAAAGAAGTAAAATGCCACTGTTTTAGTACTCTGGAAACAGAATCTACTAAAACAAGGCAAAATGCCGTGTTTATCTCGTCAACTTGTTGGCGAGA	29290
159	SauCas9KKH	+	GTGTATGGGTCGTAGCGAACTGTTTTAGTACTCTGGAAACAGAATCTACTAAAACAAGGCAAAATGCCGTGTTTATCTCGTCAACTTGTTGGCGAGAtgctgccacaataccTCGGCCCTTCTCAGTTCGCTACGaccc	29101	TAAAATGCCACTGAGAACTCTGTTTTAGTACTCTGGAAACAGAATCTACTAAAACAAGGCAAAATGCCGTGTTTATCTCGTCAACTTGTTGGCGAGA	29291
160	SauCas9KKH	-	TGGTCTTAGGAACTTTGCTGCGTTTTAGTACTCTGGAAACAGAATCTACTAAAACAAGGCAAAATGCCGTGTTTATCTCGTCAACTTGTTGGCGAGAcgaactgagaagggcCGAGGTATTGTGGCAGCAAAGTTccta	29102	AAATTACTTACTGTTAATGGAGTTTTAGTACTCTGGAAACAGAATCTACTAAAACAAGGCAAAATGCCGTGTTTATCTCGTCAACTTGTTGGCGAGA	29292

161	SauCas9KKH	-	TGGTCTTAGGAACTTTGCTGCGTTTTAGTACTCTGGAAACAGAATCTACTAAAACAAGGCAAAATGCCGTGTTTATCTCGTCAACTTGTTGGCGAGAcgaactgagaagggcCGAGGTATTGTGGCAGCAAAGTTccta	29103	AAATTACTTACTGTTAATGGAGTTTTAGTACTCTGGAAACAGAATCTACTAAAACAAGGCAAAATGCCGTGTTTATCTCGTCAACTTGTTGGCGAGA	29293
166	ScaCas9-Sc++	+	TGTATGGGTCGTAGCGAACTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCtgctgccacaataccTCGGCCCTTCTCAGTTCGCTACGaccc	29104	ATGCCACTGAGAACTCTCTTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGC	29294
167	SpyCas9-SpRY	+	TGTATGGGTCGTAGCGAACTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCtgctgccacaataccTCGGCCCTTCTCAGTTCGCTACGaccc	29105	GTAAAATGCCACTGAGAACTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGC	29295
168	SpyCas9-SpRY	-	GGTCTTAGGAACTTTGCTGCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCcgaactgagaagggcCGAGGTATTGTGGCAGCAAAGTTccta	29106	AATTACTTACTGTTAATGGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGC	29296
174	SauCas9KKH	+	GGTGTATGGGTCGTAGCGAACGTTTTAGTACTCTGGAAACAGAATCTACTAAAACAAGGCAAAATGCCGTGTTTATCTCGTCAACTTGTTGGCGAGAgctgccacaataccTCGGCCCTTCTCAGTTCGCTACGAccca	29107	TAAAATGCCACTGAGAACTCTGTTTTAGTACTCTGGAAACAGAATCTACTAAAACAAGGCAAAATGCCGTGTTTATCTCGTCAACTTGTTGGCGAGA	29297
175	SauriCas9-KKH	+	GGTGTATGGGTCGTAGCGAACGTTTTAGTACTCTGGAAACAGAATCTACTAAAACAAGGCAAAATGCCGTGTTTATCTCGTCAACTTGTTGGCGAGAgctgccacaataccTCGGCCCTTCTCAGTTCGCTACGAccca	29108	AAATGCCACTGAGAACTCTCTGTTTTAGTACTCTGGAAACAGAATCTACTAAAACAAGGCAAAATGCCGTGTTTATCTCGTCAACTTGTTGGCGAGA	29298
177	SpyCas9-NG	+	GTGTATGGGTCGTAGCGAACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCgctgccacaataccTCGGCCCTTCTCAGTTCGCTACGAccca	29109	TGCCACTGAGAACTCTCTTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGC	29299
181	SpyCas9-SpRY	+	GTGTATGGGTCGTAGCGAACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCgctgccacaataccTCGGCCCTTCTCAGTTCGCTACGAccca	29110	TAAAATGCCACTGAGAACTCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGC	29300
182	SpyCas9-SpRY	-	TGGTCTTAGGAACTTTGCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCgaactgagaagggcCGAGGTATTGTGGCAGCAAAGTTCctaa	29111	ATTACTTACTGTTAATGGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGC	29301
187	SauCas9	+	ttGGGTGTATGGGTCGTAGCGAAGTTTTAGTACTCTGGAAACAGAATCTACTAAAACAAGGCAAAATGCCGTGTTTATCT	29112	taAAAAAGAAGTAAAATGCCACTGTTTTAGTACTCTGGAAACAGAATCTACTAAAACAA	29302

			CGTCAACTTGTTGGCGAGActgccacaataccTCGGCCCTTCTCAGTTCGCTACGACCcat		GGCAAAATGCCGTGTTTATCTCGTCAACTTGTTGGCGAGA	
188	SauCas9KKH	+	GGGTGTATGGGTCGTAGCGAAGTTTTAGTACTCTGGAAACAGAATCTACTAAAACAAGGCAAAATGCCGTGTTTATCTCGTCAACTTGTTGGCGAGActgccacaataccTCGGCCCTTCTCAGTTCGCTACGACCcat	29113	TAAAATGCCACTGAGAACTCTGTTTTAGTACTCTGGAAACAGAATCTACTAAAACAAGGCAAAATGCCGTGTTTATCTCGTCAACTTGTTGGCGAGA	29303
191	ScaCas9-Sc++	+	GGTGTATGGGTCGTAGCGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCctgccacaataccTCGGCCCTTCTCAGTTCGCTACGACCcat	29114	ATGCCACTGAGAACTCTCTTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGC	29304
192	SpyCas9-SpRY	+	GGTGTATGGGTCGTAGCGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCctgccacaataccTCGGCCCTTCTCAGTTCGCTACGACCcat	29115	AAAATGCCACTGAGAACTCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGC	29305
193	SpyCas9-SpRY	-	TTGGTCTTAGGAACTTTGCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCaactgagaagggcCGAGGTATTGTGGCAGCAAAGTTCCtaag	29116	TTACTTACTGTTAATGGAATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGC	29306
194	BlatCas9	-	gtttTGGTCTTAGGAACTTTGCTGCTATAGTTCCTTACTGAAAGGTAAGTTGCTATAGTAAGGGCAACAGACCCGAGGCGTTGGGGATCGCCTAGCCCGTGTTTACGGGCTCTCCCCATATTCAAAATAATGACAGACGAGCACCTTGGAGCATTTATCTCCGAGGTGCTaactgagaagggcCGAGGTATTGTGGCAGCAAAGTTCCtaag	29117	aaatTACTTACTGTTAATGGAATGCTATAGTTCCTTACTGAAAGGTAAGTTGCTATAGTAAGGGCAACAGACCCGAGGCGTTGGGGATCGCCTAGCCCGTGTTTACGGGCTCTCCCCATATTCAAAATAATGACAGACGAGCACCTTGGAGCATTTATCTCCGAGGTGCT	29307
195	BlatCas9	-	gtttTGGTCTTAGGAACTTTGCTGCTATAGTTCCTTACTGAAAGGTAAGTTGCTATAGTAAGGGCAACAGACCCGAGGCGTTGGGGATCGCCTAGCCCGTGTTTACGGGCTCTCCCCATATTCAAAATAATGACAGACGAGCACCTTGGAGCATTTATCTCCGAGGTGCTaactgagaagggcCGAGGTATTGTGGCAGCAAAGTTCCtaag	29118	aaatTACTTACTGTTAATGGAATGCTATAGTTCCTTACTGAAAGGTAAGTTGCTATAGTAAGGGCAACAGACCCGAGGCGTTGGGGATCGCCTAGCCCGTGTTTACGGGCTCTCCCCATATTCAAAATAATGACAGACGAGCACCTTGGAGCATTTATCTCCGAGGTGCT	29308
198	SauCas9KKH	+	TGGGTGTATGGGTCGTAGCGAGTTTTAGTACTCTGGAAACAGAATCTACTAAAACAAGGCAAAATGCCGTGTTTATCTCGTCAACTTGTTGGCGAGAtgccacaataccTCGGCCCTTCTCAGTTCGCTACGACCcata	29119	AAAATGCCACTGAGAACTCTCGTTTTAGTACTCTGGAAACAGAATCTACTAAAACAAGGCAAAATGCCGTGTTTATCTCGTCAACTTGTTGGCGAGA	29309
199	SpyCas9-NG	-	TTTGGTCTTAGGAACTTTGCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCactgagaagggcCGAGGTATTGTGGCAGCAAAGTTCCTaaga	29120	TACTTACTGTTAATGGAATCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGC	29310

203	SpyCas9-SpRY	-	TTTGGTCTTAGGAACTTTGCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCactgagaagggcCGAGGTATTGTGGCAGCAAAGTTCCTaaga	29121	TACTTACTGTTAATGGAATCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGC	29311
204	SpyCas9-SpRY	+	GGGTGTATGGGTCGTAGCGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCtgccacaataccTCGGCCCTTCTCAGTTCGCTACGACCcata	29122	AAATGCCACTGAGAACTCTCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGC	29312
208	ScaCas9-Sc++	-	TTTTGGTCTTAGGAACTTTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCctgagaagggcCGAGGTATTGTGGCAGCAAAGTTCCTAagac	29123	TTACTTACTGTTAATGGAATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGC	29313
209	SpyCas9-SpRY	-	TTTTGGTCTTAGGAACTTTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCctgagaagggcCGAGGTATTGTGGCAGCAAAGTTCCTAagac	29124	ACTTACTGTTAATGGAATCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGC	29314
210	SpyCas9-SpRY	+	TGGGTGTATGGGTCGTAGCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCgccacaataccTCGGCCCTTCTCAGTTCGCTACGACCCatac	29125	AATGCCACTGAGAACTCTCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGC	29315
211	BlatCas9	-	tggtTTTGGTCTTAGGAACTTTGGCTATAGTTCCTTACTGAAAGGTAAGTTGCTATAGTAAGGGCAACAGACCCGAGGCGTTGGGGATCGCCTAGCCCGTGTTTACGGGCTCTCCCCATATTCAAAATAATGACAGACGAGCACCTTGGAGCATTTATCTCCGAGGTGCTctgagaagggcCGAGGTATTGTGGCAGCAAAGTTCCTAagac	29126	aaatTACTTACTGTTAATGGAATGCTATAGTTCCTTACTGAAAGGTAAGTTGCTATAGTAAGGGCAACAGACCCGAGGCGTTGGGGATCGCCTAGCCCGTGTTTACGGGCTCTCCCCATATTCAAAATAATGACAGACGAGCACCTTGGAGCATTTATCTCCGAGGTGCT	29316
214	Nme2Cas9	-	tgTGGTTTTGGTCTTAGGAACTTTGTTGTAGCTCCCTTTCTCATTTCGGAAACGAAATGAGAACCGTTGCTACAATAAGGCCGTCTGAAAAGATGTGCCGCAACGCTCTGCCCCTTAAAGCTTCTGCTTTAAGGGGCATCGTTTAtgagaagggcCGAGGTATTGTGGCAGCAAAGTTCCTAAgacc	29127	gtAAATTACTTACTGTTAATGGAAGTTGTAGCTCCCTTTCTCATTTCGGAAACGAAATGAGAACCGTTGCTACAATAAGGCCGTCTGAAAAGATGTGCCGCAACGCTCTGCCCCTTAAAGCTTCTGCTTTAAGGGGCATCGTTTA	29317
215	SpyCas9-SpRY	+	TTGGGTGTATGGGTCGTAGCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCccacaataccTCGGCCCTTCTCAGTTCGCTACGACCCAtaca	29128	ATGCCACTGAGAACTCTCTTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGC	29318
217	SpyCas9-SpRY	-	GTTTTGGTCTTAGGAACTTTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCtgagaagggcCGAGGTATTGTGGCAGCAAAGTTCCTAAgacc	29129	CTTACTGTTAATGGAATCAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGC	29319

218	BlatCas9	-	gtggTTTTGGTCTTAGGAACTTTGCTATAGTTCCTTACTGAAAGGTAAGTTGCTATAGTAAGGGCAACAGACCCGAGGCGTTGGGGATCGCCTAGCCCGTGTTTACGGGCTCTCCCCATATTCAAAATAATGACAGACGAGCACCTTGGAGCATTTATCTCCGAGGTGCTtgagaagggcCGAGGTATTGTGGCAGCAAAGTTCCTAAgacc	29130	cttaCTGTTAATGGAATCAGCCAGCTATAGTTCCTTACTGAAAGGTAAGTTGCTATAGTAAGGGCAACAGACCCGAGGCGTTGGGGATCGCCTAGCCCGTGTTTACGGGCTCTCCCCATATTCAAAATAATGACAGACGAGCACCTTGGAGCATTTATCTCCGAGGTGCT	29320
221	SpyCas9-NG	+	TTTGGGTGTATGGGTCGTAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCcacaataccTCGGCCCTTCTCAGTTCGCTACGACCCATacac	29131	TGCCACTGAGAACTCTCTTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGC	29321
224	SpyCas9-NG	-	GGTTTTGGTCTTAGGAACTTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCgagaagggcCGAGGTATTGTGGCAGCAAAGTTCCTAAGacca	29132	TACTTACTGTTAATGGAATCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGC	29322
228	SpyCas9-SpRY	+	TTTGGGTGTATGGGTCGTAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCcacaataccTCGGCCCTTCTCAGTTCGCTACGACCCATacac	29133	TGCCACTGAGAACTCTCTTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGC	29323
230	SpyCas9-SpRY	-	GGTTTTGGTCTTAGGAACTTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCgagaagggcCGAGGTATTGTGGCAGCAAAGTTCCTAAGacca	29134	TTACTGTTAATGGAATCAGCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGC	29324
231	BlatCas9	+	tcctTTGGGTGTATGGGTCGTAGGCTATAGTTCCTTACTGAAAGGTAAGTTGCTATAGTAAGGGCAACAGACCCGAGGCGTTGGGGATCGCCTAGCCCGTGTTTACGGGCTCTCCCCATATTCAAAATAATGACAGACGAGCACCTTGGAGCATTTATCTCCGAGGTGCTcacaataccTCGGCCCTTCTCAGTTCGCTACGACCCATacac	29135	aaaaTGCCACTGAGAACTCTCTTGCTATAGTTCCTTACTGAAAGGTAAGTTGCTATAGTAAGGGCAACAGACCCGAGGCGTTGGGGATCGCCTAGCCCGTGTTTACGGGCTCTCCCCATATTCAAAATAATGACAGACGAGCACCTTGGAGCATTTATCTCCGAGGTGCT	29325
232	BlatCas9	+	tcctTTGGGTGTATGGGTCGTAGGCTATAGTTCCTTACTGAAAGGTAAGTTGCTATAGTAAGGGCAACAGACCCGAGGCGTTGGGGATCGCCTAGCCCGTGTTTACGGGCTCTCCCCATATTCAAAATAATGACAGACGAGCACCTTGGAGCATTTATCTCCGAGGTGCTcacaataccTCGGCCCTTCTCAGTTCGCTACGACCCATacac	29136	aaaaTGCCACTGAGAACTCTCTTGCTATAGTTCCTTACTGAAAGGTAAGTTGCTATAGTAAGGGCAACAGACCCGAGGCGTTGGGGATCGCCTAGCCCGTGTTTACGGGCTCTCCCCATATTCAAAATAATGACAGACGAGCACCTTGGAGCATTTATCTCCGAGGTGCT	29326
238	SauCas9	+	atCCTTTGGGTGTATGGGTCGTAGTTTTAGTACTCTGGAAACAGAATCTACTAAAACAAGGCAAAATGCCGTGTTTATCTCGTCAACTTGTTGGCGAGAacaataccTCGGCCCTTCTCAGTTCGCTACGACCCATAcacc	29137	taAAAAAGAAGTAAAATGCCACTGTTTTAGTACTCTGGAAACAGAATCTACTAAAACAAGGCAAAATGCCGTGTTTATCTCGTCAACTTGTTGGCGAGA	29327

239	SauCas9KKH	+	CCTTTGGGTGTATGGGTCGTAGTTTTAGTACTCTGGAAACAGAATCTACTAAAACAAGGCAAAATGCCGTGTTTATCTCGTCAACTTGTTGGCGAGAacaataccTCGGCCCTTCTCAGTTCGCTACGACCCATAcacc	29138	AAATGCCACTGAGAACTCTCTGTTTTAGTACTCTGGAAACAGAATCTACTAAAACAAGGCAAAATGCCGTGTTTATCTCGTCAACTTGTTGGCGAGA	29328
242	ScaCas9-Sc++	+	CTTTGGGTGTATGGGTCGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCacaataccTCGGCCCTTCTCAGTTCGCTACGACCCATAcacc	29139	ATGCCACTGAGAACTCTCTTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGC	29329
243	SpyCas9-SpRY	+	CTTTGGGTGTATGGGTCGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCacaataccTCGGCCCTTCTCAGTTCGCTACGACCCATAcacc	29140	GCCACTGAGAACTCTCTTAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGC	29330
246	ScaCas9-Sc++	-	TGGTTTTGGTCTTAGGAACTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCagaagggcCGAGGTATTGTGGCAGCAAAGTTCCTAAGAccaa	29141	TTACTTACTGTTAATGGAATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGC	29331
247	SpyCas9-SpRY	-	TGGTTTTGGTCTTAGGAACTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCagaagggcCGAGGTATTGTGGCAGCAAAGTTCCTAAGAccaa	29142	TACTGTTAATGGAATCAGCCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGC	29332
251	SauCas9KKH	+	TCCTTTGGGTGTATGGGTCGTGTTTTAGTACTCTGGAAACAGAATCTACTAAAACAAGGCAAAATGCCGTGTTTATCTCGTCAACTTGTTGGCGAGAcaataccTCGGCCCTTCTCAGTTCGCTACGACCCATACaccc	29143	AAATGCCACTGAGAACTCTCTGTTTTAGTACTCTGGAAACAGAATCTACTAAAACAAGGCAAAATGCCGTGTTTATCTCGTCAACTTGTTGGCGAGA	29333
252	SpyCas9-NG	+	CCTTTGGGTGTATGGGTCGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCcaataccTCGGCCCTTCTCAGTTCGCTACGACCCATACaccc	29144	TGCCACTGAGAACTCTCTTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGC	29334
256	SpyCas9-SpRY	+	CCTTTGGGTGTATGGGTCGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCcaataccTCGGCCCTTCTCAGTTCGCTACGACCCATACaccc	29145	CCACTGAGAACTCTCTTAAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGC	29335
257	SpyCas9-SpRY	-	GTGGTTTTGGTCTTAGGAACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCgaagggcCGAGGTATTGTGGCAGCAAAGTTCCTAAGACcaaa	29146	ACTGTTAATGGAATCAGCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGC	29336
258	BlatCas9	-	cctgTGGTTTTGGTCTTAGGAACGCTATAGTTCCTTACTGAAAGGTAAGTTGCTATAGTAAGGGCAACAGACCCGAGGCGTTGGGGATCGCCTAGCCCGTGTTTACGGGCTCTCCCCATAT	29147	cttaCTGTTAATGGAATCAGCCAGCTATAGTTCCTTACTGAAAGGTAAGTTGCTATAGTAAGGGCAACAGACCCGAGGCGTTGGGGAT	29337

			TCAAAATAATGACAGACGAGCACCTTGGAGCATTTATCT CCGAGGTGCTgaagggcCGAGGTATTGTGGCAGCAAAGTTC CTAAGACCaaa		CGCCTAGCCCGTGTTTACGGGCTCTCCCC ATATTCAAAATAATGACAGACGAGCACCT TGGAGCATTTATCTCCGAGGTGCT	
264	ScaCas9-Sc++	+	TCCTTTGGGTGTATGGGTCGGTTTTAGAGCTAGAAATAGC AAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAG TGGCACCGAGTCGGTGCaataccTCGGCCCTTCTCAGTTCGC TACGACCCATACAccca	29148	ATGCCACTGAGAACTCTCTTGTTTTAGAG CTAGAAATAGCAAGTTAAAATAAGGCTA GTCCGTTATCAACTTGAAAAAGTGGCACC GAGTCGGTGC	29338
265	SpyCas9-SpRY	+	TCCTTTGGGTGTATGGGTCGGTTTTAGAGCTAGAAATAGC AAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAG TGGCACCGAGTCGGTGCaataccTCGGCCCTTCTCAGTTCGC TACGACCCATACAccca	29149	CACTGAGAACTCTCTTAAGAGTTTTAGAG CTAGAAATAGCAAGTTAAAATAAGGCTA GTCCGTTATCAACTTGAAAAAGTGGCACC GAGTCGGTGC	29339
266	SpyCas9-SpRY	-	TGTGGTTTTGGTCTTAGGAAGTTTTAGAGCTAGAAATAGC AAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAG TGGCACCGAGTCGGTGCaagggcCGAGGTATTGTGGCAGCA AAGTTCCTAAGACCaaaa	29150	CTGTTAATGGAATCAGCCAAGTTTTAGAG CTAGAAATAGCAAGTTAAAATAAGGCTA GTCCGTTATCAACTTGAAAAAGTGGCACC GAGTCGGTGC	29340
268	SauriCas9-KKH	+	AATCCTTTGGGTGTATGGGTCGTTTTAGTACTCTGGAAAC AGAATCTACTAAAACAAGGCAAAATGCCGTGTTTATCTC GTCAACTTGTTGGCGAGAataccTCGGCCCTTCTCAGTTCGC TACGACCCATACACCcaa	29151	AAATGCCACTGAGAACTCTCTGTTTTAGT ACTCTGGAAACAGAATCTACTAAAACAAG GCAAAATGCCGTGTTTATCTCGTCAACTT GTTGGCGAGA	29341
269	SpyCas9-SpRY	+	ATCCTTTGGGTGTATGGGTCGTTTTAGAGCTAGAAATAGC AAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAG TGGCACCGAGTCGGTGCataccTCGGCCCTTCTCAGTTCGCT ACGACCCATACACCcaa	29152	ACTGAGAACTCTCTTAAGACGTTTTAGAG CTAGAAATAGCAAGTTAAAATAAGGCTA GTCCGTTATCAACTTGAAAAAGTGGCACC GAGTCGGTGC	29342
270	SpyCas9-SpRY	-	CTGTGGTTTTGGTCTTAGGAGTTTTAGAGCTAGAAATAGC AAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAG TGGCACCGAGTCGGTGCagggcCGAGGTATTGTGGCAGCAA AGTTCCTAAGACCAaaac	29153	TGTTAATGGAATCAGCCAAAGTTTTAGAG CTAGAAATAGCAAGTTAAAATAAGGCTA GTCCGTTATCAACTTGAAAAAGTGGCACC GAGTCGGTGC	29343
271	BlatCas9	+	tcaaTCCTTTGGGTGTATGGGTCGCTATAGTTCCTTACTGAA AGGTAAGTTGCTATAGTAAGGGCAACAGACCCGAGGCGT TGGGGATCGCCTAGCCCGTGTTTACGGGCTCTCCCCATAT TCAAAATAATGACAGACGAGCACCTTGGAGCATTTATCT CCGAGGTGCTataccTCGGCCCTTCTCAGTTCGCTACGACCC ATACACCcaa	29154	tgccACTGAGAACTCTCTTAAGAGCTATAGT TCCTTACTGAAAGGTAAGTTGCTATAGTA AGGGCAACAGACCCGAGGCGTTGGGGAT CGCCTAGCCCGTGTTTACGGGCTCTCCCC ATATTCAAAATAATGACAGACGAGCACCT TGGAGCATTTATCTCCGAGGTGCT	29344
272	BlatCas9	+	tcaaTCCTTTGGGTGTATGGGTCGCTATAGTTCCTTACTGAA AGGTAAGTTGCTATAGTAAGGGCAACAGACCCGAGGCGT TGGGGATCGCCTAGCCCGTGTTTACGGGCTCTCCCCATAT TCAAAATAATGACAGACGAGCACCTTGGAGCATTTATCT CCGAGGTGCTataccTCGGCCCTTCTCAGTTCGCTACGACCC ATACACCcaa	29155	tgccACTGAGAACTCTCTTAAGAGCTATAGT TCCTTACTGAAAGGTAAGTTGCTATAGTA AGGGCAACAGACCCGAGGCGTTGGGGAT CGCCTAGCCCGTGTTTACGGGCTCTCCCC ATATTCAAAATAATGACAGACGAGCACCT TGGAGCATTTATCTCCGAGGTGCT	29345

274	BlatCas9	+	tcaaTCCTTTGGGTGTATGGGTCGCTATAGTTCCTTACTGAAAGGTAAGTTGCTATAGTAAGGGCAACAGACCCGAGGCGTTGGGGATCGCCTAGCCCGTGTTTACGGGCTCTCCCCATATTCAAAATAATGACAGACGAGCACCTTGGAGCATTTATCTCCGAGGTGCTataccTCGGCCCTTCTCAGTTCGCTACGACCCATACACCcaa	29156	tgccACTGAGAACTCTCTTAAGAGCTATAGTTCCTTACTGAAAGGTAAGTTGCTATAGTAAGGGCAACAGACCCGAGGCGTTGGGGATCGCCTAGCCCGTGTTTACGGGCTCTCCCCATATTCAAAATAATGACAGACGAGCACCTTGGAGCATTTATCTCCGAGGTGCT	29346
275	SauCas9KKH	+	CAATCCTTTGGGTGTATGGGTGTTTTAGTACTCTGGAAACAGAATCTACTAAAACAAGGCAAAATGCCGTGTTTATCTCGTCAACTTGTTGGCGAGAtaccTCGGCCCTTCTCAGTTCGCTACGACCCATACACCcaaa	29157	ACTCTCTTAAGACTACCTTTCGTTTTAGTACTCTGGAAACAGAATCTACTAAAACAAGGCAAAATGCCGTGTTTATCTCGTCAACTTGTTGGCGAGA	29347
276	SpyCas9-NG	+	AATCCTTTGGGTGTATGGGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCtaccTCGGCCCTTCTCAGTTCGCTACGACCCATACACCcaaa	29158	TGCCACTGAGAACTCTCTTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGC	29348
280	SpyCas9-SpRY	+	AATCCTTTGGGTGTATGGGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCtaccTCGGCCCTTCTCAGTTCGCTACGACCCATACACCcaaa	29159	CTGAGAACTCTCTTAAGACTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGC	29349
281	SpyCas9-SpRY	-	CCTGTGGTTTTGGTCTTAGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCgggcCGAGGTATTGTGGCAGCAAAGTTCCTAAGACCAAaacc	29160	GTTAATGGAATCAGCCAAAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGC	29350
286	ScaCas9-Sc++	+	CAATCCTTTGGGTGTATGGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCaccTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCaaag	29161	ATGCCACTGAGAACTCTCTTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGC	29351
287	SpyCas9-SpRY	+	CAATCCTTTGGGTGTATGGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCaccTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCaaag	29162	TGAGAACTCTCTTAAGACTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGC	29352
288	SpyCas9-SpRY	-	GCCTGTGGTTTTGGTCTTAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCggcCGAGGTATTGTGGCAGCAAAGTTCCTAAGACCAAAacca	29163	TTAATGGAATCAGCCAAAATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGC	29353
293	SpyCas9-NG	-	AGCCTGTGGTTTTGGTCTTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCgcCGAGGTATTGTGGCAGCAAAGTTCCTAAGACCAAAAccac	29164	TGGAATCAGCCAAAATCTTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGC	29354

297	SpyCas9-SpRY	-	AGCCTGTGGTTTTGGTCTTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCgcCGAGGTATTGTGGCAGCAAAGTTCCTAAGACCAAAAccac	29165	TAATGGAATCAGCCAAAATCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGC	29355
298	SpyCas9-SpRY	+	TCAATCCTTTGGGTGTATGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCccTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAaagg	29166	GAGAACTCTCTTAAGACTACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGC	29356
299	BlatCas9	-	tcaaGCCTGTGGTTTTGGTCTTAGCTATAGTTCCTTACTGAAAAGGTAAGTTGCTATAGTAAGGGCAACAGACCCGAGGCGTTGGGGATCGCCTAGCCCGTGTTTACGGGCTCTCCCCATATTCAAAATAATGACAGACGAGCACCTTGGAGCATTTATCTCCGAGGTGCTgcCGAGGTATTGTGGCAGCAAAGTTCCTAAGACCAAAAccac	29167	gttaATGGAATCAGCCAAAATCTGCTATAGTTCCTTACTGAAAGGTAAGTTGCTATAGTAAGGGCAACAGACCCGAGGCGTTGGGGATCGCCTAGCCCGTGTTTACGGGCTCTCCCCATATTCAAAATAATGACAGACGAGCACCTTGGAGCATTTATCTCCGAGGTGCT	29357
300	BlatCas9	-	tcaaGCCTGTGGTTTTGGTCTTAGCTATAGTTCCTTACTGAAAGGTAAGTTGCTATAGTAAGGGCAACAGACCCGAGGCGTTGGGGATCGCCTAGCCCGTGTTTACGGGCTCTCCCCATATTCAAAATAATGACAGACGAGCACCTTGGAGCATTTATCTCCGAGGTGCTgcCGAGGTATTGTGGCAGCAAAGTTCCTAAGACCAAAAccac	29168	gttaATGGAATCAGCCAAAATCTGCTATAGTTCCTTACTGAAAGGTAAGTTGCTATAGTAAGGGCAACAGACCCGAGGCGTTGGGGATCGCCTAGCCCGTGTTTACGGGCTCTCCCCATATTCAAAATAATGACAGACGAGCACCTTGGAGCATTTATCTCCGAGGTGCT	29358
306	SauCas9	-	ctCAAGCCTGTGGTTTTGGTCTTGTTTTAGTACTCTGGAAACAGAATCTACTAAAACAAGGCAAAATGCCGTGTTTATCTCGTCAACTTGTTGGCGAGAcCGAGGTATTGTGGCAGCAAAGTTCCTAAGACCAAAACcaca	29169	gaATCAGCCAAAATCTTAAGCTGGTTTTAGTACTCTGGAAACAGAATCTACTAAAACAAGGCAAAATGCCGTGTTTATCTCGTCAACTTGTTGGCGAGA	29359
307	SauCas9KKH	-	CAAGCCTGTGGTTTTGGTCTTGTTTTAGTACTCTGGAAACAGAATCTACTAAAACAAGGCAAAATGCCGTGTTTATCTCGTCAACTTGTTGGCGAGAcCGAGGTATTGTGGCAGCAAAGTTCCTAAGACCAAAACcaca	29170	TTAATGGAATCAGCCAAAATCGTTTTAGTACTCTGGAAACAGAATCTACTAAAACAAGGCAAAATGCCGTGTTTATCTCGTCAACTTGTTGGCGAGA	29360
310	ScaCas9-Sc++	-	AAGCCTGTGGTTTTGGTCTTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCcCGAGGTATTGTGGCAGCAAAGTTCCTAAGACCAAAACcaca	29171	ATGGAATCAGCCAAAATCTTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGC	29361
311	SpyCas9	-	AAGCCTGTGGTTTTGGTCTTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCcCGAGGTATTGTGGCAGCAAAGTTCCTAAGACCAAAACcaca	29172	CAGCCAAAATCTTAAGCTGCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGC	29362
314	SpyCas9-SpRY	-	AAGCCTGTGGTTTTGGTCTTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAG	29173	AATGGAATCAGCCAAAATCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTA	29363

			TGGCACCGAGTCGGTGCcCGAGGTATTGTGGCAGCAAAG TTCCTAAGACCAAAACcaca		GTCCGTTATCAACTTGAAAAAGTGGCACC GAGTCGGTGC	
315	SpyCas9-NG	+	CTCAATCCTTTGGGTGTATGGTTTTAGAGCTAGAAATAGC AAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAG TGGCACCGAGTCGGTGCcTCGGCCCTTCTCAGTTCGCTAC GACCCATACACCCAAagga	29174	TGCCACTGAGAACTCTCTTAGTTTTAGAG CTAGAAATAGCAAGTTAAAATAAGGCTA GTCCGTTATCAACTTGAAAAAGTGGCACC GAGTCGGTGC	29364
318	SpyCas9-NG	-	AAGCCTGTGGTTTTGGTCTTGTTTTAGAGCTAGAAATAGC AAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAG TGGCACCGAGTCGGTGCcCGAGGTATTGTGGCAGCAAAG TTCCTAAGACCAAAACcaca	29175	TGGAATCAGCCAAAATCTTAGTTTTAGAG CTAGAAATAGCAAGTTAAAATAAGGCTA GTCCGTTATCAACTTGAAAAAGTGGCACC GAGTCGGTGC	29365
322	SpyCas9-SpRY	+	CTCAATCCTTTGGGTGTATGGTTTTAGAGCTAGAAATAGC AAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAG TGGCACCGAGTCGGTGCcTCGGCCCTTCTCAGTTCGCTAC GACCCATACACCCAAagga	29176	AGAACTCTCTTAAGACTACCGTTTTAGAG CTAGAAATAGCAAGTTAAAATAAGGCTA GTCCGTTATCAACTTGAAAAAGTGGCACC GAGTCGGTGC	29366
328	SauCas9	-	acTCAAGCCTGTGGTTTTGGTCTGTTTTAGTACTCTGGAAA CAGAATCTACTAAAACAAGGCAAAATGCCGTGTTTATCT CGTCAACTTGTTGGCGAGACGAGGTATTGTGGCAGCAAA GTTCCTAAGACCAAAACCacag	29177	gaATCAGCCAAAATCTTAAGCTGGTTTTAG TACTCTGGAAACAGAATCTACTAAAACAA GGCAAAATGCCGTGTTTATCTCGTCAACT TGTTGGCGAGA	29367
329	SauCas9KKH	-	TCAAGCCTGTGGTTTTGGTCTGTTTTAGTACTCTGGAAAC AGAATCTACTAAAACAAGGCAAAATGCCGTGTTTATCTC GTCAACTTGTTGGCGAGACGAGGTATTGTGGCAGCAAAG TTCCTAAGACCAAAACCacag	29178	TTAATGGAATCAGCCAAAATCGTTTTAGT ACTCTGGAAACAGAATCTACTAAAACAAG GCAAAATGCCGTGTTTATCTCGTCAACTT GTTGGCGAGA	29368
330	SauriCas9	-	TCAAGCCTGTGGTTTTGGTCTGTTTTAGTACTCTGGAAAC AGAATCTACTAAAACAAGGCAAAATGCCGTGTTTATCTC GTCAACTTGTTGGCGAGACGAGGTATTGTGGCAGCAAAG TTCCTAAGACCAAAACCacag	29179	ATCAGCCAAAATCTTAAGCTGGTTTTAGT ACTCTGGAAACAGAATCTACTAAAACAAG GCAAAATGCCGTGTTTATCTCGTCAACTT GTTGGCGAGA	29369
331	SauriCas9-KKH	-	TCAAGCCTGTGGTTTTGGTCTGTTTTAGTACTCTGGAAAC AGAATCTACTAAAACAAGGCAAAATGCCGTGTTTATCTC GTCAACTTGTTGGCGAGACGAGGTATTGTGGCAGCAAAG TTCCTAAGACCAAAACCacag	29180	TAATGGAATCAGCCAAAATCTGTTTTAGT ACTCTGGAAACAGAATCTACTAAAACAAG GCAAAATGCCGTGTTTATCTCGTCAACTT GTTGGCGAGA	29370
334	ScaCas9-Sc++	+	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGC AAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAG TGGCACCGAGTCGGTGCTCGGCCCTTCTCAGTTCGCTACG ACCCATACACCCAAAggat	29181	TTAAGACTACCTTTCTCCAAGTTTTAGAGC TAGAAATAGCAAGTTAAAATAAGGCTAGT CCGTTATCAACTTGAAAAAGTGGCACCGA GTCGGTGC	29371
335	SpyCas9	+	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGC AAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAG TGGCACCGAGTCGGTGCTCGGCCCTTCTCAGTTCGCTACG ACCCATACACCCAAAggat	29182	TAAGACTACCTTTCTCCAAAGTTTTAGAG CTAGAAATAGCAAGTTAAAATAAGGCTA GTCCGTTATCAACTTGAAAAAGTGGCACC GAGTCGGTGC	29372

338	SpyCas9-SpRY	+	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAggat	29183	GAACTCTCTTAAGACTACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGC	29373
341	ScaCas9-Sc++	-	CAAGCCTGTGGTTTTGGTCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCGAGGTATTGTGGCAGCAAAGTTCCTAAGACCAAAACCacag	29184	ATGGAATCAGCCAAAATCTTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGC	29374
342	SpyCas9-SpRY	-	CAAGCCTGTGGTTTTGGTCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCGAGGTATTGTGGCAGCAAAGTTCCTAAGACCAAAACCacag	29185	ATGGAATCAGCCAAAATCTTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGC	29375
343	SpyCas9-NG	+	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAggat	29186	TGCCACTGAGAACTCTCTTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGC	29376
346	BlatCas9	+	agacCTCAATCCTTTGGGTGTATGCTATAGTTCCTTACTGAAAGGTAAGTTGCTATAGTAAGGGCAACAGACCCGAGGCGTTGGGGATCGCCTAGCCCGTGTTTACGGGCTCTCCCCATATTCAAAATAATGACAGACGAGCACCTTGGAGCATTTATCTCCGAGGTGCTTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAggat	29187	tgagAACTCTCTTAAGACTACCTGCTATAGTTCCTTACTGAAAGGTAAGTTGCTATAGTAAGGGCAACAGACCCGAGGCGTTGGGGATCGCCTAGCCCGTGTTTACGGGCTCTCCCCATATTCAAAATAATGACAGACGAGCACCTTGGAGCATTTATCTCCGAGGTGCT	29377
347	BlatCas9	+	agacCTCAATCCTTTGGGTGTATGCTATAGTTCCTTACTGAAAGGTAAGTTGCTATAGTAAGGGCAACAGACCCGAGGCGTTGGGGATCGCCTAGCCCGTGTTTACGGGCTCTCCCCATATTCAAAATAATGACAGACGAGCACCTTGGAGCATTTATCTCCGAGGTGCTTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAggat	29188	tgagAACTCTCTTAAGACTACCTGCTATAGTTCCTTACTGAAAGGTAAGTTGCTATAGTAAGGGCAACAGACCCGAGGCGTTGGGGATCGCCTAGCCCGTGTTTACGGGCTCTCCCCATATTCAAAATAATGACAGACGAGCACCTTGGAGCATTTATCTCCGAGGTGCT	29378
351	SauCas9KKH	-	CTCAAGCCTGTGGTTTTGGTCGTTTTAGTACTCTGGAAACAGAATCTACTAAAACAAGGCAAAATGCCGTGTTTATCTCGTCAACTTGTTGGCGAGAGAGGTATTGTGGCAGCAAAGTTCCTAAGACCAAAACCAcagg	29189	TTAATGGAATCAGCCAAAATCGTTTTAGTACTCTGGAAACAGAATCTACTAAAACAAGGCAAAATGCCGTGTTTATCTCGTCAACTTGTTGGCGAGA	29379
352	SauriCas9	+	GACCTCAATCCTTTGGGTGTAGTTTTAGTACTCTGGAAACAGAATCTACTAAAACAAGGCAAAATGCCGTGTTTATCTCGTCAACTTGTTGGCGAGACGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGgatt	29190	CTTAAGACTACCTTTCTCCAAGTTTTAGTACTCTGGAAACAGAATCTACTAAAACAAGGCAAAATGCCGTGTTTATCTCGTCAACTTGTTGGCGAGA	29380
353	SauriCas9-KKH	+	GACCTCAATCCTTTGGGTGTAGTTTTAGTACTCTGGAAACAGAATCTACTAAAACAAGGCAAAATGCCGTGTTTATCTC	29191	CTTAAGACTACCTTTCTCCAAGTTTTAGTACTCTGGAAACAGAATCTACTAAAACAAGG	29381

			GTCAACTTGTTGGCGAGACGGCCCTTCTCAGTTCGCTACG ACCCATACACCCAAAGgatt		CAAAATGCCGTGTTTATCTCGTCAACTTGT TGGCGAGA	
354	SauriCas9-KKH	-	CTCAAGCCTGTGGTTTTGGTCGTTTTAGTACTCTGGAAAC AGAATCTACTAAAACAAGGCAAAATGCCGTGTTTATCTC GTCAACTTGTTGGCGAGAGAGGTATTGTGGCAGCAAAGT TCCTAAGACCAAAACCAcagg	29192	TAATGGAATCAGCCAAAATCTGTTTTAGT ACTCTGGAAACAGAATCTACTAAAACAAG GCAAAATGCCGTGTTTATCTCGTCAACTT GTTGGCGAGA	29382
357	ScaCas9-Sc++	+	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGC AAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAG TGGCACCGAGTCGGTGCCGGCCCTTCTCAGTTCGCTACGA CCCATACACCCAAAGgatt	29193	TTAAGACTACCTTTCTCCAAGTTTTAGAGC TAGAAATAGCAAGTTAAAATAAGGCTAGT CCGTTATCAACTTGAAAAAGTGGCACCGA GTCGGTGC	29383
358	SpyCas9	+	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGC AAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAG TGGCACCGAGTCGGTGCCGGCCCTTCTCAGTTCGCTACGA CCCATACACCCAAAGgatt	29194	TAAGACTACCTTTCTCCAAAGTTTTAGAG CTAGAAATAGCAAGTTAAAATAAGGCTA GTCCGTTATCAACTTGAAAAAGTGGCACC GAGTCGGTGC	29384
361	SpyCas9-SpRY	+	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGC AAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAG TGGCACCGAGTCGGTGCCGGCCCTTCTCAGTTCGCTACGA CCCATACACCCAAAGgatt	29195	AACTCTCTTAAGACTACCTTGTTTTAGAGC TAGAAATAGCAAGTTAAAATAAGGCTAGT CCGTTATCAACTTGAAAAAGTGGCACCGA GTCGGTGC	29385
362	SpyCas9-NG	+	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGC AAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAG TGGCACCGAGTCGGTGCCGGCCCTTCTCAGTTCGCTACGA CCCATACACCCAAAGgatt	29196	TAAGACTACCTTTCTCCAAAGTTTTAGAG CTAGAAATAGCAAGTTAAAATAAGGCTA GTCCGTTATCAACTTGAAAAAGTGGCACC GAGTCGGTGC	29386
365	SpyCas9-SpRY	-	TCAAGCCTGTGGTTTTGGTCGTTTTAGAGCTAGAAATAGC AAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAG TGGCACCGAGTCGGTGCGAGGTATTGTGGCAGCAAAGTT CCTAAGACCAAAACCAcagg	29197	TGGAATCAGCCAAAATCTTAGTTTTAGAG CTAGAAATAGCAAGTTAAAATAAGGCTA GTCCGTTATCAACTTGAAAAAGTGGCACC GAGTCGGTGC	29387
366	St1Cas9	-	TCAAGCCTGTGGTTTTGGTCGTCTTTGTACTCTGGTACCA GAAGCTACAAAGATAAGGCTTCATGCCGAAATCAACACC CTGTCATTTTATGGCAGGGTGTTTTGAGGTATTGTGGCAG CAAAGTTCCTAAGACCAAAACCAcagg	29198	GTGTAAATTACTTACTGTTAGTCTTTGTAC TCTGGTACCAGAAGCTACAAAGATAAGGC TTCATGCCGAAATCAACACCCTGTCATTTT ATGGCAGGGTGTTTT	29388
369	SauCas9	+	caAGACCTCAATCCTTTGGGTGTGTTTTAGTACTCTGGAAA CAGAATCTACTAAAACAAGGCAAAATGCCGTGTTTATCT CGTCAACTTGTTGGCGAGAGGCCCTTCTCAGTTCGCTACG ACCCATACACCCAAAGGattg	29199	taAAAAAGAAGTAAAATGCCACTGTTTTAG TACTCTGGAAACAGAATCTACTAAAACAA GGCAAAATGCCGTGTTTATCTCGTCAACT TGTTGGCGAGA	29389
370	SauCas9KKH	+	AGACCTCAATCCTTTGGGTGTGTTTTAGTACTCTGGAAAC AGAATCTACTAAAACAAGGCAAAATGCCGTGTTTATCTC GTCAACTTGTTGGCGAGAGGCCCTTCTCAGTTCGCTACGA CCCATACACCCAAAGGattg	29200	ACTCTCTTAAGACTACCTTTCGTTTTAGTA CTCTGGAAACAGAATCTACTAAAACAAGG CAAAATGCCGTGTTTATCTCGTCAACTTGT TGGCGAGA	29390

371	SauCas9	+	caAGACCTCAATCCTTTGGGTGTGTTTTAGTACTCTGGAAACAGAATCTACTAAAACAAGGCAAAATGCCGTGTTTATCTCGTCAACTTGTTGGCGAGAGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGattg	29201	taAAAAAGAAGTAAAATGCCACTGTTTTAGTACTCTGGAAACAGAATCTACTAAAACAAGGCAAAATGCCGTGTTTATCTCGTCAACTTGTTGGCGAGA	29391
372	SauCas9KKH	+	AGACCTCAATCCTTTGGGTGTGTTTTAGTACTCTGGAAACAGAATCTACTAAAACAAGGCAAAATGCCGTGTTTATCTCGTCAACTTGTTGGCGAGAGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGattg	29202	ACTCTCTTAAGACTACCTTTCGTTTTAGTACTCTGGAAACAGAATCTACTAAAACAAGGCAAAATGCCGTGTTTATCTCGTCAACTTGTTGGCGAGA	29392
375	SauCas9KKH	-	ACTCAAGCCTGTGGTTTTGGTGTTTTAGTACTCTGGAAACAGAATCTACTAAAACAAGGCAAAATGCCGTGTTTATCTCGTCAACTTGTTGGCGAGAAGGTATTGTGGCAGCAAAGTTCCTAAGACCAAAACCACaggc	29203	AATCAGCCAAAATCTTAAGCTGTTTTAGTACTCTGGAAACAGAATCTACTAAAACAAGGCAAAATGCCGTGTTTATCTCGTCAACTTGTTGGCGAGA	29393
376	SauriCas9	+	AGACCTCAATCCTTTGGGTGTGTTTTAGTACTCTGGAAACAGAATCTACTAAAACAAGGCAAAATGCCGTGTTTATCTCGTCAACTTGTTGGCGAGAGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGattg	29204	CTTAAGACTACCTTTCTCCAAGTTTTAGTACTCTGGAAACAGAATCTACTAAAACAAGGCAAAATGCCGTGTTTATCTCGTCAACTTGTTGGCGAGA	29394
377	SauriCas9-KKH	+	AGACCTCAATCCTTTGGGTGTGTTTTAGTACTCTGGAAACAGAATCTACTAAAACAAGGCAAAATGCCGTGTTTATCTCGTCAACTTGTTGGCGAGAGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGattg	29205	CTTAAGACTACCTTTCTCCAAGTTTTAGTACTCTGGAAACAGAATCTACTAAAACAAGGCAAAATGCCGTGTTTATCTCGTCAACTTGTTGGCGAGA	29395
380	ScaCas9-Sc++	+	GACCTCAATCCTTTGGGTGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGattg	29206	TTAAGACTACCTTTCTCCAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGC	29396
381	SpyCas9-SpRY	+	GACCTCAATCCTTTGGGTGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGattg	29207	ACTCTCTTAAGACTACCTTTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGC	29397
382	SpyCas9-SpRY	-	CTCAAGCCTGTGGTTTTGGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAGGTATTGTGGCAGCAAAGTTCCTAAGACCAAAACCACaggc	29208	GGAATCAGCCAAAATCTTAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGC	29398

Table 4B. Exemplary template RNA sequences and second nick gRNA spacer sequences

Table 4B provides design of RNA components of gene modifying systems for correcting the pathogenic R261Q, mutation in PAH. The gRNA spacers from Table 1B were filtered, e.g., filtered by occurrence within 15 nt of the desired editing location and use of a Tier 1 Cas enzyme. For

each gRNA ID, this table details the sequence of a complete template RNA, optional second-nick gRNA, and Cas variant for use in a Cas-RT fusion gene modifying polypeptide. For exemplification, PBS sequences and post-edit homology regions (after the location of the edit) are set to 12 nt and 30 nt, respectively. Additionally, a second-nick gRNA is selected with preference for a distance near 100 nt from the first nick and a first preference for a design resulting in a PAM-in system, as described elsewhere in this application.

ID	Cas species	strand	Template RNA	SEQ ID NO	second-nick gRNA	SEQ ID NO
1	Nme2 Cas9	-	tcTTGGGTGGCCTGGCCTTCCAAGGTTGTAG CTCCCTTTCTCATTTCGGAAACGAAATGAGA ACCGTTGCTACAATAAGGCCGTCTGAAAAG ATGTGCCGCAACGCTCTGCCCCTTAAAGCTT CTGCTTTAAGGGGCATCGTTTAgtctgatgtactgtg tgcagtggaagacTCGGAAGGCCaggc	29399	gcAGCAGGAAAAGATGGCGCTCATGTTGTAGCTCCCT TTCTCATTTCGGAAACGAAATGAGAACCGTTGCTACA ATAAGGCCGTCTGAAAAGATGTGCCGCAACGCTCTGC CCCTTAAAGCTTCTGCTTTAAGGGGCATCGTTTA	29576
2	SpyCas9-SpRY	-	GGGTGGCCTGGCCTTCCAAGGTTTTAGAGC TAGAAATAGCAAGTTAAAATAAGGCTAGTC CGTTATCAACTTGAAAAAGTGGCACCGAGT CGGTGCgtctgatgtactgtgtgcagtggaagacTCGGAAG GCCaggc	29400	AGGAAAAGATGGCGCTCATTGTTTTAGAGCTAGAAAT AGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGA AAAAGTGGCACCGAGTCGGTGC	29577
3	BlatCas9	-	cttgGGTGGCCTGGCCTTCCAAGGCTATAGTT CCTTACTGAAAGGTAAGTTGCTATAGTAAG GGCAACAGACCCGAGGCGTTGGGGATCGCC TAGCCCGTGTTTACGGGCTCTCCCCATATTC AAAATAATGACAGACGAGCACCTTGGAGCA TTTATCTCCGAGGTGCTgtctgatgtactgtgtgcagtgg aagacTCGGAAGGCCaggc	29401	agcaGGAAAAGATGGCGCTCATTGCTATAGTTCCTTAC TGAAAGGTAAGTTGCTATAGTAAGGGCAACAGACCC GAGGCGTTGGGGATCGCCTAGCCCGTGTTTACGGGCT CTCCCCATATTCAAAATAATGACAGACGAGCACCTTG GAGCATTTATCTCCGAGGTGCT	29578
4	SauCas9KKH	+	CTGTGTGCAGTGGAAGACTTGGTTTTAGTAC TCTGGAAACAGAATCTACTAAAACAAGGCA AAATGCCGTGTTTATCTCGTCAACTTGTTGG CGAGAcgggatttcttgggtggcctggccttcCGAGTCTTC CActgc	29402	CTGACTCAGTGGTGATGAGCTGTTTTAGTACTCTGGA AACAGAATCTACTAAAACAAGGCAAAATGCCGTGTTT ATCTCGTCAACTTGTTGGCGAGA	29579
5	SauriCas9-KKH	+	CTGTGTGCAGTGGAAGACTTGGTTTTAGTAC TCTGGAAACAGAATCTACTAAAACAAGGCA AAATGCCGTGTTTATCTCGTCAACTTGTTGG CGAGAcgggatttcttgggtggcctggccttcCGAGTCTTC CActgc	29403	TGACTCAGTGGTGATGAGCTTGTTTTAGTACTCTGGA AACAGAATCTACTAAAACAAGGCAAAATGCCGTGTTT ATCTCGTCAACTTGTTGGCGAGA	29580

8	SpyCas9-SpRY	+	TGTGTGCAGTGGAAGACTTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCcgggatttcttgggtggcctggccttcCGAGTCTTCCACtgc	29404	GGTGATGAGCTTTGAGTTTTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGC	29581
10	SpyCas9-SpRY	-	TGGGTGGCCTGGCCTTCCAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCtctgatgtactgtgtgcagtggaagacTCGGAAGGCCAggcc	29405	GGAAAAGATGGCGCTCATTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGC	29582
13	SauCas9KKH	+	ACTGTGTGCAGTGGAAGACTTGTTTTAGTACTCTGGAAACAGAATCTACTAAAACAAGGCAAAATGCCGTGTTTATCTCGTCAACTTGTTGGCGAGAgggatttcttgggtggcctggccttcCGAGTCTTCCACTgca	29406	CTGACTCAGTGGTGATGAGCTGTTTTAGTACTCTGGAAACAGAATCTACTAAAACAAGGCAAAATGCCGTGTTTATCTCGTCAACTTGTTGGCGAGA	29583
14	SpyCas9-NG	-	TTGGGTGGCCTGGCCTTCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCctgatgtactgtgtgcagtggaagacTCGGAAGGCCAGgcca	29407	GGAAAAGATGGCGCTCATTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGC	29584
17	SpyCas9-NG	+	CTGTGTGCAGTGGAAGACTTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCgggatttcttgggtggcctggccttcCGAGTCTTCCACTgca	29408	CTCAGTGGTGATGAGCTTTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGC	29585
21	SpyCas9-SpRY	-	TTGGGTGGCCTGGCCTTCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCctgatgtactgtgtgcagtggaagacTCGGAAGGCCAGgcca	29409	GAAAAGATGGCGCTCATTGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGC	29586
23	SpyCas9-SpRY	+	CTGTGTGCAGTGGAAGACTTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCgggatttcttgggtggcctggccttcCGAGTCTTCCACTgca	29410	GTGATGAGCTTTGAGTTTTCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGC	29587
29	SauCas9	+	tgTACTGTGTGCAGTGGAAGACTGTTTTAGTACTCTGGAAACAGAATCTACTAAAACAAGGCAAAATGCCGTGTTTATCTCGTCAACTTGTTGGCGAGAggatttcttgggtggcctggccttcCGAGTCTTCCACTgcac	29411	ctCTGACTCAGTGGTGATGAGCTGTTTTAGTACTCTGGAAACAGAATCTACTAAAACAAGGCAAAATGCCGTGTTTATCTCGTCAACTTGTTGGCGAGA	29588

30	SauCas9KKH	+	TACTGTGTGCAGTGGAAGACTGTTTTAGTACTCTGGAAACAGAATCTACTAAAACAAGGCAAAATGCCGTGTTTATCTCGTCAACTTGTTGGCGAGAggatttcttgggtggcctggccttcCGAGTCTTCCACTgcac	29412	CTGACTCAGTGGTGATGAGCTGTTTTAGTACTCTGGAAACAGAATCTACTAAAACAAGGCAAAATGCCGTGTTTATCTCGTCAACTTGTTGGCGAGA	29589
33	ScaCas9-Sc++	-	CTTGGGTGGCCTGGCCTTCCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCtgatgtactgtgtgcagtggaagacTCGGAAGGCCAGGccac	29413	AAAGATGGCGCTCATTGTGCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGC	29590
34	SpyCas9-SpRY	-	CTTGGGTGGCCTGGCCTTCCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCtgatgtactgtgtgcagtggaagacTCGGAAGGCCAGGccac	29414	AAAAGATGGCGCTCATTGTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGC	29591
37	ScaCas9-Sc++	+	ACTGTGTGCAGTGGAAGACTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCggatttcttgggtggcctggccttcCGAGTCTTCCACTgcac	29415	ACTCAGTGGTGATGAGCTTTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGC	29592
38	SpyCas9	+	ACTGTGTGCAGTGGAAGACTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCggatttcttgggtggcctggccttcCGAGTCTTCCACTgcac	29416	TCCTAGTGCCTCTGACTCAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGC	29593
41	SpyCas9-SpRY	+	ACTGTGTGCAGTGGAAGACTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCggatttcttgggtggcctggccttcCGAGTCTTCCACTgcac	29417	TGATGAGCTTTGAGTTTTCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGC	29594
42	SpyCas9-NG	+	ACTGTGTGCAGTGGAAGACTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCggatttcttgggtggcctggccttcCGAGTCTTCCACTgcac	29418	CTCAGTGGTGATGAGCTTTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGC	29595
45	BlatCas9	-	tttcTTGGGTGGCCTGGCCTTCCGCTATAGTTCCTTACTGAAAGGTAAGTTGCTATAGTAAGGGCAACAGACCCGAGGCGTTGGGGATCGCCTAGCCCGTGTTTACGGGCTCTCCCCATATTCAAAATAATGACAGACGAGCACCTTGGAGCAT	29419	ggaaAAGATGGCGCTCATTGTGCGCTATAGTTCCTTACTGAAAGGTAAGTTGCTATAGTAAGGGCAACAGACCCGAGGCGTTGGGGATCGCCTAGCCCGTGTTTACGGGCTCTCCCCATATTCAAAATAATGACAGACGAGCACCTTGGAGCATTTATCTCCGAGGTGCT	29596

			TTATCTCCGAGGTGCTtgatgtactgtgtgcagtggaagacTCGGAAGGCCAGGccac			
51	SauCas9	+	atGTACTGTGTGCAGTGGAAGACGTTTTAGTACTCTGGAAACAGAATCTACTAAAACAAGGCAAAATGCCGTGTTTATCTCGTCAACTTGTTGGCGAGAgatttcttgggtggcctggccttcCGAGTCTTCCACTGcaca	29420	ctCTGACTCAGTGGTGATGAGCTGTTTTAGTACTCTGGAAACAGAATCTACTAAAACAAGGCAAAATGCCGTGTTTATCTCGTCAACTTGTTGGCGAGA	29597
52	SauCas9KKH	+	GTACTGTGTGCAGTGGAAGACGTTTTAGTACTCTGGAAACAGAATCTACTAAAACAAGGCAAAATGCCGTGTTTATCTCGTCAACTTGTTGGCGAGAgatttcttgggtggcctggccttcCGAGTCTTCCACTGcaca	29421	AGTTTTCTTTCTTCTTTTCATGTTTTAGTACTCTGGAAACAGAATCTACTAAAACAAGGCAAAATGCCGTGTTTATCTCGTCAACTTGTTGGCGAGA	29598
53	SauriCas9	+	GTACTGTGTGCAGTGGAAGACGTTTTAGTACTCTGGAAACAGAATCTACTAAAACAAGGCAAAATGCCGTGTTTATCTCGTCAACTTGTTGGCGAGAgatttcttgggtggcctggccttcCGAGTCTTCCACTGcaca	29422	TTCTTTTCATCCCAGCTTGCAGTTTTAGTACTCTGGAAACAGAATCTACTAAAACAAGGCAAAATGCCGTGTTTATCTCGTCAACTTGTTGGCGAGA	29599
54	SauriCas9-KKH	+	GTACTGTGTGCAGTGGAAGACGTTTTAGTACTCTGGAAACAGAATCTACTAAAACAAGGCAAAATGCCGTGTTTATCTCGTCAACTTGTTGGCGAGAgatttcttgggtggcctggccttcCGAGTCTTCCACTGcaca	29423	TGACTCAGTGGTGATGAGCTTGTTTTAGTACTCTGGAAACAGAATCTACTAAAACAAGGCAAAATGCCGTGTTTATCTCGTCAACTTGTTGGCGAGA	29600
55	SauriCas9-KKH	-	TTCTTGGGTGGCCTGGCCTTCGTTTTAGTACTCTGGAAACAGAATCTACTAAAACAAGGCAAAATGCCGTGTTTATCTCGTCAACTTGTTGGCGAGAgatgtactgtgtgcagtggaagacTCGGAAGGCCAGGCcacc	29424	AAAAGATGGCGCTCATTGTGCGTTTTAGTACTCTGGAAACAGAATCTACTAAAACAAGGCAAAATGCCGTGTTTATCTCGTCAACTTGTTGGCGAGA	29601
60	ScaCas9-Sc++	+	TACTGTGTGCAGTGGAAGACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCgatttcttgggtggcctggccttcCGAGTCTTCCACTGcaca	29425	ACTCAGTGGTGATGAGCTTTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGC	29602
61	SpyCas9-SpRY	+	TACTGTGTGCAGTGGAAGACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCgatttcttgggtggcctggccttcCGAGTCTTCCACTGcaca	29426	GATGAGCTTTGAGTTTTCTTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGC	29603

62	SpyCas9-SpRY	-	TCTTGGGTGGCCTGGCCTTCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCgatgtactgtgtgcagtggaagacTCGGAAGGCCAGGCcacc	29427	AAAGATGGCGCTCATTGTGCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGC	29604
65	SauCas9KKH	-	TTTCTTGGGTGGCCTGGCCTTGTTTTAGTACTCTGGAAACAGAATCTACTAAAACAAGGCAAAATGCCGTGTTTATCTCGTCAACTTGTTGGCGAGAatgtactgtgtgcagtggaagacTCGGAAGGCCAGGCCaccc	29428	AAGATGGCGCTCATTGTGCCTGTTTTAGTACTCTGGAAACAGAATCTACTAAAACAAGGCAAAATGCCGTGTTTATCTCGTCAACTTGTTGGCGAGA	29605
66	SauCas9KKH	+	TGTACTGTGTGCAGTGGAAGAGTTTTAGTACTCTGGAAACAGAATCTACTAAAACAAGGCAAAATGCCGTGTTTATCTCGTCAACTTGTTGGCGAGAatttcttgggtggcctggccttcCGAGTCTTCCACTGCacac	29429	AGTTTTCTTTCTTCTTTTCATGTTTTAGTACTCTGGAAACAGAATCTACTAAAACAAGGCAAAATGCCGTGTTTATCTCGTCAACTTGTTGGCGAGA	29606
67	SauCas9KKH	-	TTTCTTGGGTGGCCTGGCCTTGTTTTAGTACTCTGGAAACAGAATCTACTAAAACAAGGCAAAATGCCGTGTTTATCTCGTCAACTTGTTGGCGAGAatgtactgtgtgcagtggaagacTCGGAAGGCCAGGCCaccc	29430	AAGATGGCGCTCATTGTGCCTGTTTTAGTACTCTGGAAACAGAATCTACTAAAACAAGGCAAAATGCCGTGTTTATCTCGTCAACTTGTTGGCGAGA	29607
70	SpyCas9-SpRY	+	GTACTGTGTGCAGTGGAAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCatttcttgggtggcctggccttcCGAGTCTTCCACTGCacac	29431	ATGAGCTTTGAGTTTTCTTTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGC	29608
71	SpyCas9-SpRY	-	TTCTTGGGTGGCCTGGCCTTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCatgtactgtgtgcagtggaagacTCGGAAGGCCAGGCCaccc	29432	AAGATGGCGCTCATTGTGCCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGC	29609
73	SauCas9KKH	-	ATTTCTTGGGTGGCCTGGCCTGTTTTAGTACTCTGGAAACAGAATCTACTAAAACAAGGCAAAATGCCGTGTTTATCTCGTCAACTTGTTGGCGAGAtgtactgtgtgcagtggaagacTCGGAAGGCCAGGCCAccca	29433	AAGATGGCGCTCATTGTGCCTGTTTTAGTACTCTGGAAACAGAATCTACTAAAACAAGGCAAAATGCCGTGTTTATCTCGTCAACTTGTTGGCGAGA	29610
74	SpyCas9-SpRY	+	TGTACTGTGTGCAGTGGAAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCtttcttgggtggcctggccttcCGAGTCTTCCACTGCAcaca	29434	TGAGCTTTGAGTTTTCTTTCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGC	29611

75	SpyCas9-SpRY	-	TTTCTTGGGTGGCCTGGCCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCtgtactgtgtgcagtggaagacTCGGAAGGCCAGGCCAccca	29435	AGATGGCGCTCATTGTGCCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGC	29612
78	SpyCas9-SpRY	+	ATGTACTGTGTGCAGTGGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCttcttgggtggcctggccttcCGAGTCTTCCACTGCACacag	29436	GAGCTTTGAGTTTTCTTTCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGC	29613
79	SpyCas9-SpRY	-	ATTTCTTGGGTGGCCTGGCCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCgtactgtgtgcagtggaagacTCGGAAGGCCAGGCCACcaa	29437	GATGGCGCTCATTGTGCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGC	29614
81	SpyCas9-NG	+	GATGTACTGTGTGCAGTGGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCtcttgggtggcctggccttcCGAGTCTTCCACTGCACAcagt	29438	TTCTTTCTTCTTTTCATCCCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGC	29615
85	SpyCas9-SpRY	+	GATGTACTGTGTGCAGTGGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCtcttgggtggcctggccttcCGAGTCTTCCACTGCACAcagt	29439	AGCTTTGAGTTTTCTTTCTTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGC	29616
86	SpyCas9-SpRY	-	GATTTCTTGGGTGGCCTGGCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCtactgtgtgcagtggaagacTCGGAAGGCCAGGCCACCcaag	29440	ATGGCGCTCATTGTGCCTGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGC	29617
87	BlatCas9	-	cgggATTTCTTGGGTGGCCTGGCGCTATAGTTCCTTACTGAAAGGTAAGTTGCTATAGTAAGGGCAACAGACCCGAGGCGTTGGGGATCGCCTAGCCCGTGTTTACGGGCTCTCCCCATATTCAAAATAATGACAGACGAGCACCTTGGAGCATTTATCTCCGAGGTGCTtactgtgtgcagtggaagacTCGGAAGGCCAGGCCACCcaag	29441	aaagATGGCGCTCATTGTGCCTGGCTATAGTTCCTTACTGAAAGGTAAGTTGCTATAGTAAGGGCAACAGACCCGAGGCGTTGGGGATCGCCTAGCCCGTGTTTACGGGCTCTCCCCATATTCAAAATAATGACAGACGAGCACCTTGGAGCATTTATCTCCGAGGTGCT	29618
88	BlatCas9	-	cgggATTTCTTGGGTGGCCTGGCGCTATAGTTCCTTACTGAAAGGTAAGTTGCTATAGTAAGGGCAACAGACCCGAGGCGTTGGGGATCGCC	29442	aaagATGGCGCTCATTGTGCCTGGCTATAGTTCCTTACTGAAAGGTAAGTTGCTATAGTAAGGGCAACAGACCCGAGGCGTTGGGGATCGCCTAGCCCGTGTTTACGGGCTC	29619

			TAGCCCGTGTTTACGGGCTCTCCCCATATTC AAAATAATGACAGACGAGCACCTTGGAGCA TTTATCTCCGAGGTGCTtactgtgtgcagtggaagacT CGGAAGGCCAGGCCACCcaag		TCCCCATATTCAAAATAATGACAGACGAGCACCTTGG AGCATTTATCTCCGAGGTGCT	
91	Nme2 Cas9	-	ctCGGGATTTCTTGGGTGGCCTGGGTTGTAG CTCCCTTTCTCATTTCGGAAACGAAATGAGA ACCGTTGCTACAATAAGGCCGTCTGAAAAG ATGTGCCGCAACGCTCTGCCCCTTAAAGCTT CTGCTTTAAGGGGCATCGTTTAactgtgtgcagtgg aagacTCGGAAGGCCAGGCCACCCaaga	2944 3	gcAGCAGGAAAAGATGGCGCTCATGTTGTAGCTCCCT TTCTCATTTCGGAAACGAAATGAGAACCGTTGCTACA ATAAGGCCGTCTGAAAAGATGTGCCGCAACGCTCTGC CCCTTAAAGCTTCTGCTTTAAGGGGCATCGTTTA	2962 0
94	ScaCas 9-Sc++	+	TGATGTACTGTGTGCAGTGGGTTTTAGAGCT AGAAATAGCAAGTTAAAATAAGGCTAGTCC GTTATCAACTTGAAAAAGTGGCACCGAGTC GGTGCcttgggtggcctggccttcCGAGTCTTCCACTG CACACagta	2944 4	TTTCTTTCTTCTTTTCATCCGTTTTAGAGCTAGAAATA GCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAA AAAGTGGCACCGAGTCGGTGC	2962 1
95	SpyCa s9-SpRY	+	TGATGTACTGTGTGCAGTGGGTTTTAGAGCT AGAAATAGCAAGTTAAAATAAGGCTAGTCC GTTATCAACTTGAAAAAGTGGCACCGAGTC GGTGCcttgggtggcctggccttcCGAGTCTTCCACTG CACACagta	2944 5	GCTTTGAGTTTTCTTTCTTCGTTTTAGAGCTAGAAATA GCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAA AAAGTGGCACCGAGTCGGTGC	2962 2
96	SpyCa s9-SpRY	-	GGATTTCTTGGGTGGCCTGGGTTTTAGAGCT AGAAATAGCAAGTTAAAATAAGGCTAGTCC GTTATCAACTTGAAAAAGTGGCACCGAGTC GGTGCactgtgtgcagtggaagacTCGGAAGGCCAGG CCACCCaaga	2944 6	TGGCGCTCATTGTGCCTGGCGTTTTAGAGCTAGAAAT AGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGA AAAAGTGGCACCGAGTCGGTGC	2962 3
97	BlatCa s9	+	gtctGATGTACTGTGTGCAGTGGGCTATAGTT CCTTACTGAAAGGTAAGTTGCTATAGTAAG GGCAACAGACCCGAGGCGTTGGGGATCGCC TAGCCCGTGTTTACGGGCTCTCCCCATATTC AAAATAATGACAGACGAGCACCTTGGAGCA TTTATCTCCGAGGTGCTcttgggtggcctggccttcCG AGTCTTCCACTGCACACagta	2944 7	tgagCTTTGAGTTTTCTTTCTTCGCTATAGTTCCTTACTG AAAGGTAAGTTGCTATAGTAAGGGCAACAGACCCGA GGCGTTGGGGATCGCCTAGCCCGTGTTTACGGGCTCT CCCCATATTCAAAATAATGACAGACGAGCACCTTGGA GCATTTATCTCCGAGGTGCT	2962 4
98	BlatCa s9	-	tcggGATTTCTTGGGTGGCCTGGGCTATAGTT CCTTACTGAAAGGTAAGTTGCTATAGTAAG GGCAACAGACCCGAGGCGTTGGGGATCGCC TAGCCCGTGTTTACGGGCTCTCCCCATATTC AAAATAATGACAGACGAGCACCTTGGAGCA TTTATCTCCGAGGTGCTactgtgtgcagtggaagacTC GGAAGGCCAGGCCACCCaaga	2944 8	aaagATGGCGCTCATTGTGCCTGGCTATAGTTCCTTACT GAAAGGTAAGTTGCTATAGTAAGGGCAACAGACCCG AGGCGTTGGGGATCGCCTAGCCCGTGTTTACGGGCTC TCCCCATATTCAAAATAATGACAGACGAGCACCTTGG AGCATTTATCTCCGAGGTGCT	2962 5

99	BlatCas9	-	tcggGATTTCTTGGGTGGCCTGGGCTATAGTTCCTTACTGAAAGGTAAGTTGCTATAGTAAGGGCAACAGACCCGAGGCGTTGGGGATCGCCTAGCCCGTGTTTACGGGCTCTCCCCATATTCAAAATAATGACAGACGAGCACCTTGGAGCATTTATCTCCGAGGTGCTactgtgtgcagtggaagacTCGGAAGGCCAGGCCACCCaaga	29449	aaagATGGCGCTCATTGTGCCTGGCTATAGTTCCTTACTGAAAGGTAAGTTGCTATAGTAAGGGCAACAGACCCGAGGCGTTGGGGATCGCCTAGCCCGTGTTTACGGGCTCTCCCCATATTCAAAATAATGACAGACGAGCACCTTGGAGCATTTATCTCCGAGGTGCT	29626
100	BlatCas9	+	gtctGATGTACTGTGTGCAGTGGGCTATAGTTCCTTACTGAAAGGTAAGTTGCTATAGTAAGGGCAACAGACCCGAGGCGTTGGGGATCGCCTAGCCCGTGTTTACGGGCTCTCCCCATATTCAAAATAATGACAGACGAGCACCTTGGAGCATTTATCTCCGAGGTGCTcttgggtggcctggccttcCGAGTCTTCCACTGCACACagta	29450	tgagCTTTGAGTTTTCTTTCTTCGCTATAGTTCCTTACTGAAAGGTAAGTTGCTATAGTAAGGGCAACAGACCCGAGGCGTTGGGGATCGCCTAGCCCGTGTTTACGGGCTCTCCCCATATTCAAAATAATGACAGACGAGCACCTTGGAGCATTTATCTCCGAGGTGCT	29627
101	BlatCas9	-	tcggGATTTCTTGGGTGGCCTGGGCTATAGTTCCTTACTGAAAGGTAAGTTGCTATAGTAAGGGCAACAGACCCGAGGCGTTGGGGATCGCCTAGCCCGTGTTTACGGGCTCTCCCCATATTCAAAATAATGACAGACGAGCACCTTGGAGCATTTATCTCCGAGGTGCTactgtgtgcagtggaagacTCGGAAGGCCAGGCCACCCaaga	29451	aaagATGGCGCTCATTGTGCCTGGCTATAGTTCCTTACTGAAAGGTAAGTTGCTATAGTAAGGGCAACAGACCCGAGGCGTTGGGGATCGCCTAGCCCGTGTTTACGGGCTCTCCCCATATTCAAAATAATGACAGACGAGCACCTTGGAGCATTTATCTCCGAGGTGCT	29628
106	SauCas9KKH	+	TCTGATGTACTGTGTGCAGTGGTTTTAGTACTCTGGAAACAGAATCTACTAAAACAAGGCAAAATGCCGTGTTTATCTCGTCAACTTGTTGGCGAGAttgggtggcctggccttcCGAGTCTTCCACTGCACACAgtac	29452	AGTTTTCTTTCTTCTTTTCATGTTTTAGTACTCTGGAAACAGAATCTACTAAAACAAGGCAAAATGCCGTGTTTATCTCGTCAACTTGTTGGCGAGA	29629
107	SauriCas9-KKH	+	TCTGATGTACTGTGTGCAGTGGTTTTAGTACTCTGGAAACAGAATCTACTAAAACAAGGCAAAATGCCGTGTTTATCTCGTCAACTTGTTGGCGAGAttgggtggcctggccttcCGAGTCTTCCACTGCACACAgtac	29453	GTTTTCTTTCTTCTTTTCATCGTTTTAGTACTCTGGAAACAGAATCTACTAAAACAAGGCAAAATGCCGTGTTTATCTCGTCAACTTGTTGGCGAGA	29630
110	SpyCas9-SpRY	+	CTGATGTACTGTGTGCAGTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCttgggtggcctggccttcCGAGTCTTCCACTGCACACAgtac	29454	CTTTGAGTTTTCTTTCTTCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGC	29631
112	SpyCas9-SpRY	-	GGGATTTCTTGGGTGGCCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTC	29455	GGCGCTCATTGTGCCTGGCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGC	29632

			GGTGCctgtgtgcagtggaagacTCGGAAGGCCAGGC CACCCAagaa			
115	SauCas9KKH	+	GTCTGATGTACTGTGTGCAGTGTTTTAGTAC TCTGGAAACAGAATCTACTAAAACAAGGCA AAATGCCGTGTTTATCTCGTCAACTTGTTGG CGAGAtgggtggcctggccttcCGAGTCTTCCACTGC ACACAGtaca	29456	AGTTTTCTTTCTTCTTTTCATGTTTTAGTACTCTGGAA ACAGAATCTACTAAAACAAGGCAAAATGCCGTGTTTA TCTCGTCAACTTGTTGGCGAGA	29633
116	SpyCas9-NG	+	TCTGATGTACTGTGTGCAGTGTTTTAGAGCT AGAAATAGCAAGTTAAAATAAGGCTAGTCC GTTATCAACTTGAAAAAGTGGCACCGAGTC GGTGCtgggtggcctggccttcCGAGTCTTCCACTGC ACACAGtaca	29457	TTCTTTCTTCTTTTCATCCCGTTTTAGAGCTAGAAATA GCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAA AAAGTGGCACCGAGTCGGTGC	29634
119	SpyCas9-NG	-	CGGGATTTCTTGGGTGGCCTGTTTTAGAGCT AGAAATAGCAAGTTAAAATAAGGCTAGTCC GTTATCAACTTGAAAAAGTGGCACCGAGTC GGTGCtgtgtgcagtggaagacTCGGAAGGCCAGGC CACCCAAgaaa	29458	CGCTCATTGTGCCTGGCAACGTTTTAGAGCTAGAAAT AGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGA AAAAGTGGCACCGAGTCGGTGC	29635
123	SpyCas9-SpRY	+	TCTGATGTACTGTGTGCAGTGTTTTAGAGCT AGAAATAGCAAGTTAAAATAAGGCTAGTCC GTTATCAACTTGAAAAAGTGGCACCGAGTC GGTGCtgggtggcctggccttcCGAGTCTTCCACTGC ACACAGtaca	29459	TTTGAGTTTTCTTTCTTCTTGTTTTAGAGCTAGAAATA GCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAA AAAGTGGCACCGAGTCGGTGC	29636
125	SpyCas9-SpRY	-	CGGGATTTCTTGGGTGGCCTGTTTTAGAGCT AGAAATAGCAAGTTAAAATAAGGCTAGTCC GTTATCAACTTGAAAAAGTGGCACCGAGTC GGTGCtgtgtgcagtggaagacTCGGAAGGCCAGGC CACCCAAgaaa	29460	GCGCTCATTGTGCCTGGCAAGTTTTAGAGCTAGAAAT AGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGA AAAAGTGGCACCGAGTCGGTGC	29637
132	SauCas9	+	caTGTCTGATGTACTGTGTGCAGGTTTTAGTA CTCTGGAAACAGAATCTACTAAAACAAGGC AAAATGCCGTGTTTATCTCGTCAACTTGTTG GCGAGAgggtggcctggccttcCGAGTCTTCCACTG CACACAGTacat	29461	ctCTGACTCAGTGGTGATGAGCTGTTTTAGTACTCTGG AAACAGAATCTACTAAAACAAGGCAAAATGCCGTGT TTATCTCGTCAACTTGTTGGCGAGA	29638
133	SauCas9KKH	+	TGTCTGATGTACTGTGTGCAGGTTTTAGTAC TCTGGAAACAGAATCTACTAAAACAAGGCA AAATGCCGTGTTTATCTCGTCAACTTGTTGG CGAGAgggtggcctggccttcCGAGTCTTCCACTGC ACACAGTacat	29462	AGTTTTCTTTCTTCTTTTCATGTTTTAGTACTCTGGAA ACAGAATCTACTAAAACAAGGCAAAATGCCGTGTTTA TCTCGTCAACTTGTTGGCGAGA	29639

136	ScaCas9-Sc++	+	GTCTGATGTACTGTGTGCAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCgggtggcctggccttcCGAGTCTTCCACTGCACACAGTacat	29463	TTTCTTTCTTCTTTTCATCCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGC	29640
137	SpyCas9	+	GTCTGATGTACTGTGTGCAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCgggtggcctggccttcCGAGTCTTCCACTGCACACAGTacat	29464	CTTTTCATCCCAGCTTGCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGC	29641
140	SpyCas9-SpRY	+	GTCTGATGTACTGTGTGCAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCgggtggcctggccttcCGAGTCTTCCACTGCACACAGTacat	29465	TTGAGTTTTCTTTCTTCTTTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGC	29642
143	ScaCas9-Sc++	-	TCGGGATTTCTTGGGTGGCCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCgtgtgcagtggaagacTCGGAAGGCCAGGCCACCCAAGaaat	29466	CGCTCATTGTGCCTGGCAACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGC	29643
144	SpyCas9	-	TCGGGATTTCTTGGGTGGCCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCgtgtgcagtggaagacTCGGAAGGCCAGGCCACCCAAGaaat	29467	CGCTCATTGTGCCTGGCAACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGC	29644
147	SpyCas9-SpRY	-	TCGGGATTTCTTGGGTGGCCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCgtgtgcagtggaagacTCGGAAGGCCAGGCCACCCAAGaaat	29468	CGCTCATTGTGCCTGGCAACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGC	29645
148	SpyCas9-NG	+	GTCTGATGTACTGTGTGCAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCgggtggcctggccttcCGAGTCTTCCACTGCACACAGTacat	29469	TTCTTTCTTCTTTTCATCCCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGC	29646
151	SpyCas9-NG	-	TCGGGATTTCTTGGGTGGCCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCgtgtgcagtggaagacTCGGAAGGCCAGGCCACCCAAGaaat	29470	CGCTCATTGTGCCTGGCAACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGC	29647

154	BlatCas9	-	ctctCGGGATTTCTTGGGTGGCCGCTATAGTTCCTTACTGAAAGGTAAGTTGCTATAGTAAGGGCAACAGACCCGAGGCGTTGGGGATCGCCTAGCCCGTGTTTACGGGCTCTCCCCATATTCAAAATAATGACAGACGAGCACCTTGGAGCATTTATCTCCGAGGTGCTgtgtgcagtggaagacTCGGAAGGCCAGGCCACCCAAGaaat	29471	gcgcTCATTGTGCCTGGCAACTGGCTATAGTTCCTTACTGAAAGGTAAGTTGCTATAGTAAGGGCAACAGACCCGAGGCGTTGGGGATCGCCTAGCCCGTGTTTACGGGCTCTCCCCATATTCAAAATAATGACAGACGAGCACCTTGGAGCATTTATCTCCGAGGTGCT	29648
160	Nme2Cas9	-	tcCTCTCGGGATTTCTTGGGTGGCGTTGTAGCTCCCTTTCTCATTTCGGAAACGAAATGAGAACCGTTGCTACAATAAGGCCGTCTGAAAAGATGTGCCGCAACGCTCTGCCCCTTAAAGCTTCTGCTTTAAGGGGCATCGTTTAtgtgcagtggaagacTCGGAAGGCCAGGCCACCCAAGAaatc	29472	gcAGCAGGAAAAGATGGCGCTCATGTTGTAGCTCCCTTTCTCATTTCGGAAACGAAATGAGAACCGTTGCTACAATAAGGCCGTCTGAAAAGATGTGCCGCAACGCTCTGCCCCTTAAAGCTTCTGCTTTAAGGGGCATCGTTTA	29649
161	SauCas9	+	ccATGTCTGATGTACTGTGTGCAGTTTTAGTACTCTGGAAACAGAATCTACTAAAACAAGGCAAAATGCCGTGTTTATCTCGTCAACTTGTTGGCGAGAggtggcctggccttcCGAGTCTTCCACTGCACACAGTAcatc	29473	ctCTGACTCAGTGGTGATGAGCTGTTTTAGTACTCTGGAAACAGAATCTACTAAAACAAGGCAAAATGCCGTGTTTATCTCGTCAACTTGTTGGCGAGA	29650
162	SauCas9KKH	+	ATGTCTGATGTACTGTGTGCAGTTTTAGTACTCTGGAAACAGAATCTACTAAAACAAGGCAAAATGCCGTGTTTATCTCGTCAACTTGTTGGCGAGAggtggcctggccttcCGAGTCTTCCACTGCACACAGTAcatc	29474	AGTTTTCTTTCTTCTTTTCATGTTTTAGTACTCTGGAAACAGAATCTACTAAAACAAGGCAAAATGCCGTGTTTATCTCGTCAACTTGTTGGCGAGA	29651
163	SauriCas9	+	ATGTCTGATGTACTGTGTGCAGTTTTAGTACTCTGGAAACAGAATCTACTAAAACAAGGCAAAATGCCGTGTTTATCTCGTCAACTTGTTGGCGAGAggtggcctggccttcCGAGTCTTCCACTGCACACAGTAcatc	29475	TTCTTTTCATCCCAGCTTGCAGTTTTAGTACTCTGGAAACAGAATCTACTAAAACAAGGCAAAATGCCGTGTTTATCTCGTCAACTTGTTGGCGAGA	29652
164	SauriCas9-KKH	+	ATGTCTGATGTACTGTGTGCAGTTTTAGTACTCTGGAAACAGAATCTACTAAAACAAGGCAAAATGCCGTGTTTATCTCGTCAACTTGTTGGCGAGAggtggcctggccttcCGAGTCTTCCACTGCACACAGTAcatc	29476	GTTTTCTTTCTTCTTTTCATCGTTTTAGTACTCTGGAAACAGAATCTACTAAAACAAGGCAAAATGCCGTGTTTATCTCGTCAACTTGTTGGCGAGA	29653
165	SauriCas9	-	TCTCGGGATTTCTTGGGTGGCGTTTTAGTACTCTGGAAACAGAATCTACTAAAACAAGGCAAAATGCCGTGTTTATCTCGTCAACTTGTTGGCGAGAtgtgcagtggaagacTCGGAAGGCCAGGCCACCCAAGAaatc	29477	GGCGCTCATTGTGCCTGGCAAGTTTTAGTACTCTGGAAACAGAATCTACTAAAACAAGGCAAAATGCCGTGTTTATCTCGTCAACTTGTTGGCGAGA	29654

166	SauriCas9-KKH	-	TCTCGGGATTTCTTGGGTGGCGTTTTAGTACTCTGGAAACAGAATCTACTAAAACAAGGCAAAATGCCGTGTTTATCTCGTCAACTTGTTGGCGAGAtgtgcagtggaagacTCGGAAGGCCAGGCCACCCAAGAaatc	29478	GCTCATTGTGCCTGGCAACTGGTTTTAGTACTCTGGAAACAGAATCTACTAAAACAAGGCAAAATGCCGTGTTTATCTCGTCAACTTGTTGGCGAGA	29655
169	ScaCas9-Sc++	+	TGTCTGATGTACTGTGTGCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCggtggcctggccttcCGAGTCTTCCACTGCACACAGTAcatc	29479	TTTCTTTCTTCTTTTCATCCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGC	29656
170	SpyCas9-SpRY	+	TGTCTGATGTACTGTGTGCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCggtggcctggccttcCGAGTCTTCCACTGCACACAGTAcatc	29480	TGAGTTTTCTTTCTTCTTTTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGC	29657
173	ScaCas9-Sc++	-	CTCGGGATTTCTTGGGTGGCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCtgtgcagtggaagacTCGGAAGGCCAGGCCACCCAAGAaatc	29481	CGCTCATTGTGCCTGGCAACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGC	29658
174	SpyCas9-SpRY	-	CTCGGGATTTCTTGGGTGGCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCtgtgcagtggaagacTCGGAAGGCCAGGCCACCCAAGAaatc	29482	GCTCATTGTGCCTGGCAACTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGC	29659
175	BlatCas9	-	cctcTCGGGATTTCTTGGGTGGCGCTATAGTTCCTTACTGAAAGGTAAGTTGCTATAGTAAGGGCAACAGACCCGAGGCGTTGGGGATCGCCTAGCCCGTGTTTACGGGCTCTCCCCATATTCAAAATAATGACAGACGAGCACCTTGGAGCATTTATCTCCGAGGTGCTtgtgcagtggaagacTCGGAAGGCCAGGCCACCCAAGAaatc	29483	gcgcTCATTGTGCCTGGCAACTGGCTATAGTTCCTTACTGAAAGGTAAGTTGCTATAGTAAGGGCAACAGACCCGAGGCGTTGGGGATCGCCTAGCCCGTGTTTACGGGCTCTCCCCATATTCAAAATAATGACAGACGAGCACCTTGGAGCATTTATCTCCGAGGTGCT	29660
176	BlatCas9	-	cctcTCGGGATTTCTTGGGTGGCGCTATAGTTCCTTACTGAAAGGTAAGTTGCTATAGTAAGGGCAACAGACCCGAGGCGTTGGGGATCGCCTAGCCCGTGTTTACGGGCTCTCCCCATATTCAAAATAATGACAGACGAGCACCTTGGAGCATTTATCTCCGAGGTGCTtgtgcagtggaagacTCGGAAGGCCAGGCCACCCAAGAaatc	29484	gcgcTCATTGTGCCTGGCAACTGGCTATAGTTCCTTACTGAAAGGTAAGTTGCTATAGTAAGGGCAACAGACCCGAGGCGTTGGGGATCGCCTAGCCCGTGTTTACGGGCTCTCCCCATATTCAAAATAATGACAGACGAGCACCTTGGAGCATTTATCTCCGAGGTGCT	29661

179	SauCas9KKH	+	CATGTCTGATGTACTGTGTGCGTTTTAGTACTCTGGAAACAGAATCTACTAAAACAAGGCAAAATGCCGTGTTTATCTCGTCAACTTGTTGGCGAGAgtggcctggccttcCGAGTCTTCCACTGCACACAGTACatca	29485	AGTTTTCTTTCTTCTTTTCATGTTTTAGTACTCTGGAAACAGAATCTACTAAAACAAGGCAAAATGCCGTGTTTATCTCGTCAACTTGTTGGCGAGA	29662
180	SauCas9KKH	-	CTCTCGGGATTTCTTGGGTGGGTTTTAGTACTCTGGAAACAGAATCTACTAAAACAAGGCAAAATGCCGTGTTTATCTCGTCAACTTGTTGGCGAGAgtgcagtggaagacTCGGAAGGCCAGGCCACCCAAGAAatcc	29486	CGCTCATTGTGCCTGGCAACTGTTTTAGTACTCTGGAAACAGAATCTACTAAAACAAGGCAAAATGCCGTGTTTATCTCGTCAACTTGTTGGCGAGA	29663
181	SpyCas9-NG	+	ATGTCTGATGTACTGTGTGCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCgtggcctggccttcCGAGTCTTCCACTGCACACAGTACatca	29487	TTCTTTCTTCTTTTCATCCCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGC	29664
185	SpyCas9-SpRY	+	ATGTCTGATGTACTGTGTGCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCgtggcctggccttcCGAGTCTTCCACTGCACACAGTACatca	29488	GAGTTTTCTTTCTTCTTTTCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGC	29665
186	SpyCas9-SpRY	-	TCTCGGGATTTCTTGGGTGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCgtgcagtggaagacTCGGAAGGCCAGGCCACCCAAGAAatcc	29489	CTCATTGTGCCTGGCAACTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGC	29666
189	ScaCas9-Sc++	+	CATGTCTGATGTACTGTGTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCtggcctggccttcCGAGTCTTCCACTGCACACAGTACAtcag	29490	TTTCTTTCTTCTTTTCATCCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGC	29667
190	SpyCas9-SpRY	+	CATGTCTGATGTACTGTGTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCtggcctggccttcCGAGTCTTCCACTGCACACAGTACAtcag	29491	AGTTTTCTTTCTTCTTTTCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGC	29668
191	SpyCas9-SpRY	-	CTCTCGGGATTTCTTGGGTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCtgcagtggaagacTCGGAAGGCCAGGCCACCCAAGAAAtccc	29492	TCATTGTGCCTGGCAACTGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGC	29669

193	SauriCas9-KKH	+	TCCATGTCTGATGTACTGTGTGTTTTAGTACTCTGGAAACAGAATCTACTAAAACAAGGCAAAATGCCGTGTTTATCTCGTCAACTTGTTGGCGAGAggcctggccttcCGAGTCTTCCACTGCACACAGTACATcaga	29493	GTTTTCTTTCTTCTTTTCATCGTTTTAGTACTCTGGAAACAGAATCTACTAAAACAAGGCAAAATGCCGTGTTTATCTCGTCAACTTGTTGGCGAGA	29670
194	SpyCas9-NG	-	CCTCTCGGGATTTCTTGGGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCgcagtggaagacTCGGAAGGCCAGGCCACCCAAGAAATcccg	29494	CATTGTGCCTGGCAACTGGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGC	29671
198	SpyCas9-SpRY	-	CCTCTCGGGATTTCTTGGGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCgcagtggaagacTCGGAAGGCCAGGCCACCCAAGAAATcccg	29495	CATTGTGCCTGGCAACTGGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGC	29672
199	SpyCas9-SpRY	+	CCATGTCTGATGTACTGTGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCggcctggccttcCGAGTCTTCCACTGCACACAGTACATcaga	29496	GTTTTCTTTCTTCTTTTCATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGC	29673
203	SauCas9KKH	+	ATCCATGTCTGATGTACTGTGGTTTTAGTACTCTGGAAACAGAATCTACTAAAACAAGGCAAAATGCCGTGTTTATCTCGTCAACTTGTTGGCGAGAgcctggccttcCGAGTCTTCCACTGCACACAGTACATCagac	29497	AGTTTTCTTTCTTCTTTTCATGTTTTAGTACTCTGGAAACAGAATCTACTAAAACAAGGCAAAATGCCGTGTTTATCTCGTCAACTTGTTGGCGAGA	29674
204	SauCas9KKH	+	ATCCATGTCTGATGTACTGTGGTTTTAGTACTCTGGAAACAGAATCTACTAAAACAAGGCAAAATGCCGTGTTTATCTCGTCAACTTGTTGGCGAGAgcctggccttcCGAGTCTTCCACTGCACACAGTACATCagac	29498	AGTTTTCTTTCTTCTTTTCATGTTTTAGTACTCTGGAAACAGAATCTACTAAAACAAGGCAAAATGCCGTGTTTATCTCGTCAACTTGTTGGCGAGA	29675
209	ScaCas9-Sc++	-	TCCTCTCGGGATTTCTTGGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCcagtggaagacTCGGAAGGCCAGGCCACCCAAGAAATCccga	29499	TTGTGCCTGGCAACTGGTAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGC	29676
210	SpyCas9	-	TCCTCTCGGGATTTCTTGGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCcagtggaagacTCGGAAGGCCAGGCCACCCAAGAAATCccga	29500	TGTGCCTGGCAACTGGTAGCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGC	29677

213	SpyCas9-SpRY	-	TCCTCTCGGGATTTCTTGGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCcagtggaagacTCGGAAGGCCAGGCCACCCAAGAAATCccga	29501	ATTGTGCCTGGCAACTGGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGC	29678
214	SpyCas9-NG	+	TCCATGTCTGATGTACTGTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCgcctggccttcCGAGTCTTCCACTGCACACAGTACATCagac	29502	TTCTTTCTTCTTTTCATCCCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGC	29679
217	SpyCas9-NG	-	TCCTCTCGGGATTTCTTGGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCcagtggaagacTCGGAAGGCCAGGCCACCCAAGAAATCccga	29503	CATTGTGCCTGGCAACTGGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGC	29680
221	SpyCas9-SpRY	+	TCCATGTCTGATGTACTGTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCgcctggccttcCGAGTCTTCCACTGCACACAGTACATCagac	29504	TTTTCTTTCTTCTTTTCATCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGC	29681
222	BlatCas9	-	ctttCCTCTCGGGATTTCTTGGGGCTATAGTTCCTTACTGAAAGGTAAGTTGCTATAGTAAGGGCAACAGACCCGAGGCGTTGGGGATCGCCTAGCCCGTGTTTACGGGCTCTCCCCATATTCAAAATAATGACAGACGAGCACCTTGGAGCATTTATCTCCGAGGTGCTcagtggaagacTCGGAAGGCCAGGCCACCCAAGAAATCccga	29505	gcgcTCATTGTGCCTGGCAACTGGCTATAGTTCCTTACTGAAAGGTAAGTTGCTATAGTAAGGGCAACAGACCCGAGGCGTTGGGGATCGCCTAGCCCGTGTTTACGGGCTCTCCCCATATTCAAAATAATGACAGACGAGCACCTTGGAGCATTTATCTCCGAGGTGCT	29682
223	BlatCas9	-	ctttCCTCTCGGGATTTCTTGGGGCTATAGTTCCTTACTGAAAGGTAAGTTGCTATAGTAAGGGCAACAGACCCGAGGCGTTGGGGATCGCCTAGCCCGTGTTTACGGGCTCTCCCCATATTCAAAATAATGACAGACGAGCACCTTGGAGCATTTATCTCCGAGGTGCTcagtggaagacTCGGAAGGCCAGGCCACCCAAGAAATCccga	29506	gcgcTCATTGTGCCTGGCAACTGGCTATAGTTCCTTACTGAAAGGTAAGTTGCTATAGTAAGGGCAACAGACCCGAGGCGTTGGGGATCGCCTAGCCCGTGTTTACGGGCTCTCCCCATATTCAAAATAATGACAGACGAGCACCTTGGAGCATTTATCTCCGAGGTGCT	29683
226	Nme2Cas9	-	tgCTTTCCTCTCGGGATTTCTTGGGTTGTAGCTCCCTTTCTCATTTCGGAAACGAAATGAGAACCGTTGCTACAATAAGGCCGTCTGAAAAGATGTGCCGCAACGCTCTGCCCCTTAAAGCTTCTGCTTTAAGGGGCATCGTTTAagtggaagacTCGGAAGGCCAGGCCACCCAAGAAATCCgag	29507	gcAGCAGGAAAAGATGGCGCTCATGTTGTAGCTCCCTTTCTCATTTCGGAAACGAAATGAGAACCGTTGCTACAATAAGGCCGTCTGAAAAGATGTGCCGCAACGCTCTGCCCCTTAAAGCTTCTGCTTTAAGGGGCATCGTTTA	29684

227	SauriCas9	-	TTTCCTCTCGGGATTTCTTGGGTTTTAGTACTCTGGAAACAGAATCTACTAAAACAAGGCAAAATGCCGTGTTTATCTCGTCAACTTGTTGGCGAGAagtggaagacTCGGAAGGCCAGGCCACCCAAGAAATCCcgag	29508	ATTGTGCCTGGCAACTGGTAGGTTTTAGTACTCTGGAAACAGAATCTACTAAAACAAGGCAAAATGCCGTGTTTATCTCGTCAACTTGTTGGCGAGA	29685
228	SauriCas9-KKH	-	TTTCCTCTCGGGATTTCTTGGGTTTTAGTACTCTGGAAACAGAATCTACTAAAACAAGGCAAAATGCCGTGTTTATCTCGTCAACTTGTTGGCGAGAagtggaagacTCGGAAGGCCAGGCCACCCAAGAAATCCcgag	29509	ATTGTGCCTGGCAACTGGTAGGTTTTAGTACTCTGGAAACAGAATCTACTAAAACAAGGCAAAATGCCGTGTTTATCTCGTCAACTTGTTGGCGAGA	29686
231	ScaCas9-Sc++	+	ATCCATGTCTGATGTACTGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCcctggccttcCGAGTCTTCCACTGCACACAGTACATCAgaca	29510	TTTCTTTCTTCTTTTCATCCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGC	29687
232	SpyCas9-SpRY	+	ATCCATGTCTGATGTACTGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCcctggccttcCGAGTCTTCCACTGCACACAGTACATCAgaca	29511	TTTCTTTCTTCTTTTCATCCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGC	29688
235	ScaCas9-Sc++	-	TTCCTCTCGGGATTTCTTGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCagtggaagacTCGGAAGGCCAGGCCACCCAAGAAATCCcgag	29512	TTGTGCCTGGCAACTGGTAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGC	29689
236	SpyCas9-SpRY	-	TTCCTCTCGGGATTTCTTGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCagtggaagacTCGGAAGGCCAGGCCACCCAAGAAATCCcgag	29513	TTGTGCCTGGCAACTGGTAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGC	29690
237	BlatCas9	-	gcttTCCTCTCGGGATTTCTTGGGCTATAGTTCCTTACTGAAAGGTAAGTTGCTATAGTAAGGGCAACAGACCCGAGGCGTTGGGGATCGCCTAGCCCGTGTTTACGGGCTCTCCCCATATTCAAAATAATGACAGACGAGCACCTTGGAGCATTTATCTCCGAGGTGCTagtggaagacTCGGAAGGCCAGGCCACCCAAGAAATCCcgag	29514	gcgcTCATTGTGCCTGGCAACTGGCTATAGTTCCTTACTGAAAGGTAAGTTGCTATAGTAAGGGCAACAGACCCGAGGCGTTGGGGATCGCCTAGCCCGTGTTTACGGGCTCTCCCCATATTCAAAATAATGACAGACGAGCACCTTGGAGCATTTATCTCCGAGGTGCT	29691
238	BlatCas9	-	gcttTCCTCTCGGGATTTCTTGGGCTATAGTTCCTTACTGAAAGGTAAGTTGCTATAGTAAGGGCAACAGACCCGAGGCGTTGGGGATCGCCT	29515	gcgcTCATTGTGCCTGGCAACTGGCTATAGTTCCTTACTGAAAGGTAAGTTGCTATAGTAAGGGCAACAGACCCGAGGCGTTGGGGATCGCCTAGCCCGTGTTTACGGGCTC	29692

			AGCCCGTGTTTACGGGCTCTCCCCATATTCAAAATAATGACAGACGAGCACCTTGGAGCATTTATCTCCGAGGTGCTagtggaagacTCGGAAGGCCAGGCCACCCAAGAAATCCcgag		TCCCCATATTCAAAATAATGACAGACGAGCACCTTGGAGCATTTATCTCCGAGGTGCT	
239	SauCas9KKH	-	CTTTCCTCTCGGGATTTCTTGGTTTTAGTACTCTGGAAACAGAATCTACTAAAACAAGGCAAAATGCCGTGTTTATCTCGTCAACTTGTTGGCGAGAgtggaagacTCGGAAGGCCAGGCCACCCAAGAAATCCCgaga	29516	TTGTGCCTGGCAACTGGTAGCGTTTTAGTACTCTGGAAACAGAATCTACTAAAACAAGGCAAAATGCCGTGTTTATCTCGTCAACTTGTTGGCGAGA	29693
240	SpyCas9-NG	+	GATCCATGTCTGATGTACTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCctggccttcCGAGTCTTCCACTGCACACAGTACATCAGacat	29517	TTCTTTCTTCTTTTCATCCCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGC	29694
243	SpyCas9-NG	-	TTTCCTCTCGGGATTTCTTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCgtggaagacTCGGAAGGCCAGGCCACCCAAGAAATCCCgaga	29518	TGTGCCTGGCAACTGGTAGCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGC	29695
247	SpyCas9-SpRY	+	GATCCATGTCTGATGTACTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCctggccttcCGAGTCTTCCACTGCACACAGTACATCAGacat	29519	TTCTTTCTTCTTTTCATCCCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGC	29696
249	SpyCas9-SpRY	-	TTTCCTCTCGGGATTTCTTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCgtggaagacTCGGAAGGCCAGGCCACCCAAGAAATCCCgaga	29520	TGTGCCTGGCAACTGGTAGCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGC	29697
250	BlatCas9	+	ttggATCCATGTCTGATGTACTGGCTATAGTTCCTTACTGAAAGGTAAGTTGCTATAGTAAGGGCAACAGACCCGAGGCGTTGGGGATCGCCTAGCCCGTGTTTACGGGCTCTCCCCATATTCAAAATAATGACAGACGAGCACCTTGGAGCATTTATCTCCGAGGTGCTctggccttcCGAGTCTTCCACTGCACACAGTACATCAGacat	29521	gagtTTTCTTTCTTCTTTTCATCGCTATAGTTCCTTACTGAAAGGTAAGTTGCTATAGTAAGGGCAACAGACCCGAGGCGTTGGGGATCGCCTAGCCCGTGTTTACGGGCTCTCCCCATATTCAAAATAATGACAGACGAGCACCTTGGAGCATTTATCTCCGAGGTGCT	29698
251	BlatCas9	+	ttggATCCATGTCTGATGTACTGGCTATAGTTCCTTACTGAAAGGTAAGTTGCTATAGTAAGGGCAACAGACCCGAGGCGTTGGGGATCGCCTAGCCCGTGTTTACGGGCTCTCCCCATATTCA	29522	gagtTTTCTTTCTTCTTTTCATCGCTATAGTTCCTTACTGAAAGGTAAGTTGCTATAGTAAGGGCAACAGACCCGAGGCGTTGGGGATCGCCTAGCCCGTGTTTACGGGCTCT	29699

			AAATAATGACAGACGAGCACCTTGGAGCAT TTATCTCCGAGGTGCTctggccttcCGAGTCTTCC ACTGCACACAGTACATCAGacat		CCCCATATTCAAAATAATGACAGACGAGCACCTTGGA GCATTTATCTCCGAGGTGCT	
254	ScaCas 9-Sc++	+	GGATCCATGTCTGATGTACTGTTTTAGAGCT AGAAATAGCAAGTTAAAATAAGGCTAGTCC GTTATCAACTTGAAAAAGTGGCACCGAGTC GGTGCtggccttcCGAGTCTTCCACTGCACACAG TACATCAGAcatg	2952 3	TTTCTTTCTTCTTTTCATCCGTTTTAGAGCTAGAAATA GCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAA AAAGTGGCACCGAGTCGGTGC	2970 0
255	SpyCa s9- SpRY	+	GGATCCATGTCTGATGTACTGTTTTAGAGCT AGAAATAGCAAGTTAAAATAAGGCTAGTCC GTTATCAACTTGAAAAAGTGGCACCGAGTC GGTGCtggccttcCGAGTCTTCCACTGCACACAG TACATCAGAcatg	2952 4	TCTTTCTTCTTTTCATCCCAGTTTTAGAGCTAGAAATA GCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAA AAAGTGGCACCGAGTCGGTGC	2970 1
258	ScaCas 9-Sc++	-	CTTTCCTCTCGGGATTTCTTGTTTTAGAGCT AGAAATAGCAAGTTAAAATAAGGCTAGTCC GTTATCAACTTGAAAAAGTGGCACCGAGTC GGTGCtggaagacTCGGAAGGCCAGGCCACCCA AGAAATCCCGagag	2952 5	TGTGCCTGGCAACTGGTAGCGTTTTAGAGCTAGAAAT AGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGA AAAAGTGGCACCGAGTCGGTGC	2970 2
259	SpyCa s9	-	CTTTCCTCTCGGGATTTCTTGTTTTAGAGCT AGAAATAGCAAGTTAAAATAAGGCTAGTCC GTTATCAACTTGAAAAAGTGGCACCGAGTC GGTGCtggaagacTCGGAAGGCCAGGCCACCCA AGAAATCCCGagag	2952 6	TGTGCCTGGCAACTGGTAGCGTTTTAGAGCTAGAAAT AGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGA AAAAGTGGCACCGAGTCGGTGC	2970 3
262	SpyCa s9- SpRY	-	CTTTCCTCTCGGGATTTCTTGTTTTAGAGCT AGAAATAGCAAGTTAAAATAAGGCTAGTCC GTTATCAACTTGAAAAAGTGGCACCGAGTC GGTGCtggaagacTCGGAAGGCCAGGCCACCCA AGAAATCCCGagag	2952 7	GTGCCTGGCAACTGGTAGCTGTTTTAGAGCTAGAAAT AGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGA AAAAGTGGCACCGAGTCGGTGC	2970 4
263	SpyCa s9-NG	-	CTTTCCTCTCGGGATTTCTTGTTTTAGAGCT AGAAATAGCAAGTTAAAATAAGGCTAGTCC GTTATCAACTTGAAAAAGTGGCACCGAGTC GGTGCtggaagacTCGGAAGGCCAGGCCACCCA AGAAATCCCGagag	2952 8	GTGCCTGGCAACTGGTAGCTGTTTTAGAGCTAGAAAT AGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGA AAAAGTGGCACCGAGTCGGTGC	2970 5
267	SauriC as9	-	TGCTTTCCTCTCGGGATTTCTGTTTTAGTACT CTGGAAACAGAATCTACTAAAACAAGGCAA AATGCCGTGTTTATCTCGTCAACTTGTTGGC GAGAggaagacTCGGAAGGCCAGGCCACCCAA GAAATCCCGAgagg	2952 9	GTGCCTGGCAACTGGTAGCTGGTTTTAGTACTCTGGA AACAGAATCTACTAAAACAAGGCAAAATGCCGTGTTT ATCTCGTCAACTTGTTGGCGAGA	2970 6

268	SauriCas9-KKH	-	TGCTTTCCTCTCGGGATTTCTGTTTTAGTACTCTGGAAACAGAATCTACTAAAACAAGGCAAAATGCCGTGTTTATCTCGTCAACTTGTTGGCGAGAggaagacTCGGAAGGCCAGGCCACCCAAGAAATCCCGAgagg	29530	GTGCCTGGCAACTGGTAGCTGGTTTTAGTACTCTGGAAACAGAATCTACTAAAACAAGGCAAAATGCCGTGTTTATCTCGTCAACTTGTTGGCGAGA	29707
271	ScaCas9-Sc++	-	GCTTTCCTCTCGGGATTTCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCggaagacTCGGAAGGCCAGGCCACCCAAGAAATCCCGAgagg	29531	TGCCTGGCAACTGGTAGCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGC	29708
272	SpyCas9	-	GCTTTCCTCTCGGGATTTCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCggaagacTCGGAAGGCCAGGCCACCCAAGAAATCCCGAgagg	29532	GCCTGGCAACTGGTAGCTGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGC	29709
275	SpyCas9-SpRY	-	GCTTTCCTCTCGGGATTTCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCggaagacTCGGAAGGCCAGGCCACCCAAGAAATCCCGAgagg	29533	TGCCTGGCAACTGGTAGCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGC	29710
276	SpyCas9-NG	+	TGGATCCATGTCTGATGTACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCggccttcCGAGTCTTCCACTGCACACAGTACATCAGACatgg	29534	TTCTTTCTTCTTTTCATCCCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGC	29711
279	SpyCas9-NG	-	GCTTTCCTCTCGGGATTTCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCggaagacTCGGAAGGCCAGGCCACCCAAGAAATCCCGAgagg	29535	GTGCCTGGCAACTGGTAGCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGC	29712
283	SpyCas9-SpRY	+	TGGATCCATGTCTGATGTACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCggccttcCGAGTCTTCCACTGCACACAGTACATCAGACatgg	29536	CTTTCTTCTTTTCATCCCAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGC	29713
286	SauCas9	-	gcCTGCTTTCCTCTCGGGATTTCGTTTTAGTACTCTGGAAACAGAATCTACTAAAACAAGGCAAAATGCCGTGTTTATCTCGTCAACTTGTTGGCGAGAgaagacTCGGAAGGCCAGGCCACCCAAGAAATCCCGAGagga	29537	ttGTGCCTGGCAACTGGTAGCTGGTTTTAGTACTCTGGAAACAGAATCTACTAAAACAAGGCAAAATGCCGTGTTTATCTCGTCAACTTGTTGGCGAGA	29714

287	SauCas9KKH	-	CTGCTTTCCTCTCGGGATTTCGTTTTAGTACTCTGGAAACAGAATCTACTAAAACAAGGCAAAATGCCGTGTTTATCTCGTCAACTTGTTGGCGAGAgaagacTCGGAAGGCCAGGCCACCCAAGAAATCCCGAGagga	29538	GTGCCTGGCAACTGGTAGCTGGTTTTAGTACTCTGGAAACAGAATCTACTAAAACAAGGCAAAATGCCGTGTTTATCTCGTCAACTTGTTGGCGAGA	29715
288	SauCas9	-	gcCTGCTTTCCTCTCGGGATTTCGTTTTAGTACTCTGGAAACAGAATCTACTAAAACAAGGCAAAATGCCGTGTTTATCTCGTCAACTTGTTGGCGAGAgaagacTCGGAAGGCCAGGCCACCCAAGAAATCCCGAGagga	29539	ttGTGCCTGGCAACTGGTAGCTGGTTTTAGTACTCTGGAAACAGAATCTACTAAAACAAGGCAAAATGCCGTGTTTATCTCGTCAACTTGTTGGCGAGA	29716
289	SauCas9KKH	-	CTGCTTTCCTCTCGGGATTTCGTTTTAGTACTCTGGAAACAGAATCTACTAAAACAAGGCAAAATGCCGTGTTTATCTCGTCAACTTGTTGGCGAGAgaagacTCGGAAGGCCAGGCCACCCAAGAAATCCCGAGagga	29540	GTGCCTGGCAACTGGTAGCTGGTTTTAGTACTCTGGAAACAGAATCTACTAAAACAAGGCAAAATGCCGTGTTTATCTCGTCAACTTGTTGGCGAGA	29717
292	SauriCas9	-	CTGCTTTCCTCTCGGGATTTCGTTTTAGTACTCTGGAAACAGAATCTACTAAAACAAGGCAAAATGCCGTGTTTATCTCGTCAACTTGTTGGCGAGAgaagacTCGGAAGGCCAGGCCACCCAAGAAATCCCGAGagga	29541	GTGCCTGGCAACTGGTAGCTGGTTTTAGTACTCTGGAAACAGAATCTACTAAAACAAGGCAAAATGCCGTGTTTATCTCGTCAACTTGTTGGCGAGA	29718
293	SauriCas9-KKH	-	CTGCTTTCCTCTCGGGATTTCGTTTTAGTACTCTGGAAACAGAATCTACTAAAACAAGGCAAAATGCCGTGTTTATCTCGTCAACTTGTTGGCGAGAgaagacTCGGAAGGCCAGGCCACCCAAGAAATCCCGAGagga	29542	GTGCCTGGCAACTGGTAGCTGGTTTTAGTACTCTGGAAACAGAATCTACTAAAACAAGGCAAAATGCCGTGTTTATCTCGTCAACTTGTTGGCGAGA	29719
296	ScaCas9-Sc++	+	TTGGATCCATGTCTGATGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCgccttcCGAGTCTTCCACTGCACACAGTACATCAGACAtgga	29543	TTTCTTCTTTTCATCCCAGCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGC	29720
297	SpyCas9-SpRY	+	TTGGATCCATGTCTGATGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCgccttcCGAGTCTTCCACTGCACACAGTACATCAGACAtgga	29544	TTTCTTCTTTTCATCCCAGCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGC	29721
300	ScaCas9-Sc++	-	TGCTTTCCTCTCGGGATTTCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCgaagacTCGGAAGGCCAGGCCACCCAAGAAATCCCGAGagga	29545	GCCTGGCAACTGGTAGCTGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGC	29722

301	SpyCas9-SpRY	-	TGCTTTCCTCTCGGGATTTCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCgaagacTCGGAAGGCCAGGCCACCCAAGAAATCCCGAGagga	29546	GCCTGGCAACTGGTAGCTGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGC	29723
302	SauCas9KKH	-	CCTGCTTTCCTCTCGGGATTTGTTTTAGTACTCTGGAAACAGAATCTACTAAAACAAGGCAAAATGCCGTGTTTATCTCGTCAACTTGTTGGCGAGAaagacTCGGAAGGCCAGGCCACCCAAGAAATCCCGAGAggaa	29547	CCTGGCAACTGGTAGCTGGAGGTTTTAGTACTCTGGAAACAGAATCTACTAAAACAAGGCAAAATGCCGTGTTTATCTCGTCAACTTGTTGGCGAGA	29724
303	SpyCas9-SpRY	+	CTTGGATCCATGTCTGATGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCccttcCGAGTCTTCCACTGCACACAGTACATCAGACATggat	29548	TTCTTCTTTTCATCCCAGCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGC	29725
304	SpyCas9-SpRY	-	CTGCTTTCCTCTCGGGATTTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCaagacTCGGAAGGCCAGGCCACCCAAGAAATCCCGAGAggaa	29549	CCTGGCAACTGGTAGCTGGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGC	29726
305	SpyCas9-SpRY	+	GCTTGGATCCATGTCTGATGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCcttcCGAGTCTTCCACTGCACACAGTACATCAGACATGgatc	29550	TCTTCTTTTCATCCCAGCTTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGC	29727
306	SpyCas9-SpRY	-	CCTGCTTTCCTCTCGGGATTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCagacTCGGAAGGCCAGGCCACCCAAGAAATCCCGAGAGgaaa	29551	CTGGCAACTGGTAGCTGGAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGC	29728
308	SpyCas9-SpRY	+	GGCTTGGATCCATGTCTGATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCttcCGAGTCTTCCACTGCACACAGTACATCAGACATGGatcc	29552	CTTCTTTTCATCCCAGCTTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGC	29729
309	SpyCas9-SpRY	-	GCCTGCTTTCCTCTCGGGATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCgacTCGGAAGGCCAGGCCACCCAAGAAATCCCGAGAGGaaag	29553	TGGCAACTGGTAGCTGGAGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGC	29730

310	SpyCas9-NG	+	GGGCTTGGATCCATGTCTGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCtcCGAGTCTTCCACTGCACACAGTACATCAGACATGGAtcca	29554	CTTTTCATCCCAGCTTGCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGC	29731
314	SpyCas9-SpRY	+	GGGCTTGGATCCATGTCTGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCtcCGAGTCTTCCACTGCACACAGTACATCAGACATGGAtcca	29555	TTCTTTTCATCCCAGCTTGCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGC	29732
315	SpyCas9-SpRY	-	GGCCTGCTTTCCTCTCGGGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCacTCGGAAGGCCAGGCCACCCAAGAAATCCCGAGAGGAaagc	29556	GGCAACTGGTAGCTGGAGGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGC	29733
316	BlatCas9	+	catgGGCTTGGATCCATGTCTGAGCTATAGTTCCTTACTGAAAGGTAAGTTGCTATAGTAAGGGCAACAGACCCGAGGCGTTGGGGATCGCCTAGCCCGTGTTTACGGGCTCTCCCCATATTCAAAATAATGACAGACGAGCACCTTGGAGCATTTATCTCCGAGGTGCTtcCGAGTCTTCCACTGCACACAGTACATCAGACATGGAtcca	29557	tcttTCTTCTTTTCATCCCAGCTGCTATAGTTCCTTACTGAAAGGTAAGTTGCTATAGTAAGGGCAACAGACCCGAGGCGTTGGGGATCGCCTAGCCCGTGTTTACGGGCTCTCCCCATATTCAAAATAATGACAGACGAGCACCTTGGAGCATTTATCTCCGAGGTGCT	29734
317	BlatCas9	+	catgGGCTTGGATCCATGTCTGAGCTATAGTTCCTTACTGAAAGGTAAGTTGCTATAGTAAGGGCAACAGACCCGAGGCGTTGGGGATCGCCTAGCCCGTGTTTACGGGCTCTCCCCATATTCAAAATAATGACAGACGAGCACCTTGGAGCATTTATCTCCGAGGTGCTtcCGAGTCTTCCACTGCACACAGTACATCAGACATGGAtcca	29558	tcttTCTTCTTTTCATCCCAGCTGCTATAGTTCCTTACTGAAAGGTAAGTTGCTATAGTAAGGGCAACAGACCCGAGGCGTTGGGGATCGCCTAGCCCGTGTTTACGGGCTCTCCCCATATTCAAAATAATGACAGACGAGCACCTTGGAGCATTTATCTCCGAGGTGCT	29735
321	ScaCas9-Sc++	+	TGGGCTTGGATCCATGTCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCcCGAGTCTTCCACTGCACACAGTACATCAGACATGGATccaa	29559	TCTTTTCATCCCAGCTTGCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGC	29736
322	SpyCas9-SpRY	+	TGGGCTTGGATCCATGTCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCcCGAGTCTTCCACTGCACACAGTACATCAGACATGGATccaa	29560	TCTTTTCATCCCAGCTTGCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGC	29737

323	SpyCas9-SpRY	-	TGGCCTGCTTTCCTCTCGGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCcTCGGAAGGCCAGGCCACCCAAGAAATCCCGAGAGGAAagca	29561	GCAACTGGTAGCTGGAGGACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGC	29738
324	BlatCas9	-	ggctGGCCTGCTTTCCTCTCGGGGCTATAGTTCCTTACTGAAAGGTAAGTTGCTATAGTAAGGGCAACAGACCCGAGGCGTTGGGGATCGCCTAGCCCGTGTTTACGGGCTCTCCCCATATTCAAAATAATGACAGACGAGCACCTTGGAGCATTTATCTCCGAGGTGCTcTCGGAAGGCCAGGCCACCCAAGAAATCCCGAGAGGAAagca	29562	ctggCAACTGGTAGCTGGAGGACGCTATAGTTCCTTACTGAAAGGTAAGTTGCTATAGTAAGGGCAACAGACCCGAGGCGTTGGGGATCGCCTAGCCCGTGTTTACGGGCTCTCCCCATATTCAAAATAATGACAGACGAGCACCTTGGAGCATTTATCTCCGAGGTGCT	29739
325	BlatCas9	-	ggctGGCCTGCTTTCCTCTCGGGGCTATAGTTCCTTACTGAAAGGTAAGTTGCTATAGTAAGGGCAACAGACCCGAGGCGTTGGGGATCGCCTAGCCCGTGTTTACGGGCTCTCCCCATATTCAAAATAATGACAGACGAGCACCTTGGAGCATTTATCTCCGAGGTGCTcTCGGAAGGCCAGGCCACCCAAGAAATCCCGAGAGGAAagca	29563	ctggCAACTGGTAGCTGGAGGACGCTATAGTTCCTTACTGAAAGGTAAGTTGCTATAGTAAGGGCAACAGACCCGAGGCGTTGGGGATCGCCTAGCCCGTGTTTACGGGCTCTCCCCATATTCAAAATAATGACAGACGAGCACCTTGGAGCATTTATCTCCGAGGTGCT	29740
327	SpyCas9-SpRY	+	ATGGGCTTGGATCCATGTCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCGAGTCTTCCACTGCACACAGTACATCAGACATGGATCcaag	29564	CTTTTCATCCCAGCTTGCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGC	29741
329	SpyCas9-SpRY	-	CTGGCCTGCTTTCCTCTCGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTCGGAAGGCCAGGCCACCCAAGAAATCCCGAGAGGAAAgcag	29565	CAACTGGTAGCTGGAGGACAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGC	29742
332	SpyCas9-NG	+	CATGGGCTTGGATCCATGTCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGAGTCTTCCACTGCACACAGTACATCAGACATGGATCCaagc	29566	TTTTCATCCCAGCTTGCACTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGC	29743
335	SpyCas9-NG	-	GCTGGCCTGCTTTCCTCTCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCGGAAGGCCAGGCCACCCAAGAAATCCCGAGAGGAAAGcagg	29567	GCAACTGGTAGCTGGAGGACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGC	29744

339	SpyCas9-SpRY	+	CATGGGCTTGGATCCATGTCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGAGTCTTCCACTGCACACAGTACATCAGACATGGATCCaagc	29568	TTTTCATCCCAGCTTGCACTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGC	29745
341	SpyCas9-SpRY	-	GCTGGCCTGCTTTCCTCTCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCGGAAGGCCAGGCCACCCAAGAAATCCCGAGAGGAAAGcagg	29569	AACTGGTAGCTGGAGGACAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGC	29746
350	ScaCas9-Sc++	+	ACATGGGCTTGGATCCATGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAGTCTTCCACTGCACACAGTACATCAGACATGGATCCAagcc	29570	CTTTTCATCCCAGCTTGCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGC	29747
351	SpyCas9-SpRY	+	ACATGGGCTTGGATCCATGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAGTCTTCCACTGCACACAGTACATCAGACATGGATCCAagcc	29571	TTTCATCCCAGCTTGCACTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGC	29748
354	ScaCas9-Sc++	-	GGCTGGCCTGCTTTCCTCTCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGGAAGGCCAGGCCACCCAAGAAATCCCGAGAGGAAAGCaggc	29572	GTAGCTGGAGGACAGTACTCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGC	29749
355	SpyCas9	-	GGCTGGCCTGCTTTCCTCTCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGGAAGGCCAGGCCACCCAAGAAATCCCGAGAGGAAAGCaggc	29573	TAGCTGGAGGACAGTACTCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGC	29750
358	SpyCas9-SpRY	-	GGCTGGCCTGCTTTCCTCTCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGGAAGGCCAGGCCACCCAAGAAATCCCGAGAGGAAAGCaggc	29574	ACTGGTAGCTGGAGGACAGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGC	29751
359	SpyCas9-NG	-	GGCTGGCCTGCTTTCCTCTCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGGAAGGCCAGGCCACCCAAGAAATCCCGAGAGGAAAGCaggc	29575	GCAACTGGTAGCTGGAGGACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGC	29752

Table 4C. Exemplary template RNA sequences and second nick gRNA spacer sequences

Table 4C provides design of RNA components of gene modifying systems for correcting the pathogenic R243Q, mutation in PAH. The gRNA spacers from Table 1C were filtered, e.g., filtered by occurrence within 15 nt of the desired editing location and use of a Tier 1 Cas enzyme. For each gRNA ID, this table details the sequence of a complete template RNA, optional second-nick gRNA, and Cas variant for use in a Cas-RT fusion gene modifying polypeptide. For exemplification, PBS sequences and post-edit homology regions (after the location of the edit) are set to 12 nt and 30 nt, respectively. Additionally, a second-nick gRNA is selected with preference for a distance near 100 nt from the first nick and a first preference for a design resulting in a PAM-in system, as described elsewhere in this application.

ID	Cas species	strand	Template RNA	SEQ ID NO	second-nick gRNA	SEQ ID NO
3	ScaCas9-Sc++	-	CACTGGTTTCCGCCTCCAACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCcccgagaggaaagcaggccagccacaggTCGGAGGCGGaaac	29753	CACGGTTCGGGGGTATACATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGC	29938
4	SpyCas9-SpRY	-	CACTGGTTTCCGCCTCCAACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCcccgagaggaaagcaggccagccacaggTCGGAGGCGGaaac	29754	ACGGTTCGGGGGTATACATGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGC	29939
5	SauriCas9	+	AAGCAGGCCAGCCACAGGTTGGTTTTAGTACTCTGGAAACAGAATCTACTAAAACAAGGCAAAATGCCGTGTTTTATCTCGTCAACTTGTTGGCGAGAatcccagcttgcactggtttccgcctcCGACCTGTGGCtggc	29755	TGTGTACTACTCCACTACCTAGTTTTAGTACTCTGGAAACAGAATCTACTAAAACAAGGCAAAATGCCGTGTTTATCTCGTCAACTTGTTGGCGAGA	29940
6	SauriCas9-KKH	+	AAGCAGGCCAGCCACAGGTTGGTTTTAGTACTCTGGAAACAGAATCTACTAAAACAAGGCAAAATGCCGTGTTTATCTCGTCAACTTGTTGGCGAGAatcccagcttgcactggtttccgcctcCGACCTGTGGCtggc	29756	ATGTGTACTACTCCACTACCTGTTTTAGTACTCTGGAAACAGAATCTACTAAAACAAGGCAAAATGCCGTGTTTATCTCGTCAACTTGTTGGCGAGA	29941
9	ScaCas9-Sc++	+	AGCAGGCCAGCCACAGGTTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCatcccagcttgcactggtttccgcctcCGACCTGTGGCtggc	29757	GTGTACTACTCCACTACCTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGC	29942
10	SpyCas9-SpRY	+	AGCAGGCCAGCCACAGGTTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCatcccagcttgcactggtttccgcctcCGACCTGTGGCtggc	29758	CAGTTATGTGTACTACTCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGC	29943

11	SpyCas9-SpRY	-	GCACTGGTTTCCGCCTCCAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCccgagaggaaagcaggccagccacaggTCGGAGGCGGAaacc	29759	CGGTTCGGGGGTATACATGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGC	29944
12	BlatCas9	+	gaaaGCAGGCCAGCCACAGGTTGGCTATAGTTCCTTACTGAAAGGTAAGTTGCTATAGTAAGGGCAACAGACCCGAGGCGTTGGGGATCGCCTAGCCCGTGTTTACGGGCTCTCCCCATATTCAAAATAATGACAGACGAGCACCTTGGAGCATTTATCTCCGAGGTGCTatcccagcttgcactggtttccgcctcCGACCTGTGGCtggc	29760	gggcAGTTATGTGTACTACTCCAGCTATAGTTCCTTACTGAAAGGTAAGTTGCTATAGTAAGGGCAACAGACCCGAGGCGTTGGGGATCGCCTAGCCCGTGTTTACGGGCTCTCCCCATATTCAAAATAATGACAGACGAGCACCTTGGAGCATTTATCTCCGAGGTGCT	29945
13	BlatCas9	+	gaaaGCAGGCCAGCCACAGGTTGGCTATAGTTCCTTACTGAAAGGTAAGTTGCTATAGTAAGGGCAACAGACCCGAGGCGTTGGGGATCGCCTAGCCCGTGTTTACGGGCTCTCCCCATATTCAAAATAATGACAGACGAGCACCTTGGAGCATTTATCTCCGAGGTGCTatcccagcttgcactggtttccgcctcCGACCTGTGGCtggc	29761	gggcAGTTATGTGTACTACTCCAGCTATAGTTCCTTACTGAAAGGTAAGTTGCTATAGTAAGGGCAACAGACCCGAGGCGTTGGGGATCGCCTAGCCCGTGTTTACGGGCTCTCCCCATATTCAAAATAATGACAGACGAGCACCTTGGAGCATTTATCTCCGAGGTGCT	29946
14	SauCas9KKH	+	AAAGCAGGCCAGCCACAGGTTGTTTTAGTACTCTGGAAACAGAATCTACTAAAACAAGGCAAAATGCCGTGTTTTATCTCGTCAACTTGTTGGCGAGAtcccagcttgcactggtttccgcctcCGACCTGTGGCTggcc	29762	GTTATGTGTACTACTCCACTAGTTTTAGTACTCTGGAAACAGAATCTACTAAAACAAGGCAAAATGCCGTGTTTATCTCGTCAACTTGTTGGCGAGA	29947
15	SauriCas9-KKH	+	AAAGCAGGCCAGCCACAGGTTGTTTTAGTACTCTGGAAACAGAATCTACTAAAACAAGGCAAAATGCCGTGTTTTATCTCGTCAACTTGTTGGCGAGAtcccagcttgcactggtttccgcctcCGACCTGTGGCTggcc	29763	ATGTGTACTACTCCACTACCTGTTTTAGTACTCTGGAAACAGAATCTACTAAAACAAGGCAAAATGCCGTGTTTATCTCGTCAACTTGTTGGCGAGA	29948
17	SpyCas9-NG	+	AAGCAGGCCAGCCACAGGTTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCtcccagcttgcactggtttccgcctcCGACCTGTGGCTggcc	29764	TGTACTACTCCACTACCTAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGC	29949
21	SpyCas9-SpRY	+	AAGCAGGCCAGCCACAGGTTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCtcccagcttgcactggtttccgcctcCGACCTGTGGCTggcc	29765	AGTTATGTGTACTACTCCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGC	29950
22	SpyCas9-SpRY	-	TGCACTGGTTTCCGCCTCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCcgagaggaaagcaggccagccacaggTCGGAGGCGGAAacca	29766	GGTTCGGGGGTATACATGGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGC	29951
25	SauCas9	+	agGAAAGCAGGCCAGCCACAGGTGTTTTAGTACTCTGGAAACAGAATCTACTAAAACAAGGCAAAATGCCGT	29767	gcCTAGCGTCAAAGCCTATGTCCGTTTTAGTACTCTGGAAACAGAATCTACTAAAACAAGGCAAA	29952

			GTTTATCTCGTCAACTTGTTGGCGAGAcccagcttgcactggttccgcctcCGACCTGTGGCTGgcct		ATGCCGTGTTTATCTCGTCAACTTGTTGGCGAGA	
26	SauCas9KKH	+	GAAAGCAGGCCAGCCACAGGTGTTTTAGTACTCTGGAAACAGAATCTACTAAAACAAGGCAAAATGCCGTGTTTATCTCGTCAACTTGTTGGCGAGAcccagcttgcactggtttccgcctcCGACCTGTGGCTGgcct	29768	GTTATGTGTACTACTCCACTAGTTTTAGTACTCTGGAAACAGAATCTACTAAAACAAGGCAAAATGCCGTGTTTATCTCGTCAACTTGTTGGCGAGA	29953
29	ScaCas9-Sc++	+	AAAGCAGGCCAGCCACAGGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCcccagcttgcactggtttccgcctcCGACCTGTGGCTGgcct	29769	GTGTACTACTCCACTACCTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGC	29954
30	SpyCas9	+	AAAGCAGGCCAGCCACAGGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCcccagcttgcactggtttccgcctcCGACCTGTGGCTGgcct	29770	TGTACTACTCCACTACCTAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGC	29955
33	SpyCas9-SpRY	+	AAAGCAGGCCAGCCACAGGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCcccagcttgcactggtttccgcctcCGACCTGTGGCTGgcct	29771	GTTATGTGTACTACTCCACTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGC	29956
34	SpyCas9-NG	+	AAAGCAGGCCAGCCACAGGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCcccagcttgcactggtttccgcctcCGACCTGTGGCTGgcct	29772	TGTACTACTCCACTACCTAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGC	29957
37	SpyCas9-SpRY	-	TTGCACTGGTTTCCGCCTCCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCgagaggaaagcaggccagccacaggTCGGAGGCGGAAAccag	29773	GTTCGGGGGTATACATGGGCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGC	29958
42	SauCas9	+	gaGGAAAGCAGGCCAGCCACAGGGTTTTAGTACTCTGGAAACAGAATCTACTAAAACAAGGCAAAATGCCGTGTTTATCTCGTCAACTTGTTGGCGAGAccagcttgcactggtttccgcctcCGACCTGTGGCTGGcctg	29774	gcCTAGCGTCAAAGCCTATGTCCGTTTTAGTACTCTGGAAACAGAATCTACTAAAACAAGGCAAAATGCCGTGTTTATCTCGTCAACTTGTTGGCGAGA	29959
43	SauCas9KKH	+	GGAAAGCAGGCCAGCCACAGGGTTTTAGTACTCTGGAAACAGAATCTACTAAAACAAGGCAAAATGCCGTGTTTATCTCGTCAACTTGTTGGCGAGAccagcttgcactggtttccgcctcCGACCTGTGGCTGGcctg	29775	GTTATGTGTACTACTCCACTAGTTTTAGTACTCTGGAAACAGAATCTACTAAAACAAGGCAAAATGCCGTGTTTATCTCGTCAACTTGTTGGCGAGA	29960
44	SauriCas9	+	GGAAAGCAGGCCAGCCACAGGGTTTTAGTACTCTGGAAACAGAATCTACTAAAACAAGGCAAAATGCCGTGTTTATCTCGTCAACTTGTTGGCGAGAccagcttgcactggtttccgcctcCGACCTGTGGCTGGcctg	29776	TGTGTACTACTCCACTACCTAGTTTTAGTACTCTGGAAACAGAATCTACTAAAACAAGGCAAAATGCCGTGTTTATCTCGTCAACTTGTTGGCGAGA	29961

45	SauriCas9-KKH	+	GGAAAGCAGGCCAGCCACAGGGTTTTAGTACTCTGGAAACAGAATCTACTAAAACAAGGCAAAATGCCGTGTTTATCTCGTCAACTTGTTGGCGAGAccagcttgcactggtttccgcctcCGACCTGTGGCTGGcctg	29777	ATGTGTACTACTCCACTACCTGTTTTAGTACTCTGGAAACAGAATCTACTAAAACAAGGCAAAATGCCGTGTTTATCTCGTCAACTTGTTGGCGAGA	29962
48	ScaCas9-Sc++	+	GAAAGCAGGCCAGCCACAGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCccagcttgcactggtttccgcctcCGACCTGTGGCTGGcctg	29778	GTGTACTACTCCACTACCTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGC	29963
49	SpyCas9-SpRY	+	GAAAGCAGGCCAGCCACAGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCccagcttgcactggtttccgcctcCGACCTGTGGCTGGcctg	29779	TTATGTGTACTACTCCACTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGC	29964
50	SpyCas9-SpRY	-	CTTGCACTGGTTTCCGCCTCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCagaggaaagcaggccagccacaggTCGGAGGCGGAAACcagt	29780	TTCGGGGGTATACATGGGCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGC	29965
51	BlatCas9	-	cagcTTGCACTGGTTTCCGCCTCGCTATAGTTCCTTACTGAAAGGTAAGTTGCTATAGTAAGGGCAACAGACCCGAGGCGTTGGGGATCGCCTAGCCCGTGTTTACGGGCTCTCCCCATATTCAAAATAATGACAGACGAGCACCTTGGAGCATTTATCTCCGAGGTGCTagaggaaagcaggccagccacaggTCGGAGGCGGAAACcagt	29781	ggttCGGGGGTATACATGGGCTTGCTATAGTTCCTTACTGAAAGGTAAGTTGCTATAGTAAGGGCAACAGACCCGAGGCGTTGGGGATCGCCTAGCCCGTGTTTACGGGCTCTCCCCATATTCAAAATAATGACAGACGAGCACCTTGGAGCATTTATCTCCGAGGTGCT	29966
52	BlatCas9	-	cagcTTGCACTGGTTTCCGCCTCGCTATAGTTCCTTACTGAAAGGTAAGTTGCTATAGTAAGGGCAACAGACCCGAGGCGTTGGGGATCGCCTAGCCCGTGTTTACGGGCTCTCCCCATATTCAAAATAATGACAGACGAGCACCTTGGAGCATTTATCTCCGAGGTGCTagaggaaagcaggccagccacaggTCGGAGGCGGAAACcagt	29782	ggttCGGGGGTATACATGGGCTTGCTATAGTTCCTTACTGAAAGGTAAGTTGCTATAGTAAGGGCAACAGACCCGAGGCGTTGGGGATCGCCTAGCCCGTGTTTACGGGCTCTCCCCATATTCAAAATAATGACAGACGAGCACCTTGGAGCATTTATCTCCGAGGTGCT	29967
57	Nme2Cas9	-	ccCAGCTTGCACTGGTTTCCGCCTGTTGTAGCTCCCTTTCTCATTTCGGAAACGAAATGAGAACCGTTGCTACAATAAGGCCGTCTGAAAAGATGTGCCGCAACGCTCTGCCCCTTAAAGCTTCTGCTTTAAGGGGCATCGTTTAgaggaaagcaggccagccacaggTCGGAGGCGGAAACCagtg	29783	cgGTTCGGGGGTATACATGGGCTTGTTGTAGCTCCCTTTCTCATTTCGGAAACGAAATGAGAACCGTTGCTACAATAAGGCCGTCTGAAAAGATGTGCCGCAACGCTCTGCCCCTTAAAGCTTCTGCTTTAAGGGGCATCGTTTA	29968
58	SauCas9KKH	+	AGGAAAGCAGGCCAGCCACAGGTTTTAGTACTCTGGAAACAGAATCTACTAAAACAAGGCAAAATGCCGTGTTTATCTCGTCAACTTGTTGGCGAGAcagcttgcactggtttccgcctcCGACCTGTGGCTGGCctgc	29784	TTATGTGTACTACTCCACTACGTTTTAGTACTCTGGAAACAGAATCTACTAAAACAAGGCAAAATGCCGTGTTTATCTCGTCAACTTGTTGGCGAGA	29969

59	SpyCas9-SpRY	+	GGAAAGCAGGCCAGCCACAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCcagcttgcactggtttccgcctcCGACCTGTGGCTGGCctgc	29785	TATGTGTACTACTCCACTACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGC	29970
60	SpyCas9-SpRY	-	GCTTGCACTGGTTTCCGCCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCgaggaaagcaggccagccacaggTCGGAGGCGGAAACCagtg	29786	TCGGGGGTATACATGGGCTTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGC	29971
61	BlatCas9	-	ccagCTTGCACTGGTTTCCGCCTGCTATAGTTCCTTACTGAAAGGTAAGTTGCTATAGTAAGGGCAACAGACCCGAGGCGTTGGGGATCGCCTAGCCCGTGTTTACGGGCTCTCCCCATATTCAAAATAATGACAGACGAGCACCTTGGAGCATTTATCTCCGAGGTGCTgaggaaagcaggccagccacaggTCGGAGGCGGAAACCagtg	29787	ggttCGGGGGTATACATGGGCTTGCTATAGTTCCTTACTGAAAGGTAAGTTGCTATAGTAAGGGCAACAGACCCGAGGCGTTGGGGATCGCCTAGCCCGTGTTTACGGGCTCTCCCCATATTCAAAATAATGACAGACGAGCACCTTGGAGCATTTATCTCCGAGGTGCT	29972
62	BlatCas9	-	ccagCTTGCACTGGTTTCCGCCTGCTATAGTTCCTTACTGAAAGGTAAGTTGCTATAGTAAGGGCAACAGACCCGAGGCGTTGGGGATCGCCTAGCCCGTGTTTACGGGCTCTCCCCATATTCAAAATAATGACAGACGAGCACCTTGGAGCATTTATCTCCGAGGTGCTgaggaaagcaggccagccacaggTCGGAGGCGGAAACCagtg	29788	ggttCGGGGGTATACATGGGCTTGCTATAGTTCCTTACTGAAAGGTAAGTTGCTATAGTAAGGGCAACAGACCCGAGGCGTTGGGGATCGCCTAGCCCGTGTTTACGGGCTCTCCCCATATTCAAAATAATGACAGACGAGCACCTTGGAGCATTTATCTCCGAGGTGCT	29973
64	SauCas9KKH	-	CAGCTTGCACTGGTTTCCGCCGTTTTAGTACTCTGGAAACAGAATCTACTAAAACAAGGCAAAATGCCGTGTTTATCTCGTCAACTTGTTGGCGAGAaggaaagcaggccagccacaggTCGGAGGCGGAAACCAgtgc	29789	GGTTCGGGGGTATACATGGGCGTTTTAGTACTCTGGAAACAGAATCTACTAAAACAAGGCAAAATGCCGTGTTTATCTCGTCAACTTGTTGGCGAGA	29974
65	SpyCas9-NG	+	AGGAAAGCAGGCCAGCCACAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCagcttgcactggtttccgcctcCGACCTGTGGCTGGCCtgct	29790	TGTACTACTCCACTACCTAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGC	29975
69	SpyCas9-SpRY	+	AGGAAAGCAGGCCAGCCACAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCagcttgcactggtttccgcctcCGACCTGTGGCTGGCCtgct	29791	ATGTGTACTACTCCACTACCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGC	29976
70	SpyCas9-SpRY	-	AGCTTGCACTGGTTTCCGCCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCaggaaagcaggccagccacaggTCGGAGGCGGAAACCAgtgc	29792	CGGGGGTATACATGGGCTTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGC	29977
76	ScaCas9-Sc++	+	GAGGAAAGCAGGCCAGCCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACT	29793	GTGTACTACTCCACTACCTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGC	29978

			TGAAAAAGTGGCACCGAGTCGGTGCgcttgcactggtttccgcctcCGACCTGTGGCTGGCCTgctt			
77	SpyCas9	+	GAGGAAAGCAGGCCAGCCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCgcttgcactggtttccgcctcCGACCTGTGGCTGGCCTgctt	29794	TGTACTACTCCACTACCTAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGC	29979
80	SpyCas9-SpRY	+	GAGGAAAGCAGGCCAGCCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCgcttgcactggtttccgcctcCGACCTGTGGCTGGCCTgctt	29795	TGTGTACTACTCCACTACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGC	29980
81	SpyCas9-NG	+	GAGGAAAGCAGGCCAGCCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCgcttgcactggtttccgcctcCGACCTGTGGCTGGCCTgctt	29796	TGTACTACTCCACTACCTAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGC	29981
84	SpyCas9-SpRY	-	CAGCTTGCACTGGTTTCCGCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCggaaagcaggccagccacaggTCGGAGGCGGAAACCAGtgca	29797	GGGGGTATACATGGGCTTGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGC	29982
86	SauriCas9	+	GAGAGGAAAGCAGGCCAGCCAGTTTTAGTACTCTGGAAACAGAATCTACTAAAACAAGGCAAAATGCCGTGTTTATCTCGTCAACTTGTTGGCGAGActtgcactggtttccgcctcCGACCTGTGGCTGGCCTGcttt	29798	TGTGTACTACTCCACTACCTAGTTTTAGTACTCTGGAAACAGAATCTACTAAAACAAGGCAAAATGCCGTGTTTATCTCGTCAACTTGTTGGCGAGA	29983
87	SauriCas9-KKH	+	GAGAGGAAAGCAGGCCAGCCAGTTTTAGTACTCTGGAAACAGAATCTACTAAAACAAGGCAAAATGCCGTGTTTATCTCGTCAACTTGTTGGCGAGActtgcactggtttccgcctcCGACCTGTGGCTGGCCTGcttt	29799	TGTGTACTACTCCACTACCTAGTTTTAGTACTCTGGAAACAGAATCTACTAAAACAAGGCAAAATGCCGTGTTTATCTCGTCAACTTGTTGGCGAGA	29984
90	ScaCas9-Sc++	+	AGAGGAAAGCAGGCCAGCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCcttgcactggtttccgcctccCGACCTGTGGCTGGCCTGcttt	29800	GTGTACTACTCCACTACCTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGC	29985
91	SpyCas9-SpRY	+	AGAGGAAAGCAGGCCAGCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCcttgcactggtttccgcctccCGACCTGTGGCTGGCCTGcttt	29801	GTGTACTACTCCACTACCTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGC	29986
92	SpyCas9-SpRY	-	CCAGCTTGCACTGGTTTCCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCgaaagcaggccagccacaggTCGGAGGCGGAAACCAGTgcaa	29802	GGGGTATACATGGGCTTGGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGC	29987

93	BlatCas9	-	atccCAGCTTGCACTGGTTTCCGGCTATAGTTCCTTACTGAAAGGTAAGTTGCTATAGTAAGGGCAACAGACCCGAGGCGTTGGGGATCGCCTAGCCCGTGTTTACGGGCTCTCCCCATATTCAAAATAATGACAGACGAGCACCTTGGAGCATTTATCTCCGAGGTGCTgaaagcaggccagccacaggTCGGAGGCGGAAACCAGTgcaa	29803	gttcGGGGGTATACATGGGCTTGGCTATAGTTCCTTACTGAAAGGTAAGTTGCTATAGTAAGGGCAACAGACCCGAGGCGTTGGGGATCGCCTAGCCCGTGTTTACGGGCTCTCCCCATATTCAAAATAATGACAGACGAGCACCTTGGAGCATTTATCTCCGAGGTGCT	29988
96	Nme2Cas9	-	tcATCCCAGCTTGCACTGGTTTCCGTTGTAGCTCCCTTTCTCATTTCGGAAACGAAATGAGAACCGTTGCTACAATAAGGCCGTCTGAAAAGATGTGCCGCAACGCTCTGCCCCTTAAAGCTTCTGCTTTAAAAgcaggccagccacaggTCGGAGGCGGAAACCAGTGcaag	29804	cgGTTCGGGGGTATACATGGGCTTGTTGTAGCTCCCTTTCTCATTTCGGAAACGAAATGAGAACCGTTGCTACAATAAGGCCGTCTGAAAAGATGTGCCGCAACGCTCTGCCCCTTAAAGCTTCTGCTTTAAGGGGCATCGTTTA	29989
97	PpnCas9	+	tccCGAGAGGAAAGCAGGCCAGCCGTTGTAGCTCCCTTTTTCATTTCGCGAAAGCGAAATGAAAAACGTTGTTACAATAAGAGATGAATTTCTCGCAAAGCTCTGCCTCTTGAAATTTCGGTTTCAAGAGGCATCttgcactggtttccgcctcCGACCTGTGGCTGGCCTGCtttc	29805	ctaGCGTCAAAGCCTATGTCCCTGGTTGTAGCTCCCTTTTTCATTTCGCGAAAGCGAAATGAAAAACGTTGTTACAATAAGAGATGAATTTCTCGCAAAGCTCTGCCTCTTGAAATTTCGGTTTCAAGAGGCATC	29990
98	SauCas9KKH	+	CGAGAGGAAAGCAGGCCAGCCGTTTTAGTACTCTGGAAACAGAATCTACTAAAACAAGGCAAAATGCCGTGTTTTATCTCGTCAACTTGTTGGCGAGAttgcactggtttccgcctcCGACCTGTGGCTGGCCTGCtttc	29806	ATGTGTACTACTCCACTACCTGTTTTAGTACTCTGGAAACAGAATCTACTAAAACAAGGCAAAATGCCGTGTTTATCTCGTCAACTTGTTGGCGAGA	29991
99	SauCas9KKH	+	CGAGAGGAAAGCAGGCCAGCCGTTTTAGTACTCTGGAAACAGAATCTACTAAAACAAGGCAAAATGCCGTGTTTATCTCGTCAACTTGTTGGCGAGAttgcactggtttccgcctcCGACCTGTGGCTGGCCTGCtttc	29807	ATGTGTACTACTCCACTACCTGTTTTAGTACTCTGGAAACAGAATCTACTAAAACAAGGCAAAATGCCGTGTTTATCTCGTCAACTTGTTGGCGAGA	29992
102	SauriCas9-KKH	+	CGAGAGGAAAGCAGGCCAGCCGTTTTAGTACTCTGGAAACAGAATCTACTAAAACAAGGCAAAATGCCGTGTTTATCTCGTCAACTTGTTGGCGAGAttgcactggtttccgcctcCGACCTGTGGCTGGCCTGCtttc	29808	TGTGTACTACTCCACTACCTAGTTTTAGTACTCTGGAAACAGAATCTACTAAAACAAGGCAAAATGCCGTGTTTATCTCGTCAACTTGTTGGCGAGA	29993
103	SpyCas9-SpRY	+	GAGAGGAAAGCAGGCCAGCCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCttgcactggtttccgcctcCGACCTGTGGCTGGCCTGCtttc	29809	TGTACTACTCCACTACCTAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGC	29994
104	SpyCas9-SpRY	-	CCCAGCTTGCACTGGTTTCCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCaaagcaggccagccacaggTCGGAGGCGGAAACCAGTGcaag	29810	GGGTATACATGGGCTTGGATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGC	29995
105	BlatCas9	-	catcCCAGCTTGCACTGGTTTCCGCTATAGTTCCTTACTGAAAGGTAAGTTGCTATAGTAAGGGCAACAGACCCGAGGCGTTGGGGATCGCCTAGCCCGTGTTTACGGGCT	29811	ggggTATACATGGGCTTGGATCCGCTATAGTTCCTTACTGAAAGGTAAGTTGCTATAGTAAGGGCAACAGACCCGAGGCGTTGGGGATCGCCTAGCCC	29996

			CTCCCCATATTCAAAATAATGACAGACGAGCACCTT GGAGCATTTATCTCCGAGGTGCTaaagcaggccagccacaggT CGGAGGCGGAAACCAGTGcaag		GTGTTTACGGGCTCTCCCCATATTCAAAATAAT GACAGACGAGCACCTTGGAGCATTTATCTCCG AGGTGCT	
106	BlatCas9	-	catcCCAGCTTGCACTGGTTTCCGCTATAGTTCCTTACT GAAAGGTAAGTTGCTATAGTAAGGGCAACAGACCCG AGGCGTTGGGGATCGCCTAGCCCGTGTTTACGGGCT CTCCCCATATTCAAAATAATGACAGACGAGCACCTT GGAGCATTTATCTCCGAGGTGCTaaagcaggccagccacaggT CGGAGGCGGAAACCAGTGcaag	29812	ggggTATACATGGGCTTGGATCCGCTATAGTTCC TTACTGAAAGGTAAGTTGCTATAGTAAGGGCA ACAGACCCGAGGCGTTGGGGATCGCCTAGCCC GTGTTTACGGGCTCTCCCCATATTCAAAATAAT GACAGACGAGCACCTTGGAGCATTTATCTCCG AGGTGCT	29997
107	BlatCas9	-	catcCCAGCTTGCACTGGTTTCCGCTATAGTTCCTTACT GAAAGGTAAGTTGCTATAGTAAGGGCAACAGACCCG AGGCGTTGGGGATCGCCTAGCCCGTGTTTACGGGCT CTCCCCATATTCAAAATAATGACAGACGAGCACCTT GGAGCATTTATCTCCGAGGTGCTaaagcaggccagccacaggT CGGAGGCGGAAACCAGTGcaag	29813	ggggTATACATGGGCTTGGATCCGCTATAGTTCC TTACTGAAAGGTAAGTTGCTATAGTAAGGGCA ACAGACCCGAGGCGTTGGGGATCGCCTAGCCC GTGTTTACGGGCTCTCCCCATATTCAAAATAAT GACAGACGAGCACCTTGGAGCATTTATCTCCG AGGTGCT	29998
108	SauCas9KKH	+	CCGAGAGGAAAGCAGGCCAGCGTTTTAGTACTCTGG AAACAGAATCTACTAAAACAAGGCAAAATGCCGTGT TTATCTCGTCAACTTGTTGGCGAGAtgcactggtttccgcctcC GACCTGTGGCTGGCCTGCTttcc	29814	ATGTGTACTACTCCACTACCTGTTTTAGTACTC TGGAAACAGAATCTACTAAAACAAGGCAAAAT GCCGTGTTTATCTCGTCAACTTGTTGGCGAGA	29999
109	SpyCas9-NG	-	TCCCAGCTTGCACTGGTTTCGTTTTAGAGCTAGAAAT AGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTG AAAAAGTGGCACCGAGTCGGTGCaagcaggccagccacaggT CGGAGGCGGAAACCAGTGCaagc	29815	TATACATGGGCTTGGATCCAGTTTTAGAGCTA GAAATAGCAAGTTAAAATAAGGCTAGTCCGTT ATCAACTTGAAAAAGTGGCACCGAGTCGGTGC	30000
112	SpyCas9-SpRY	+	CGAGAGGAAAGCAGGCCAGCGTTTTAGAGCTAGAA ATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACT TGAAAAAGTGGCACCGAGTCGGTGCtgcactggtttccgcctc CGACCTGTGGCTGGCCTGCTttcc	29816	GTACTACTCCACTACCTAAAGTTTTAGAGCTAG AAATAGCAAGTTAAAATAAGGCTAGTCCGTTA TCAACTTGAAAAAGTGGCACCGAGTCGGTGC	30001
114	SpyCas9-SpRY	-	TCCCAGCTTGCACTGGTTTCGTTTTAGAGCTAGAAAT AGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTG AAAAAGTGGCACCGAGTCGGTGCaagcaggccagccacaggT CGGAGGCGGAAACCAGTGCaagc	29817	GGTATACATGGGCTTGGATCGTTTTAGAGCTA GAAATAGCAAGTTAAAATAAGGCTAGTCCGTT ATCAACTTGAAAAAGTGGCACCGAGTCGGTGC	30002
121	ScaCas9-Sc++	-	ATCCCAGCTTGCACTGGTTTGTTTTAGAGCTAGAAAT AGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTG AAAAAGTGGCACCGAGTCGGTGCagcaggccagccacaggT CGGAGGCGGAAACCAGTGCAagct	29818	GTATACATGGGCTTGGATCCGTTTTAGAGCTA GAAATAGCAAGTTAAAATAAGGCTAGTCCGTT ATCAACTTGAAAAAGTGGCACCGAGTCGGTGC	30003
122	SpyCas9-SpRY	-	ATCCCAGCTTGCACTGGTTTGTTTTAGAGCTAGAAAT AGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTG AAAAAGTGGCACCGAGTCGGTGCagcaggccagccacaggT CGGAGGCGGAAACCAGTGCAagct	29819	GTATACATGGGCTTGGATCCGTTTTAGAGCTA GAAATAGCAAGTTAAAATAAGGCTAGTCCGTT ATCAACTTGAAAAAGTGGCACCGAGTCGGTGC	30004

123	SpyCas9-SpRY	+	CCGAGAGGAAAGCAGGCCAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCgcactggtttccgcctcCGACCTGTGGCTGGCCTGCTTtcct	29820	TACTACTCCACTACCTAAAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGC	30005
124	BlatCas9	-	ttcaTCCCAGCTTGCACTGGTTTGCTATAGTTCCTTACTGAAAGGTAAGTTGCTATAGTAAGGGCAACAGACCCGAGGCGTTGGGGATCGCCTAGCCCGTGTTTACGGGCTCTCCCCATATTCAAAATAATGACAGACGAGCACCTTGGAGCATTTATCTCCGAGGTGCTagcaggccagccacaggTCGGAGGCGGAAACCAGTGCAagct	29821	ggggTATACATGGGCTTGGATCCGCTATAGTTCCTTACTGAAAGGTAAGTTGCTATAGTAAGGGCAACAGACCCGAGGCGTTGGGGATCGCCTAGCCCGTGTTTACGGGCTCTCCCCATATTCAAAATAATGACAGACGAGCACCTTGGAGCATTTATCTCCGAGGTGCT	30006
126	Nme2Cas9	-	ttTTCATCCCAGCTTGCACTGGTTGTTGTAGCTCCCTTTCTCATTTCGGAAACGAAATGAGAACCGTTGCTACAATAAGGCCGTCTGAAAAGATGTGCCGCAACGCTCTGCCCCTTAAAGCTTCTGCTTTAAGGGGCATCGTTTAgcaggccagccacaggTCGGAGGCGGAAACCAGTGCAAgctg	29822	cgGTTCGGGGGTATACATGGGCTTGTTGTAGCTCCCTTTCTCATTTCGGAAACGAAATGAGAACCGTTGCTACAATAAGGCCGTCTGAAAAGATGTGCCGCAACGCTCTGCCCCTTAAAGCTTCTGCTTTAAGGGGCATCGTTTA	30007
127	SpyCas9-SpRY	+	CCCGAGAGGAAAGCAGGCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCcactggtttccgcctcCGACCTGTGGCTGGCCTGCTTTcctc	29823	ACTACTCCACTACCTAAAGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGC	30008
128	SpyCas9-SpRY	-	CATCCCAGCTTGCACTGGTTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCgcaggccagccacaggTCGGAGGCGGAAACCAGTGCAAgctg	29824	TATACATGGGCTTGGATCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGC	30009
129	BlatCas9	+	aatcCCGAGAGGAAAGCAGGCCAGCTATAGTTCCTTACTGAAAGGTAAGTTGCTATAGTAAGGGCAACAGACCCGAGGCGTTGGGGATCGCCTAGCCCGTGTTTACGGGCTCTCCCCATATTCAAAATAATGACAGACGAGCACCTTGGAGCATTTATCTCCGAGGTGCTcactggtttccgcctcCGACCTGTGGCTGGCCTGCTTTcctc	29825	tgtaCTACTCCACTACCTAAAGGGCTATAGTTCCTTACTGAAAGGTAAGTTGCTATAGTAAGGGCAACAGACCCGAGGCGTTGGGGATCGCCTAGCCCGTGTTTACGGGCTCTCCCCATATTCAAAATAATGACAGACGAGCACCTTGGAGCATTTATCTCCGAGGTGCT	30010
130	BlatCas9	+	aatcCCGAGAGGAAAGCAGGCCAGCTATAGTTCCTTACTGAAAGGTAAGTTGCTATAGTAAGGGCAACAGACCCGAGGCGTTGGGGATCGCCTAGCCCGTGTTTACGGGCTCTCCCCATATTCAAAATAATGACAGACGAGCACCTTGGAGCATTTATCTCCGAGGTGCTcactggtttccgcctcCGACCTGTGGCTGGCCTGCTTTcctc	29826	tgtaCTACTCCACTACCTAAAGGGCTATAGTTCCTTACTGAAAGGTAAGTTGCTATAGTAAGGGCAACAGACCCGAGGCGTTGGGGATCGCCTAGCCCGTGTTTACGGGCTCTCCCCATATTCAAAATAATGACAGACGAGCACCTTGGAGCATTTATCTCCGAGGTGCT	30011
131	BlatCas9	-	tttcATCCCAGCTTGCACTGGTTGCTATAGTTCCTTACTGAAAGGTAAGTTGCTATAGTAAGGGCAACAGACCCGAGGCGTTGGGGATCGCCTAGCCCGTGTTTACGGGCTCTCCCCATATTCAAAATAATGACAGACGAGCACCTT	29827	ggggTATACATGGGCTTGGATCCGCTATAGTTCCTTACTGAAAGGTAAGTTGCTATAGTAAGGGCAACAGACCCGAGGCGTTGGGGATCGCCTAGCCCGTGTTTACGGGCTCTCCCCATATTCAAAATAAT	30012

			GGAGCATTTATCTCCGAGGTGCTgcaggccagccacaggTCG GAGGCGGAAACCAGTGCAAgctg		GACAGACGAGCACCTTGGAGCATTTATCTCCG AGGTGCT	
132	SpyCas9-NG	+	TCCCGAGAGGAAAGCAGGCCGTTTTAGAGCTAGAAA TAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTT GAAAAAGTGGCACCGAGTCGGTGCactggtttccgcctcCGA CCTGTGGCTGGCCTGCTTTCctct	29828	GTACTACTCCACTACCTAAAGTTTTAGAGCTAG AAATAGCAAGTTAAAATAAGGCTAGTCCGTTA TCAACTTGAAAAAGTGGCACCGAGTCGGTGC	30013
136	SpyCas9-SpRY	+	TCCCGAGAGGAAAGCAGGCCGTTTTAGAGCTAGAAA TAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTT GAAAAAGTGGCACCGAGTCGGTGCactggtttccgcctcCGA CCTGTGGCTGGCCTGCTTTCctct	29829	CTACTCCACTACCTAAAGGTGTTTTAGAGCTAG AAATAGCAAGTTAAAATAAGGCTAGTCCGTTA TCAACTTGAAAAAGTGGCACCGAGTCGGTGC	30014
137	SpyCas9-SpRY	-	TCATCCCAGCTTGCACTGGTGTTTTAGAGCTAGAAAT AGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTG AAAAAGTGGCACCGAGTCGGTGCcaggccagccacaggTCG GAGGCGGAAACCAGTGCAAGctgg	29830	ATACATGGGCTTGGATCCATGTTTTAGAGCTA GAAATAGCAAGTTAAAATAAGGCTAGTCCGTT ATCAACTTGAAAAAGTGGCACCGAGTCGGTGC	30015
141	ScaCas9-Sc++	+	ATCCCGAGAGGAAAGCAGGCGTTTTAGAGCTAGAAA TAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTT GAAAAAGTGGCACCGAGTCGGTGCctggtttccgcctcCGA CCTGTGGCTGGCCTGCTTTCCtctc	29831	TCCACTACCTAAAGGTCTCCGTTTTAGAGCTAG AAATAGCAAGTTAAAATAAGGCTAGTCCGTTA TCAACTTGAAAAAGTGGCACCGAGTCGGTGC	30016
142	SpyCas9-SpRY	+	ATCCCGAGAGGAAAGCAGGCGTTTTAGAGCTAGAAA TAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTT GAAAAAGTGGCACCGAGTCGGTGCctggtttccgcctcCGA CCTGTGGCTGGCCTGCTTTCCtctc	29832	TACTCCACTACCTAAAGGTCGTTTTAGAGCTAG AAATAGCAAGTTAAAATAAGGCTAGTCCGTTA TCAACTTGAAAAAGTGGCACCGAGTCGGTGC	30017
143	SpyCas9-SpRY	-	TTCATCCCAGCTTGCACTGGGTTTTAGAGCTAGAAAT AGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTG AAAAAGTGGCACCGAGTCGGTGCaggccagccacaggTCG GAGGCGGAAACCAGTGCAAGCtggg	29833	TACATGGGCTTGGATCCATGGTTTTAGAGCTA GAAATAGCAAGTTAAAATAAGGCTAGTCCGTT ATCAACTTGAAAAAGTGGCACCGAGTCGGTGC	30018
144	BlatCas9	+	gaaaTCCCGAGAGGAAAGCAGGCGCTATAGTTCCTTA CTGAAAGGTAAGTTGCTATAGTAAGGGCAACAGACC CGAGGCGTTGGGGATCGCCTAGCCCGTGTTTACGGG CTCTCCCCATATTCAAAATAATGACAGACGAGCACC TTGGAGCATTTATCTCCGAGGTGCTctggtttccgcctcCGA CCTGTGGCTGGCCTGCTTTCCtctc	29834	tgtaCTACTCCACTACCTAAAGGGCTATAGTTCC TTACTGAAAGGTAAGTTGCTATAGTAAGGGCA ACAGACCCGAGGCGTTGGGGATCGCCTAGCCC GTGTTTACGGGCTCTCCCCATATTCAAAATAAT GACAGACGAGCACCTTGGAGCATTTATCTCCG AGGTGCT	30019
145	BlatCas9	-	ctttTCATCCCAGCTTGCACTGGGCTATAGTTCCTTACT GAAAGGTAAGTTGCTATAGTAAGGGCAACAGACCCG AGGCGTTGGGGATCGCCTAGCCCGTGTTTACGGGCT CTCCCCATATTCAAAATAATGACAGACGAGCACCTT GGAGCATTTATCTCCGAGGTGCTaggccagccacaggTCGG AGGCGGAAACCAGTGCAAGCtggg	29835	ggggTATACATGGGCTTGGATCCGCTATAGTTCC TTACTGAAAGGTAAGTTGCTATAGTAAGGGCA ACAGACCCGAGGCGTTGGGGATCGCCTAGCCC GTGTTTACGGGCTCTCCCCATATTCAAAATAAT GACAGACGAGCACCTTGGAGCATTTATCTCCG AGGTGCT	30020

148	Nme2 Cas9	+	aaGAAATCCCGAGAGGAAAGCAGGGTTGTAGCTCCC TTTCTCATTTCGGAAACGAAATGAGAACCGTTGCTA CAATAAGGCCGTCTGAAAAGATGTGCCGCAACGCTC TGCCCCTTAAAGCTTCTGCTTTAAGGGGCATCGTTTA tggtttccgcctcCGACCTGTGGCTGGCCTGCTTTCCTctcg	29836	taCTCCACTACCTAAAGGTCTCCTGTTGTAGCTC CCTTTCTCATTTCGGAAACGAAATGAGAACCG TTGCTACAATAAGGCCGTCTGAAAAGATGTGC CGCAACGCTCTGCCCCTTAAAGCTTCTGCTTTA AGGGGCATCGTTTA	30021
149	Nme2 Cas9	-	ttCTTTTCATCCCAGCTTGCACTGGTTGTAGCTCCCTTT CTCATTTCGGAAACGAAATGAGAACCGTTGCTACAA TAAGGCCGTCTGAAAAGATGTGCCGCAACGCTCTGC CCCTTAAAGCTTCTGCTTTAAGGGGCATCGTTTAggcc agccacaggTCGGAGGCGGAAACCAGTGCAAGCTggga	29837	cgGTTCGGGGGTATACATGGGCTTGTTGTAGCT CCCTTTCTCATTTCGGAAACGAAATGAGAACC GTTGCTACAATAAGGCCGTCTGAAAAGATGTG CCGCAACGCTCTGCCCCTTAAAGCTTCTGCTTT AAGGGGCATCGTTTA	30022
150	SauriCas9-KKH	+	AAATCCCGAGAGGAAAGCAGGGTTTTAGTACTCTGG AAACAGAATCTACTAAAACAAGGCAAAATGCCGTGT TTATCTCGTCAACTTGTTGGCGAGAtggtttccgcctcCGAC CTGTGGCTGGCCTGCTTTCCTctcg	29838	ACTCCACTACCTAAAGGTCTCGTTTTAGTACTC TGGAAACAGAATCTACTAAAACAAGGCAAAAT GCCGTGTTTATCTCGTCAACTTGTTGGCGAGA	30023
151	SpyCas9-SpRY	+	AATCCCGAGAGGAAAGCAGGGTTTTAGAGCTAGAA ATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACT TGAAAAAGTGGCACCGAGTCGGTGCtggtttccgcctcCGA CCTGTGGCTGGCCTGCTTTCCTctcg	29839	ACTCCACTACCTAAAGGTCTGTTTTAGAGCTAG AAATAGCAAGTTAAAATAAGGCTAGTCCGTTA TCAACTTGAAAAAGTGGCACCGAGTCGGTGC	30024
152	SpyCas9-SpRY	-	TTTCATCCCAGCTTGCACTGGTTTTAGAGCTAGAAAT AGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTG AAAAAGTGGCACCGAGTCGGTGCggccagccacaggTCGG AGGCGGAAACCAGTGCAAGCTggga	29840	ACATGGGCTTGGATCCATGTGTTTTAGAGCTA GAAATAGCAAGTTAAAATAAGGCTAGTCCGTT ATCAACTTGAAAAAGTGGCACCGAGTCGGTGC	30025
153	BlatCas9	+	agaaATCCCGAGAGGAAAGCAGGGCTATAGTTCCTTA CTGAAAGGTAAGTTGCTATAGTAAGGGCAACAGACC CGAGGCGTTGGGGATCGCCTAGCCCGTGTTTACGGG CTCTCCCCATATTCAAAATAATGACAGACGAGCACC TTGGAGCATTTATCTCCGAGGTGCTtggtttccgcctcCGAC CTGTGGCTGGCCTGCTTTCCTctcg	29841	actcCACTACCTAAAGGTCTCCTGCTATAGTTCC TTACTGAAAGGTAAGTTGCTATAGTAAGGGCA ACAGACCCGAGGCGTTGGGGATCGCCTAGCCC GTGTTTACGGGCTCTCCCCATATTCAAAATAAT GACAGACGAGCACCTTGGAGCATTTATCTCCG AGGTGCT	30026
154	BlatCas9	-	tcttTTCATCCCAGCTTGCACTGGCTATAGTTCCTTACT GAAAGGTAAGTTGCTATAGTAAGGGCAACAGACCCG AGGCGTTGGGGATCGCCTAGCCCGTGTTTACGGGCT CTCCCCATATTCAAAATAATGACAGACGAGCACCTT GGAGCATTTATCTCCGAGGTGCTggccagccacaggTCGG AGGCGGAAACCAGTGCAAGCTggga	29842	catgGGCTTGGATCCATGTCTGAGCTATAGTTCC TTACTGAAAGGTAAGTTGCTATAGTAAGGGCA ACAGACCCGAGGCGTTGGGGATCGCCTAGCCC GTGTTTACGGGCTCTCCCCATATTCAAAATAAT GACAGACGAGCACCTTGGAGCATTTATCTCCG AGGTGCT	30027
155	SauCas9KKH	+	GAAATCCCGAGAGGAAAGCAGGTTTTAGTACTCTGG AAACAGAATCTACTAAAACAAGGCAAAATGCCGTGT TTATCTCGTCAACTTGTTGGCGAGAggtttccgcctcCGAC CTGTGGCTGGCCTGCTTTCCTCtcgg	29843	TACTCCACTACCTAAAGGTCTGTTTTAGTACTC TGGAAACAGAATCTACTAAAACAAGGCAAAAT GCCGTGTTTATCTCGTCAACTTGTTGGCGAGA	30028

156	SpyCas9-NG	-	TTTTCATCCCAGCTTGCACTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCgccagccacaggTCGGAGGCGGAAACCAGTGCAAGCTGggat	29844	CATGGGCTTGGATCCATGTCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGC	30029
160	SpyCas9-SpRY	-	TTTTCATCCCAGCTTGCACTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCgccagccacaggTCGGAGGCGGAAACCAGTGCAAGCTGggat	29845	CATGGGCTTGGATCCATGTCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGC	30030
161	SpyCas9-SpRY	+	AAATCCCGAGAGGAAAGCAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCggtttccgcctcCGACCTGTGGCTGGCCTGCTTTCCTCtcgg	29846	CTCCACTACCTAAAGGTCTCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGC	30031
167	ScaCas9-Sc++	-	CTTTTCATCCCAGCTTGCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCccagccacaggTCGGAGGCGGAAACCAGTGCAAGCTGGgatg	29847	TGGGCTTGGATCCATGTCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGC	30032
168	SpyCas9	-	CTTTTCATCCCAGCTTGCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCccagccacaggTCGGAGGCGGAAACCAGTGCAAGCTGGgatg	29848	TTCGGGGGTATACATGGGCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGC	30033
171	SpyCas9-SpRY	-	CTTTTCATCCCAGCTTGCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCccagccacaggTCGGAGGCGGAAACCAGTGCAAGCTGGgatg	29849	ATGGGCTTGGATCCATGTCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGC	30034
172	SpyCas9-NG	+	GAAATCCCGAGAGGAAAGCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCgtttccgcctcCGACCTGTGGCTGGCCTGCTTTCCTCTcggg	29850	CCACTACCTAAAGGTCTCCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGC	30035
175	SpyCas9-NG	-	CTTTTCATCCCAGCTTGCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCccagccacaggTCGGAGGCGGAAACCAGTGCAAGCTGGgatg	29851	CATGGGCTTGGATCCATGTCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGC	30036
179	SpyCas9-SpRY	+	GAAATCCCGAGAGGAAAGCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCgtttccgcctcCGACCTGTGGCTGGCCTGCTTTCCTCTcggg	29852	TCCACTACCTAAAGGTCTCCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGC	30037
183	SauriCas9	-	TTCTTTTCATCCCAGCTTGCAGTTTTAGTACTCTGGAAACAGAATCTACTAAAACAAGGCAAAATGCCGTGTT	29853	ATGTCTGATGTACTGTGTGCAGTTTTAGTACTCTGGAAACAGAATCTACTAAAACAAGGCAAAATGCCGTGTTTATCTCGTCAACTTGTTGGCGAGA	30038

			TATCTCGTCAACTTGTTGGCGAGAcagccacaggTCGGAG GCGGAAACCAGTGCAAGCTGGGatga			
184	SauriCas9-KKH	-	TTCTTTTCATCCCAGCTTGCAGTTTTAGTACTCTGGA AACAGAATCTACTAAAACAAGGCAAAATGCCGTGTT TATCTCGTCAACTTGTTGGCGAGAcagccacaggTCGGAG GCGGAAACCAGTGCAAGCTGGGatga	29854	TCCATGTCTGATGTACTGTGTGTTTTAGTACTC TGGAAACAGAATCTACTAAAACAAGGCAAAAT GCCGTGTTTATCTCGTCAACTTGTTGGCGAGA	30039
187	ScaCas9-Sc++	+	AGAAATCCCGAGAGGAAAGCGTTTTAGAGCTAGAA ATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACT TGAAAAAGTGGCACCGAGTCGGTGCtttccgcctcCGACC TGTGGCTGGCCTGCTTTCCTCTCggga	29855	CACTACCTAAAGGTCTCCTAGTTTTAGAGCTAG AAATAGCAAGTTAAAATAAGGCTAGTCCGTTA TCAACTTGAAAAAGTGGCACCGAGTCGGTGC	30040
188	SpyCas9	+	AGAAATCCCGAGAGGAAAGCGTTTTAGAGCTAGAA ATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACT TGAAAAAGTGGCACCGAGTCGGTGCtttccgcctcCGACC TGTGGCTGGCCTGCTTTCCTCTCggga	29856	TGTACTACTCCACTACCTAAGTTTTAGAGCTAG AAATAGCAAGTTAAAATAAGGCTAGTCCGTTA TCAACTTGAAAAAGTGGCACCGAGTCGGTGC	30041
191	SpyCas9-SpRY	+	AGAAATCCCGAGAGGAAAGCGTTTTAGAGCTAGAA ATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACT TGAAAAAGTGGCACCGAGTCGGTGCtttccgcctcCGACC TGTGGCTGGCCTGCTTTCCTCTCggga	29857	CCACTACCTAAAGGTCTCCTGTTTTAGAGCTAG AAATAGCAAGTTAAAATAAGGCTAGTCCGTTA TCAACTTGAAAAAGTGGCACCGAGTCGGTGC	30042
194	ScaCas9-Sc++	-	TCTTTTCATCCCAGCTTGCAGTTTTAGAGCTAGAAAT AGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTG AAAAAGTGGCACCGAGTCGGTGCcagccacaggTCGGAG GCGGAAACCAGTGCAAGCTGGGatga	29858	TGGGCTTGGATCCATGTCTGGTTTTAGAGCTAG AAATAGCAAGTTAAAATAAGGCTAGTCCGTTA TCAACTTGAAAAAGTGGCACCGAGTCGGTGC	30043
195	SpyCas9-SpRY	-	TCTTTTCATCCCAGCTTGCAGTTTTAGAGCTAGAAAT AGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTG AAAAAGTGGCACCGAGTCGGTGCcagccacaggTCGGAG GCGGAAACCAGTGCAAGCTGGGatga	29859	TGGGCTTGGATCCATGTCTGGTTTTAGAGCTAG AAATAGCAAGTTAAAATAAGGCTAGTCCGTTA TCAACTTGAAAAAGTGGCACCGAGTCGGTGC	30044
196	SpyCas9-NG	+	AGAAATCCCGAGAGGAAAGCGTTTTAGAGCTAGAA ATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACT TGAAAAAGTGGCACCGAGTCGGTGCtttccgcctcCGACC TGTGGCTGGCCTGCTTTCCTCTCggga	29860	CCACTACCTAAAGGTCTCCTGTTTTAGAGCTAG AAATAGCAAGTTAAAATAAGGCTAGTCCGTTA TCAACTTGAAAAAGTGGCACCGAGTCGGTGC	30045
199	BlatCas9	+	ccaaGAAATCCCGAGAGGAAAGCGCTATAGTTCCTTA CTGAAAGGTAAGTTGCTATAGTAAGGGCAACAGACC CGAGGCGTTGGGGATCGCCTAGCCCGTGTTTACGGG CTCTCCCCATATTCAAAATAATGACAGACGAGCACC TTGGAGCATTTATCTCCGAGGTGCTtttccgcctcCGACCT GTGGCTGGCCTGCTTTCCTCTCggga	29861	actcCACTACCTAAAGGTCTCCTGCTATAGTTCC TTACTGAAAGGTAAGTTGCTATAGTAAGGGCA ACAGACCCGAGGCGTTGGGGATCGCCTAGCCC GTGTTTACGGGCTCTCCCCATATTCAAAATAAT GACAGACGAGCACCTTGGAGCATTTATCTCCG AGGTGCT	30046
203	Nme2Cas9	+	acCCAAGAAATCCCGAGAGGAAAGGTTGTAGCTCCCT TTCTCATTTCGGAAACGAAATGAGAACCGTTGCTAC AATAAGGCCGTCTGAAAAGATGTGCCGCAACGCTCT	29862	taCTCCACTACCTAAAGGTCTCCTGTTGTAGCTC CCTTTCTCATTTCGGAAACGAAATGAGAACCG TTGCTACAATAAGGCCGTCTGAAAAGATGTGC	30047

			GCCCCTTAAAGCTTCTGCTTTAAGGGGCATCGTTTAttccgcctcCGACCTGTGGCTGGCCTGCTTTCCTCTCGgat		CGCAACGCTCTGCCCCTTAAAGCTTCTGCTTTAAGGGGCATCGTTTA	
204	PpnCas9	-	tttCTTCTTTTCATCCCAGCTTGCGTTGTAGCTCCCTTTTTCATTTCGCGAAAGCGAAATGAAAAACGTTGTTACAATAAGAGATGAATTTCTCGCAAAGCTCTGCCTCTTGAAATTTCGGTTTCAAGAGGCATCagccacaggTCGGAGGCGGAAACCAGTGCAAGCTGGGAtgaa	29863	aacTGGTAGCTGGAGGACAGTACTGTTGTAGCTCCCTTTTTCATTTCGCGAAAGCGAAATGAAAAACGTTGTTACAATAAGAGATGAATTTCTCGCAAAGCTCTGCCTCTTGAAATTTCGGTTTCAAGAGGCATC	30048
205	SauCas9KKH	-	CTTCTTTTCATCCCAGCTTGCGTTTTAGTACTCTGGAAACAGAATCTACTAAAACAAGGCAAAATGCCGTGTTTATCTCGTCAACTTGTTGGCGAGAagccacaggTCGGAGGCGGAAACCAGTGCAAGCTGGGAtgaa	29864	ATACATGGGCTTGGATCCATGGTTTTAGTACTCTGGAAACAGAATCTACTAAAACAAGGCAAAATGCCGTGTTTATCTCGTCAACTTGTTGGCGAGA	30049
206	SauCas9KKH	-	CTTCTTTTCATCCCAGCTTGCGTTTTAGTACTCTGGAAACAGAATCTACTAAAACAAGGCAAAATGCCGTGTTTATCTCGTCAACTTGTTGGCGAGAagccacaggTCGGAGGCGGAAACCAGTGCAAGCTGGGAtgaa	29865	ATACATGGGCTTGGATCCATGGTTTTAGTACTCTGGAAACAGAATCTACTAAAACAAGGCAAAATGCCGTGTTTATCTCGTCAACTTGTTGGCGAGA	30050
207	SauriCas9	+	CAAGAAATCCCGAGAGGAAAGGTTTTAGTACTCTGGAAACAGAATCTACTAAAACAAGGCAAAATGCCGTGTTTTATCTCGTCAACTTGTTGGCGAGAttccgcctcCGACCTGTGGCTGGCCTGCTTTCCTCTCGgat	29866	TGTGTACTACTCCACTACCTAGTTTTAGTACTCTGGAAACAGAATCTACTAAAACAAGGCAAAATGCCGTGTTTATCTCGTCAACTTGTTGGCGAGA	30051
208	SauriCas9-KKH	+	CAAGAAATCCCGAGAGGAAAGGTTTTAGTACTCTGGAAACAGAATCTACTAAAACAAGGCAAAATGCCGTGTTTTATCTCGTCAACTTGTTGGCGAGAttccgcctcCGACCTGTGGCTGGCCTGCTTTCCTCTCGgat	29867	ACTCCACTACCTAAAGGTCTCGTTTTAGTACTCTGGAAACAGAATCTACTAAAACAAGGCAAAATGCCGTGTTTATCTCGTCAACTTGTTGGCGAGA	30052
211	ScaCas9-Sc++	+	AAGAAATCCCGAGAGGAAAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCttccgcctcCGACCTGTGGCTGGCCTGCTTTCCTCTCGgat	29868	CACTACCTAAAGGTCTCCTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGC	30053
212	SpyCas9-SpRY	+	AAGAAATCCCGAGAGGAAAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCttccgcctcCGACCTGTGGCTGGCCTGCTTTCCTCTCGgat	29869	CACTACCTAAAGGTCTCCTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGC	30054
213	SpyCas9-SpRY	-	TTCTTTTCATCCCAGCTTGCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCagccacaggTCGGAGGCGGAAACCAGTGCAAGCTGGGAtgaa	29870	GGGCTTGGATCCATGTCTGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGC	30055
214	BlatCas9	+	cccaAGAAATCCCGAGAGGAAAGGCTATAGTTCCTTACTGAAAGGTAAGTTGCTATAGTAAGGGCAACAGACCCGAGGCGTTGGGGATCGCCTAGCCCGTGTTTACGGGCTCTCCCCATATTCAAAATAATGACAGACGAGCACC	29871	ctccACTACCTAAAGGTCTCCTAGCTATAGTTCCTTACTGAAAGGTAAGTTGCTATAGTAAGGGCAACAGACCCGAGGCGTTGGGGATCGCCTAGCCCGTGTTTACGGGCTCTCCCCATATTCAAAATAAT	30056

			TTGGAGCATTTATCTCCGAGGTGCTttccgcctcCGACCT GTGGCTGGCCTGCTTTCCTCTCGgat		GACAGACGAGCACCTTGGAGCATTTATCTCCG AGGTGCT	
215	BlatCas9	+	cccaAGAAATCCCGAGAGGAAAGGCTATAGTTCCTTA CTGAAAGGTAAGTTGCTATAGTAAGGGCAACAGACC CGAGGCGTTGGGGATCGCCTAGCCCGTGTTTACGGG CTCTCCCCATATTCAAAATAATGACAGACGAGCACC TTGGAGCATTTATCTCCGAGGTGCTttccgcctcCGACCT GTGGCTGGCCTGCTTTCCTCTCGgat	29872	ctccACTACCTAAAGGTCTCCTAGCTATAGTTCC TTACTGAAAGGTAAGTTGCTATAGTAAGGGCA ACAGACCCGAGGCGTTGGGGATCGCCTAGCCC GTGTTTACGGGCTCTCCCCATATTCAAAATAAT GACAGACGAGCACCTTGGAGCATTTATCTCCG AGGTGCT	30057
217	SauCas9KKH	+	CCAAGAAATCCCGAGAGGAAAGTTTTAGTACTCTGG AAACAGAATCTACTAAAACAAGGCAAAATGCCGTGT TTATCTCGTCAACTTGTTGGCGAGAtccgcctcCGACCTG TGGCTGGCCTGCTTTCCTCTCGGgatt	29873	ACCTAAAGGTCTCCTAGTGCCGTTTTAGTACTC TGGAAACAGAATCTACTAAAACAAGGCAAAAT GCCGTGTTTATCTCGTCAACTTGTTGGCGAGA	30058
218	SauriCas9-KKH	+	CCAAGAAATCCCGAGAGGAAAGTTTTAGTACTCTGG AAACAGAATCTACTAAAACAAGGCAAAATGCCGTGT TTATCTCGTCAACTTGTTGGCGAGAtccgcctcCGACCTG TGGCTGGCCTGCTTTCCTCTCGGgatt	29874	ACTCCACTACCTAAAGGTCTCGTTTTAGTACTC TGGAAACAGAATCTACTAAAACAAGGCAAAAT GCCGTGTTTATCTCGTCAACTTGTTGGCGAGA	30059
219	SpyCas9-SpRY	-	CTTCTTTTCATCCCAGCTTGGTTTTAGAGCTAGAAAT AGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTG AAAAAGTGGCACCGAGTCGGTGCgccacaggTCGGAGG CGGAAACCAGTGCAAGCTGGGATgaaa	29875	GGCTTGGATCCATGTCTGATGTTTTAGAGCTAG AAATAGCAAGTTAAAATAAGGCTAGTCCGTTA TCAACTTGAAAAAGTGGCACCGAGTCGGTGC	30060
220	SpyCas9-SpRY	+	CAAGAAATCCCGAGAGGAAAGTTTTAGAGCTAGAA ATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACT TGAAAAAGTGGCACCGAGTCGGTGCtccgcctcCGACCT GTGGCTGGCCTGCTTTCCTCTCGGgatt	29876	ACTACCTAAAGGTCTCCTAGGTTTTAGAGCTA GAAATAGCAAGTTAAAATAAGGCTAGTCCGTT ATCAACTTGAAAAAGTGGCACCGAGTCGGTGC	30061
224	SauCas9KKH	+	CCCAAGAAATCCCGAGAGGAAGTTTTAGTACTCTGG AAACAGAATCTACTAAAACAAGGCAAAATGCCGTGT TTATCTCGTCAACTTGTTGGCGAGAccgcctcCGACCTG TGGCTGGCCTGCTTTCCTCTCGGGattt	29877	ACCTAAAGGTCTCCTAGTGCCGTTTTAGTACTC TGGAAACAGAATCTACTAAAACAAGGCAAAAT GCCGTGTTTATCTCGTCAACTTGTTGGCGAGA	30062
225	SpyCas9-NG	+	CCAAGAAATCCCGAGAGGAAGTTTTAGAGCTAGAAA TAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTT GAAAAAGTGGCACCGAGTCGGTGCccgcctcCGACCTG TGGCTGGCCTGCTTTCCTCTCGGGattt	29878	ACTACCTAAAGGTCTCCTAGGTTTTAGAGCTA GAAATAGCAAGTTAAAATAAGGCTAGTCCGTT ATCAACTTGAAAAAGTGGCACCGAGTCGGTGC	30063
229	SpyCas9-SpRY	+	CCAAGAAATCCCGAGAGGAAGTTTTAGAGCTAGAAA TAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTT GAAAAAGTGGCACCGAGTCGGTGCccgcctcCGACCTG TGGCTGGCCTGCTTTCCTCTCGGGattt	29879	CTACCTAAAGGTCTCCTAGTGTTTTAGAGCTAG AAATAGCAAGTTAAAATAAGGCTAGTCCGTTA TCAACTTGAAAAAGTGGCACCGAGTCGGTGC	30064
230	SpyCas9-SpRY	-	TCTTCTTTTCATCCCAGCTTGTTTTAGAGCTAGAAAT AGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTG	29880	GCTTGGATCCATGTCTGATGGTTTTAGAGCTAG AAATAGCAAGTTAAAATAAGGCTAGTCCGTTA TCAACTTGAAAAAGTGGCACCGAGTCGGTGC	30065

			AAAAAGTGGCACCGAGTCGGTGCccacaggTCGGAGGC GGAAACCAGTGCAAGCTGGGATGaaaa			
236	ScaCas 9-Sc++	+	CCCAAGAAATCCCGAGAGGAGTTTTAGAGCTAGAAA TAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTT GAAAAAGTGGCACCGAGTCGGTGCcgcctcCGACCTGT GGCTGGCCTGCTTTCCTCTCGGGAtttc	29881	CACTACCTAAAGGTCTCCTAGTTTTAGAGCTAG AAATAGCAAGTTAAAATAAGGCTAGTCCGTTA TCAACTTGAAAAAGTGGCACCGAGTCGGTGC	30066
237	SpyCas9-SpRY	+	CCCAAGAAATCCCGAGAGGAGTTTTAGAGCTAGAAA TAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTT GAAAAAGTGGCACCGAGTCGGTGCcgcctcCGACCTGT GGCTGGCCTGCTTTCCTCTCGGGAtttc	29882	TACCTAAAGGTCTCCTAGTGGTTTTAGAGCTAG AAATAGCAAGTTAAAATAAGGCTAGTCCGTTA TCAACTTGAAAAAGTGGCACCGAGTCGGTGC	30067
238	SpyCas9-NG	-	TTCTTCTTTTCATCCCAGCTGTTTTAGAGCTAGAAAT AGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTG AAAAAGTGGCACCGAGTCGGTGCcacaggTCGGAGGC GGAAACCAGTGCAAGCTGGGATGAaaag	29883	TGGATCCATGTCTGATGTACGTTTTAGAGCTAG AAATAGCAAGTTAAAATAAGGCTAGTCCGTTA TCAACTTGAAAAAGTGGCACCGAGTCGGTGC	30068
242	SpyCas9-SpRY	-	TTCTTCTTTTCATCCCAGCTGTTTTAGAGCTAGAAAT AGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTG AAAAAGTGGCACCGAGTCGGTGCcacaggTCGGAGGC GGAAACCAGTGCAAGCTGGGATGAaaag	29884	CTTGGATCCATGTCTGATGTGTTTTAGAGCTAG AAATAGCAAGTTAAAATAAGGCTAGTCCGTTA TCAACTTGAAAAAGTGGCACCGAGTCGGTGC	30069
243	BlatCas9	-	tcttTCTTCTTTTCATCCCAGCTGCTATAGTTCCTTACTG AAAGGTAAGTTGCTATAGTAAGGGCAACAGACCCGA GGCGTTGGGGATCGCCTAGCCCGTGTTTACGGGCTC TCCCCATATTCAAAATAATGACAGACGAGCACCTTG GAGCATTTATCTCCGAGGTGCTcacaggTCGGAGGCGG AAACCAGTGCAAGCTGGGATGAaaag	29885	catgGGCTTGGATCCATGTCTGAGCTATAGTTCC TTACTGAAAGGTAAGTTGCTATAGTAAGGGCA ACAGACCCGAGGCGTTGGGGATCGCCTAGCCC GTGTTTACGGGCTCTCCCCATATTCAAAATAAT GACAGACGAGCACCTTGGAGCATTTATCTCCG AGGTGCT	30070
244	BlatCas9	-	tcttTCTTCTTTTCATCCCAGCTGCTATAGTTCCTTACTG AAAGGTAAGTTGCTATAGTAAGGGCAACAGACCCGA GGCGTTGGGGATCGCCTAGCCCGTGTTTACGGGCTC TCCCCATATTCAAAATAATGACAGACGAGCACCTTG GAGCATTTATCTCCGAGGTGCTcacaggTCGGAGGCGG AAACCAGTGCAAGCTGGGATGAaaag	29886	catgGGCTTGGATCCATGTCTGAGCTATAGTTCC TTACTGAAAGGTAAGTTGCTATAGTAAGGGCA ACAGACCCGAGGCGTTGGGGATCGCCTAGCCC GTGTTTACGGGCTCTCCCCATATTCAAAATAAT GACAGACGAGCACCTTGGAGCATTTATCTCCG AGGTGCT	30071
249	SauriCas9-KKH	+	CACCCAAGAAATCCCGAGAGGGTTTTAGTACTCTGG AAACAGAATCTACTAAAACAAGGCAAAATGCCGTGT TTATCTCGTCAACTTGTTGGCGAGAgcctcCGACCTGTG GCTGGCCTGCTTTCCTCTCGGGATttct	29887	ACTCCACTACCTAAAGGTCTCGTTTTAGTACTC TGGAAACAGAATCTACTAAAACAAGGCAAAAT GCCGTGTTTATCTCGTCAACTTGTTGGCGAGA	30072
254	ScaCas9-Sc++	-	TTTCTTCTTTTCATCCCAGCGTTTTAGAGCTAGAAAT AGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTG AAAAAGTGGCACCGAGTCGGTGCacaggTCGGAGGCG GAAACCAGTGCAAGCTGGGATGAAaaga	29888	TTGGATCCATGTCTGATGTAGTTTTAGAGCTAG AAATAGCAAGTTAAAATAAGGCTAGTCCGTTA TCAACTTGAAAAAGTGGCACCGAGTCGGTGC	30073

255	SpyCas9-SpRY	-	TTTCTTCTTTTCATCCCAGCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCacaggTCGGAGGCGGAAACCAGTGCAAGCTGGGATGAAaaga	29889	TTGGATCCATGTCTGATGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGC	30074
256	SpyCas9-SpRY	+	ACCCAAGAAATCCCGAGAGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCgcctcCGACCTGTGGCTGGCCTGCTTTCCTCTCGGGATttct	29890	ACCTAAAGGTCTCCTAGTGCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGC	30075
257	BlatCas9	+	gccaCCCAAGAAATCCCGAGAGGGCTATAGTTCCTTACTGAAAGGTAAGTTGCTATAGTAAGGGCAACAGACCCGAGGCGTTGGGGATCGCCTAGCCCGTGTTTACGGGCTCTCCCCATATTCAAAATAATGACAGACGAGCACCTTGGAGCATTTATCTCCGAGGTGCTgcctcCGACCTGTGGCTGGCCTGCTTTCCTCTCGGGATttct	29891	ccacTACCTAAAGGTCTCCTAGTGCTATAGTTCCTTACTGAAAGGTAAGTTGCTATAGTAAGGGCAACAGACCCGAGGCGTTGGGGATCGCCTAGCCCGTGTTTACGGGCTCTCCCCATATTCAAAATAATGACAGACGAGCACCTTGGAGCATTTATCTCCGAGGTGCT	30076
258	BlatCas9	+	gccaCCCAAGAAATCCCGAGAGGGCTATAGTTCCTTACTGAAAGGTAAGTTGCTATAGTAAGGGCAACAGACCCGAGGCGTTGGGGATCGCCTAGCCCGTGTTTACGGGCTCTCCCCATATTCAAAATAATGACAGACGAGCACCTTGGAGCATTTATCTCCGAGGTGCTgcctcCGACCTGTGGCTGGCCTGCTTTCCTCTCGGGATttct	29892	ccacTACCTAAAGGTCTCCTAGTGCTATAGTTCCTTACTGAAAGGTAAGTTGCTATAGTAAGGGCAACAGACCCGAGGCGTTGGGGATCGCCTAGCCCGTGTTTACGGGCTCTCCCCATATTCAAAATAATGACAGACGAGCACCTTGGAGCATTTATCTCCGAGGTGCT	30077
260	SauCas9KKH	+	CCACCCAAGAAATCCCGAGAGGTTTTAGTACTCTGGAAACAGAATCTACTAAAACAAGGCAAAATGCCGTGTTTTATCTCGTCAACTTGTTGGCGAGAcctcCGACCTGTGGCTGGCCTGCTTTCCTCTCGGGATTtctt	29893	ACCTAAAGGTCTCCTAGTGCCGTTTTAGTACTCTGGAAACAGAATCTACTAAAACAAGGCAAAATGCCGTGTTTATCTCGTCAACTTGTTGGCGAGA	30078
261	SpyCas9-SpRY	+	CACCCAAGAAATCCCGAGAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCcctcCGACCTGTGGCTGGCCTGCTTTCCTCTCGGGATTtctt	29894	CCTAAAGGTCTCCTAGTGCCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGC	30079
263	SpyCas9-SpRY	-	CTTTCTTCTTTTCATCCCAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCcaggTCGGAGGCGGAAACCAGTGCAAGCTGGGATGAAAagaa	29895	TGGATCCATGTCTGATGTACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGC	30080
264	BlatCas9	-	tttcTTTCTTCTTTTCATCCCAGGCTATAGTTCCTTACTGAAAGGTAAGTTGCTATAGTAAGGGCAACAGACCCGAGGCGTTGGGGATCGCCTAGCCCGTGTTTACGGGCTCTCCCCATATTCAAAATAATGACAGACGAGCACCTTGGAGCATTTATCTCCGAGGTGCTcaggTCGGAGGCGGAAACCAGTGCAAGCTGGGATGAAAagaa	29896	ttggATCCATGTCTGATGTACTGGCTATAGTTCCTTACTGAAAGGTAAGTTGCTATAGTAAGGGCAACAGACCCGAGGCGTTGGGGATCGCCTAGCCCGTGTTTACGGGCTCTCCCCATATTCAAAATAATGACAGACGAGCACCTTGGAGCATTTATCTCCGAGGTGCT	30081

269	SauCas9KKH	+	GCCACCCAAGAAATCCCGAGAGTTTTAGTACTCTGGAAACAGAATCTACTAAAACAAGGCAAAATGCCGTGTTTATCTCGTCAACTTGTTGGCGAGActcCGACCTGTGGCTGGCCTGCTTTCCTCTCGGGATTTcttg	29897	ACCTAAAGGTCTCCTAGTGCCGTTTTAGTACTCTGGAAACAGAATCTACTAAAACAAGGCAAAATGCCGTGTTTATCTCGTCAACTTGTTGGCGAGA	30082
270	SpyCas9-NG	+	CCACCCAAGAAATCCCGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCctcCGACCTGTGGCTGGCCTGCTTTCCTCTCGGGATTTcttg	29898	TAAAGGTCTCCTAGTGCCTCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGC	30083
274	SpyCas9-SpRY	+	CCACCCAAGAAATCCCGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCctcCGACCTGTGGCTGGCCTGCTTTCCTCTCGGGATTTcttg	29899	CTAAAGGTCTCCTAGTGCCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGC	30084
275	SpyCas9-SpRY	-	TCTTTCTTCTTTTCATCCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCaggTCGGAGGCGGAAACCAGTGCAAGCTGGGATGAAAAgaag	29900	GGATCCATGTCTGATGTACTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGC	30085
281	SauCas9	+	caGGCCACCCAAGAAATCCCGAGGTTTTAGTACTCTGGAAACAGAATCTACTAAAACAAGGCAAAATGCCGTGTTTATCTCGTCAACTTGTTGGCGAGAtcCGACCTGTGGCTGGCCTGCTTTCCTCTCGGGATTTCttgg	29901	ctAGTGCCTCTGACTCAGTGGTGGTTTTAGTACTCTGGAAACAGAATCTACTAAAACAAGGCAAAATGCCGTGTTTATCTCGTCAACTTGTTGGCGAGA	30086
282	SauCas9KKH	+	GGCCACCCAAGAAATCCCGAGGTTTTAGTACTCTGGAAACAGAATCTACTAAAACAAGGCAAAATGCCGTGTTTATCTCGTCAACTTGTTGGCGAGAtcCGACCTGTGGCTGGCCTGCTTTCCTCTCGGGATTTCttgg	29902	ACCTAAAGGTCTCCTAGTGCCGTTTTAGTACTCTGGAAACAGAATCTACTAAAACAAGGCAAAATGCCGTGTTTATCTCGTCAACTTGTTGGCGAGA	30087
285	ScaCas9-Sc++	+	GCCACCCAAGAAATCCCGAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCtcCGACCTGTGGCTGGCCTGCTTTCCTCTCGGGATTTCttgg	29903	CTAAAGGTCTCCTAGTGCCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGC	30088
286	SpyCas9	+	GCCACCCAAGAAATCCCGAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCtcCGACCTGTGGCTGGCCTGCTTTCCTCTCGGGATTTCttgg	29904	TCCTAGTGCCTCTGACTCAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGC	30089
289	SpyCas9-SpRY	+	GCCACCCAAGAAATCCCGAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCtcCGACCTGTGGCTGGCCTGCTTTCCTCTCGGGATTTCttgg	29905	TAAAGGTCTCCTAGTGCCTCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGC	30090
290	SpyCas9-NG	+	GCCACCCAAGAAATCCCGAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTT	29906	TAAAGGTCTCCTAGTGCCTCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGC	30091

			GAAAAAGTGGCACCGAGTCGGTGCtcCGACCTGTGGC TGGCCTGCTTTCCTCTCGGGATTTCttgg			
293	SpyCas9-NG	-	TTCTTTCTTCTTTTCATCCCGTTTTAGAGCTAGAAATA GCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGA AAAAGTGGCACCGAGTCGGTGCggTCGGAGGCGGAA ACCAGTGCAAGCTGGGATGAAAAGaaga	29907	GATCCATGTCTGATGTACTGGTTTTAGAGCTAG AAATAGCAAGTTAAAATAAGGCTAGTCCGTTA TCAACTTGAAAAAGTGGCACCGAGTCGGTGC	30092
297	SpyCas9-SpRY	-	TTCTTTCTTCTTTTCATCCCGTTTTAGAGCTAGAAATA GCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGA AAAAGTGGCACCGAGTCGGTGCggTCGGAGGCGGAA ACCAGTGCAAGCTGGGATGAAAAGaaga	29908	GATCCATGTCTGATGTACTGGTTTTAGAGCTAG AAATAGCAAGTTAAAATAAGGCTAGTCCGTTA TCAACTTGAAAAAGTGGCACCGAGTCGGTGC	30093
303	SauCas9	+	ccAGGCCACCCAAGAAATCCCGAGTTTTAGTACTCTG GAAACAGAATCTACTAAAACAAGGCAAAATGCCGT GTTTATCTCGTCAACTTGTTGGCGAGAcCGACCTGTG GCTGGCCTGCTTTCCTCTCGGGATTTCTtggg	29909	ctAGTGCCTCTGACTCAGTGGTGGTTTTAGTACT CTGGAAACAGAATCTACTAAAACAAGGCAAA ATGCCGTGTTTATCTCGTCAACTTGTTGGCGAG A	30094
304	SauCas9KKH	+	AGGCCACCCAAGAAATCCCGAGTTTTAGTACTCTGG AAACAGAATCTACTAAAACAAGGCAAAATGCCGTGT TTATCTCGTCAACTTGTTGGCGAGAcCGACCTGTGGC TGGCCTGCTTTCCTCTCGGGATTTCTtggg	29910	AAGGTCTCCTAGTGCCTCTGAGTTTTAGTACTC TGGAAACAGAATCTACTAAAACAAGGCAAAAT GCCGTGTTTATCTCGTCAACTTGTTGGCGAGA	30095
305	SauriCas9	+	AGGCCACCCAAGAAATCCCGAGTTTTAGTACTCTGG AAACAGAATCTACTAAAACAAGGCAAAATGCCGTGT TTATCTCGTCAACTTGTTGGCGAGAcCGACCTGTGGC TGGCCTGCTTTCCTCTCGGGATTTCTtggg	29911	TCTCCTAGTGCCTCTGACTCAGTTTTAGTACTC TGGAAACAGAATCTACTAAAACAAGGCAAAAT GCCGTGTTTATCTCGTCAACTTGTTGGCGAGA	30096
306	SauriCas9-KKH	+	AGGCCACCCAAGAAATCCCGAGTTTTAGTACTCTGG AAACAGAATCTACTAAAACAAGGCAAAATGCCGTGT TTATCTCGTCAACTTGTTGGCGAGAcCGACCTGTGGC TGGCCTGCTTTCCTCTCGGGATTTCTtggg	29912	AGGTCTCCTAGTGCCTCTGACGTTTTAGTACTC TGGAAACAGAATCTACTAAAACAAGGCAAAAT GCCGTGTTTATCTCGTCAACTTGTTGGCGAGA	30097
309	ScaCas9-Sc++	+	GGCCACCCAAGAAATCCCGAGTTTTAGAGCTAGAAA TAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTT GAAAAAGTGGCACCGAGTCGGTGCcCGACCTGTGGC TGGCCTGCTTTCCTCTCGGGATTTCTtggg	29913	CTAAAGGTCTCCTAGTGCCTGTTTTAGAGCTAG AAATAGCAAGTTAAAATAAGGCTAGTCCGTTA TCAACTTGAAAAAGTGGCACCGAGTCGGTGC	30098
310	SpyCas9-SpRY	+	GGCCACCCAAGAAATCCCGAGTTTTAGAGCTAGAAA TAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTT GAAAAAGTGGCACCGAGTCGGTGCcCGACCTGTGGC TGGCCTGCTTTCCTCTCGGGATTTCTtggg	29914	AAAGGTCTCCTAGTGCCTCTGTTTTAGAGCTAG AAATAGCAAGTTAAAATAAGGCTAGTCCGTTA TCAACTTGAAAAAGTGGCACCGAGTCGGTGC	30099
313	ScaCas9-Sc++	-	TTTCTTTCTTCTTTTCATCCGTTTTAGAGCTAGAAATA GCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGA AAAAGTGGCACCGAGTCGGTGCgTCGGAGGCGGAAA CCAGTGCAAGCTGGGATGAAAAGAagaa	29915	ATCCATGTCTGATGTACTGTGTTTTAGAGCTAG AAATAGCAAGTTAAAATAAGGCTAGTCCGTTA TCAACTTGAAAAAGTGGCACCGAGTCGGTGC	30100

314	SpyCas9-SpRY	-	TTTCTTTCTTCTTTTCATCCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCgTCGGAGGCGGAAACCAGTGCAAGCTGGGATGAAAAGAagaa	29916	ATCCATGTCTGATGTACTGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGC	30101
315	St1Cas9	+	GGCCACCCAAGAAATCCCGAGTCTTTGTACTCTGGTACCAGAAGCTACAAAGATAAGGCTTCATGCCGAAATCAACACCCTGTCATTTTATGGCAGGGTGTTTTcCGACCTGTGGCTGGCCTGCTTTCCTCTCGGGATTTCTtggg	29917	NAGTCTTTGTACTCTGGTACCAGAAGCTACAAAGATAAGGCTTCATGCCGAAATCAACACCCTGTCATTTTATGGCAGGGTGTTTT	30102
319	SauCas9KKH	+	CAGGCCACCCAAGAAATCCCGGTTTTAGTACTCTGGAAACAGAATCTACTAAAACAAGGCAAAATGCCGTGTTTTATCTCGTCAACTTGTTGGCGAGACGACCTGTGGCTGGCCTGCTTTCCTCTCGGGATTTCTTgggt	29918	AAGGTCTCCTAGTGCCTCTGAGTTTTAGTACTCTGGAAACAGAATCTACTAAAACAAGGCAAAATGCCGTGTTTATCTCGTCAACTTGTTGGCGAGA	30103
320	SauriCas9-KKH	+	CAGGCCACCCAAGAAATCCCGGTTTTAGTACTCTGGAAACAGAATCTACTAAAACAAGGCAAAATGCCGTGTTTATCTCGTCAACTTGTTGGCGAGACGACCTGTGGCTGGCCTGCTTTCCTCTCGGGATTTCTTgggt	29919	AGGTCTCCTAGTGCCTCTGACGTTTTAGTACTCTGGAAACAGAATCTACTAAAACAAGGCAAAATGCCGTGTTTATCTCGTCAACTTGTTGGCGAGA	30104
322	SauriCas9-KKH	-	GTTTTCTTTCTTCTTTTCATCGTTTTAGTACTCTGGAAACAGAATCTACTAAAACAAGGCAAAATGCCGTGTTTATCTCGTCAACTTGTTGGCGAGATCGGAGGCGGAAACCAGTGCAAGCTGGGATGAAAAGAAgaaa	29920	TCCATGTCTGATGTACTGTGTGTTTTAGTACTCTGGAAACAGAATCTACTAAAACAAGGCAAAATGCCGTGTTTATCTCGTCAACTTGTTGGCGAGA	30105
323	SpyCas9-NG	+	AGGCCACCCAAGAAATCCCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCGACCTGTGGCTGGCCTGCTTTCCTCTCGGGATTTCTTgggt	29921	TAAAGGTCTCCTAGTGCCTCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGC	30106
327	SpyCas9-SpRY	+	AGGCCACCCAAGAAATCCCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCGACCTGTGGCTGGCCTGCTTTCCTCTCGGGATTTCTTgggt	29922	AAGGTCTCCTAGTGCCTCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGC	30107
328	SpyCas9-SpRY	-	TTTTCTTTCTTCTTTTCATCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTCGGAGGCGGAAACCAGTGCAAGCTGGGATGAAAAGAAgaaa	29923	TCCATGTCTGATGTACTGTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGC	30108
329	St1Cas9	+	AGGCCACCCAAGAAATCCCGGTCTTTGTACTCTGGTACCAGAAGCTACAAAGATAAGGCTTCATGCCGAAATCAACACCCTGTCATTTTATGGCAGGGTGTTTTCGACCTGTGGCTGGCCTGCTTTCCTCTCGGGATTTCTTgggt	29924	NAGTCTTTGTACTCTGGTACCAGAAGCTACAAAGATAAGGCTTCATGCCGAAATCAACACCCTGTCATTTTATGGCAGGGTGTTTT	30109
330	BlatCas9	-	gagtTTTCTTTCTTCTTTTCATCGCTATAGTTCCTTACTGAAAGGTAAGTTGCTATAGTAAGGGCAACAGACCCGAGGCGTTGGGGATCGCCTAGCCCGTGTTTACGGGCTC	29925	ttggATCCATGTCTGATGTACTGGCTATAGTTCCTTACTGAAAGGTAAGTTGCTATAGTAAGGGCAACAGACCCGAGGCGTTGGGGATCGCCTAGCCCG	30110

			TCCCCATATTCAAAATAATGACAGACGAGCACCTTG GAGCATTTATCTCCGAGGTGCTTCGGAGGCGGAAAC CAGTGCAAGCTGGGATGAAAAGAAgaaa		TGTTTACGGGCTCTCCCCATATTCAAAATAATG ACAGACGAGCACCTTGGAGCATTTATCTCCGA GGTGCT	
331	BlatCa s9	-	gagtTTTCTTTCTTCTTTTCATCGCTATAGTTCCTTACTG AAAGGTAAGTTGCTATAGTAAGGGCAACAGACCCGA GGCGTTGGGGATCGCCTAGCCCGTGTTTACGGGCTC TCCCCATATTCAAAATAATGACAGACGAGCACCTTG GAGCATTTATCTCCGAGGTGCTTCGGAGGCGGAAAC CAGTGCAAGCTGGGATGAAAAGAAgaaa	29926	ttggATCCATGTCTGATGTACTGGCTATAGTTCCT TACTGAAAGGTAAGTTGCTATAGTAAGGGCAA CAGACCCGAGGCGTTGGGGATCGCCTAGCCCG TGTTTACGGGCTCTCCCCATATTCAAAATAATG ACAGACGAGCACCTTGGAGCATTTATCTCCGA GGTGCT	3011 1
336	SauCa s9	+	ggCCAGGCCACCCAAGAAATCCCGTTTTAGTACTCTG GAAACAGAATCTACTAAAACAAGGCAAAATGCCGT GTTTATCTCGTCAACTTGTTGGCGAGAGACCTGTGGC TGGCCTGCTTTCCTCTCGGGATTTCTTGgggtg	29927	ctAGTGCCTCTGACTCAGTGGTGGTTTTAGTACT CTGGAAACAGAATCTACTAAAACAAGGCAAA ATGCCGTGTTTATCTCGTCAACTTGTTGGCGAG A	3011 2
337	SauCa s9KK H	+	CCAGGCCACCCAAGAAATCCCGTTTTAGTACTCTGG AAACAGAATCTACTAAAACAAGGCAAAATGCCGTGT TTATCTCGTCAACTTGTTGGCGAGAGACCTGTGGCTG GCCTGCTTTCCTCTCGGGATTTCTTGgggtg	29928	AAGGTCTCCTAGTGCCTCTGAGTTTTAGTACTC TGGAAACAGAATCTACTAAAACAAGGCAAAAT GCCGTGTTTATCTCGTCAACTTGTTGGCGAGA	3011 3
338	SauCa s9KK H	-	AGTTTTCTTTCTTCTTTTCATGTTTTAGTACTCTGGAA ACAGAATCTACTAAAACAAGGCAAAATGCCGTGTTT ATCTCGTCAACTTGTTGGCGAGACGGAGGCGGAAAC CAGTGCAAGCTGGGATGAAAAGAAGaaag	29929	ATCCATGTCTGATGTACTGTGGTTTTAGTACTC TGGAAACAGAATCTACTAAAACAAGGCAAAAT GCCGTGTTTATCTCGTCAACTTGTTGGCGAGA	3011 4
341	ScaCas 9-Sc++	+	CAGGCCACCCAAGAAATCCCGTTTTAGAGCTAGAAA TAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTT GAAAAAGTGGCACCGAGTCGGTGCGACCTGTGGCTG GCCTGCTTTCCTCTCGGGATTTCTTGgggtg	29930	GTCTCCTAGTGCCTCTGACTGTTTTAGAGCTAG AAATAGCAAGTTAAAATAAGGCTAGTCCGTTA TCAACTTGAAAAAGTGGCACCGAGTCGGTGC	3011 5
342	SpyCa s9-SpRY	+	CAGGCCACCCAAGAAATCCCGTTTTAGAGCTAGAAA TAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTT GAAAAAGTGGCACCGAGTCGGTGCGACCTGTGGCTG GCCTGCTTTCCTCTCGGGATTTCTTGgggtg	29931	AGGTCTCCTAGTGCCTCTGAGTTTTAGAGCTAG AAATAGCAAGTTAAAATAAGGCTAGTCCGTTA TCAACTTGAAAAAGTGGCACCGAGTCGGTGC	3011 6
343	SpyCa s9-SpRY	-	GTTTTCTTTCTTCTTTTCATGTTTTAGAGCTAGAAATA GCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGA AAAAGTGGCACCGAGTCGGTGCCGGAGGCGGAAAC CAGTGCAAGCTGGGATGAAAAGAAGaaag	29932	CCATGTCTGATGTACTGTGTGTTTTAGAGCTAG AAATAGCAAGTTAAAATAAGGCTAGTCCGTTA TCAACTTGAAAAAGTGGCACCGAGTCGGTGC	3011 7
350	SauCa s9KK H	+	GCCAGGCCACCCAAGAAATCCGTTTTAGTACTCTGG AAACAGAATCTACTAAAACAAGGCAAAATGCCGTGT TTATCTCGTCAACTTGTTGGCGAGAACCTGTGGCTGG CCTGCTTTCCTCTCGGGATTTCTTGGgtgg	29933	AAGGTCTCCTAGTGCCTCTGAGTTTTAGTACTC TGGAAACAGAATCTACTAAAACAAGGCAAAAT GCCGTGTTTATCTCGTCAACTTGTTGGCGAGA	3011 8

351	SauriCas9-KKH	+	GCCAGGCCACCCAAGAAATCCGTTTTAGTACTCTGGAAACAGAATCTACTAAAACAAGGCAAAATGCCGTGTTTTATCTCGTCAACTTGTTGGCGAGAACCTGTGGCTGGCCTGCTTTCCTCTCGGGATTTCTTGGgtgg	29934	AGGTCTCCTAGTGCCTCTGACGTTTTAGTACTCTGGAAACAGAATCTACTAAAACAAGGCAAAATGCCGTGTTTATCTCGTCAACTTGTTGGCGAGA	30119
353	SpyCas9-NG	+	CCAGGCCACCCAAGAAATCCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCACCTGTGGCTGGCCTGCTTTCCTCTCGGGATTTCTTGGgtgg	29935	TCTCCTAGTGCCTCTGACTCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGC	30120
357	SpyCas9-SpRY	+	CCAGGCCACCCAAGAAATCCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCACCTGTGGCTGGCCTGCTTTCCTCTCGGGATTTCTTGGgtgg	29936	GGTCTCCTAGTGCCTCTGACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGC	30121
358	SpyCas9-SpRY	-	AGTTTTCTTTCTTCTTTTCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGGAGGCGGAAACCAGTGCAAGCTGGGATGAAAAGAAGAaaga	29937	CATGTCTGATGTACTGTGTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGC	30122

Table 4D. Exemplary template RNA sequences and second nick gRNA spacer sequences

Table 4D provides design of RNA components of gene modifying systems for correcting the pathogenic IVS10-11G>A, mutation in PAH. The gRNA spacers from Table 1D were filtered, e.g., filtered by occurrence within 15 nt of the desired editing location and use of a Tier 1 Cas enzyme. For each gRNA ID, this table details the sequence of a complete template RNA, optional second-nick gRNA, and Cas variant for use in a Cas-RT fusion gene modifying polypeptide. For exemplification, PBS sequences and post-edit homology regions (after the location of the edit) are set to 12 nt and 30 nt, respectively. Additionally, a second-nick gRNA is selected with preference for a distance near 100 nt from the first nick and a first preference for a design resulting in a PAM-in system, as described elsewhere in this application.

ID	Cas species	strand	Template RNA	SEQ ID NO	second-nick gRNA	SEQ ID NO
1	SpyCas9-SpRY	-	ATAATAACTTTTCACTTAGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCgcttctctgataagcagtactgtaggccCCAAGTGAAAagtt	30123	TCTCTGCCACGTAATAGAGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGC	30272

2	SauCas 9KKH	+	TAAGCAGTACTGTAGGCCCTAGTTTTAGTACTCTGGAA ACAGAATCTACTAAAACAAGGCAAAATGCCGTGTTTAT CTCGTCAACTTGTTGGCGAGAatttaacagtgataataacttttcactTG GGGCCTACAgtac	30124	GCATTTGGGCTGTGATGTAGAGTTTTAGTACT CTGGAAACAGAATCTACTAAAACAAGGCAAA ATGCCGTGTTTATCTCGTCAACTTGTTGGCGA GA	30273
3	SpyCas 9-NG	-	GATAATAACTTTTCACTTAGGTTTTAGAGCTAGAAATA GCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAA AAGTGGCACCGAGTCGGTGCcttctctgataagcagtactgtaggccC CAAGTGAAAAgtta	30125	TCTCTGCCACGTAATAGAGGGTTTTAGAGCTA GAAATAGCAAGTTAAAATAAGGCTAGTCCGT TATCAACTTGAAAAAGTGGCACCGAGTCGGT GC	30274
6	SpyCas 9-NG	+	AAGCAGTACTGTAGGCCCTAGTTTTAGAGCTAGAAATA GCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAA AAGTGGCACCGAGTCGGTGCatttaacagtgataataacttttcactTG GGGCCTACAgtac	30126	ATTTGGGCTGTGATGTAGAAGTTTTAGAGCTA GAAATAGCAAGTTAAAATAAGGCTAGTCCGT TATCAACTTGAAAAAGTGGCACCGAGTCGGT GC	30275
10	SpyCas 9-SpRY	-	GATAATAACTTTTCACTTAGGTTTTAGAGCTAGAAATA GCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAA AAGTGGCACCGAGTCGGTGCcttctctgataagcagtactgtaggccC CAAGTGAAAAgtta	30127	CTCTGCCACGTAATAGAGGGGTTTTAGAGCTA GAAATAGCAAGTTAAAATAAGGCTAGTCCGT TATCAACTTGAAAAAGTGGCACCGAGTCGGT GC	30276
12	SpyCas 9-SpRY	+	AAGCAGTACTGTAGGCCCTAGTTTTAGAGCTAGAAATA GCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAA AAGTGGCACCGAGTCGGTGCatttaacagtgataataacttttcactTG GGGCCTACAgtac	30128	TTTGGGCTGTGATGTAGAAGGTTTTAGAGCTA GAAATAGCAAGTTAAAATAAGGCTAGTCCGT TATCAACTTGAAAAAGTGGCACCGAGTCGGT GC	30277
16	ScaCas 9-Sc++	-	TGATAATAACTTTTCACTTAGTTTTAGAGCTAGAAATA GCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAA AAGTGGCACCGAGTCGGTGCttctctgataagcagtactgtaggccCC AAGTGAAAAGttat	30129	TCTGCCACGTAATAGAGGGGGTTTTAGAGCTA GAAATAGCAAGTTAAAATAAGGCTAGTCCGT TATCAACTTGAAAAAGTGGCACCGAGTCGGT GC	30278
17	SpyCas 9	-	TGATAATAACTTTTCACTTAGTTTTAGAGCTAGAAATA GCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAA AAGTGGCACCGAGTCGGTGCttctctgataagcagtactgtaggccCC AAGTGAAAAGttat	30130	CTGCCACGTAATAGAGGGGCGTTTTAGAGCTA GAAATAGCAAGTTAAAATAAGGCTAGTCCGT TATCAACTTGAAAAAGTGGCACCGAGTCGGT GC	30279
20	SpyCas 9-SpRY	-	TGATAATAACTTTTCACTTAGTTTTAGAGCTAGAAATA GCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAA AAGTGGCACCGAGTCGGTGCttctctgataagcagtactgtaggccCC AAGTGAAAAGttat	30131	TCTGCCACGTAATAGAGGGGGTTTTAGAGCTA GAAATAGCAAGTTAAAATAAGGCTAGTCCGT TATCAACTTGAAAAAGTGGCACCGAGTCGGT GC	30280
23	ScaCas 9-Sc++	+	TAAGCAGTACTGTAGGCCCTGTTTTAGAGCTAGAAATA GCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAA AAGTGGCACCGAGTCGGTGCtttaacagtgataataacttttcactTGG GGCCTACAGtact	30132	GGGCTGTGATGTAGAAGGAAGTTTTAGAGCT AGAAATAGCAAGTTAAAATAAGGCTAGTCCG TTATCAACTTGAAAAAGTGGCACCGAGTCGGT GC	30281
24	SpyCas 9-SpRY	+	TAAGCAGTACTGTAGGCCCTGTTTTAGAGCTAGAAATA GCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAA	30133	TTGGGCTGTGATGTAGAAGGGTTTTAGAGCTA GAAATAGCAAGTTAAAATAAGGCTAGTCCGT	30282

			AAGTGGCACCGAGTCGGTGCtttaacagtgataataacttttcactTGGGGCCTACAGtact		TATCAACTTGAAAAAGTGGCACCGAGTCGGTGC	
25	SpyCas9-NG	-	TGATAATAACTTTTCACTTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCttctctgataagcagtactgtaggccCCAAGTGAAAAGttat	30134	CTGCCACGTAATAGAGGGGCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGC	30283
28	BlatCas9	-	cagtGATAATAACTTTTCACTTAGCTATAGTTCCTTACTGAAAGGTAAGTTGCTATAGTAAGGGCAACAGACCCGAGGCGTTGGGGATCGCCTAGCCCGTGTTTACGGGCTCTCCCCATATTCAAAATAATGACAGACGAGCACCTTGGAGCATTTATCTCCGAGGTGCTttctctgataagcagtactgtaggccCCAAGTGAAAAGttat	30135	ctctGCCACGTAATAGAGGGGCTGCTATAGTTCCTTACTGAAAGGTAAGTTGCTATAGTAAGGGCAACAGACCCGAGGCGTTGGGGATCGCCTAGCCCGTGTTTACGGGCTCTCCCCATATTCAAAATAATGACAGACGAGCACCTTGGAGCATTTATCTCCGAGGTGCT	30284
31	Nme2Cas9	-	aaCAGTGATAATAACTTTTCACTTGTTGTAGCTCCCTTTCTCATTTCGGAAACGAAATGAGAACCGTTGCTACAATAAGGCCGTCTGAAAAGATGTGCCGCAACGCTCTGCCCCTTAAAGCTTCTGCTTTAAGGGGCATCGTTTAtctctgataagcagtactgtaggccCCAAGTGAAAAGTtatt	30136	tcTGCCACGTAATAGAGGGGCTGGGTTGTAGCTCCCTTTCTCATTTCGGAAACGAAATGAGAACCGTTGCTACAATAAGGCCGTCTGAAAAGATGTGCCGCAACGCTCTGCCCCTTAAAGCTTCTGCTTTAAGGGGCATCGTTTA	30285
32	SauriCas9	-	AGTGATAATAACTTTTCACTTGTTTTAGTACTCTGGAAACAGAATCTACTAAAACAAGGCAAAATGCCGTGTTTATCTCGTCAACTTGTTGGCGAGAtctctgataagcagtactgtaggccCCAAGTGAAAAGTtatt	30137	CTCTGCCACGTAATAGAGGGGGTTTTAGTACTCTGGAAACAGAATCTACTAAAACAAGGCAAAATGCCGTGTTTATCTCGTCAACTTGTTGGCGAGA	30286
33	SauriCas9-KKH	-	AGTGATAATAACTTTTCACTTGTTTTAGTACTCTGGAAACAGAATCTACTAAAACAAGGCAAAATGCCGTGTTTATCTCGTCAACTTGTTGGCGAGAtctctgataagcagtactgtaggccCCAAGTGAAAAGTtatt	30138	CTCTGCCACGTAATAGAGGGGGTTTTAGTACTCTGGAAACAGAATCTACTAAAACAAGGCAAAATGCCGTGTTTATCTCGTCAACTTGTTGGCGAGA	30287
34	SauriCas9-KKH	+	GATAAGCAGTACTGTAGGCCCGTTTTAGTACTCTGGAAACAGAATCTACTAAAACAAGGCAAAATGCCGTGTTTATCTCGTCAACTTGTTGGCGAGAttaacagtgataataacttttcactTGGGGCCTACAGTactg	30139	TGGGCTGTGATGTAGAAGGAAGTTTTAGTACTCTGGAAACAGAATCTACTAAAACAAGGCAAAATGCCGTGTTTATCTCGTCAACTTGTTGGCGAGA	30288
39	ScaCas9-Sc++	-	GTGATAATAACTTTTCACTTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCtctctgataagcagtactgtaggccCCAAGTGAAAAGTtatt	30140	CTGCCACGTAATAGAGGGGCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGC	30289
40	SpyCas9	-	GTGATAATAACTTTTCACTTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCtctctgataagcagtactgtaggccCCAAGTGAAAAGTtatt	30141	CTGCCACGTAATAGAGGGGCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGC	30290
43	SpyCas9-SpRY	-	GTGATAATAACTTTTCACTTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAA	30142	CTGCCACGTAATAGAGGGGCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGT	30291

			AAGTGGCACCGAGTCGGTGCtctctgataagcagtactgtaggccCC AAGTGAAAAGTtatt		TATCAACTTGAAAAAGTGGCACCGAGTCGGT GC	
44	SpyCas 9-NG	-	GTGATAATAACTTTTCACTTGTTTTAGAGCTAGAAATA GCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAA AAGTGGCACCGAGTCGGTGCtctctgataagcagtactgtaggccCC AAGTGAAAAGTtatt	30143	CTGCCACGTAATAGAGGGGCGTTTTAGAGCTA GAAATAGCAAGTTAAAATAAGGCTAGTCCGT TATCAACTTGAAAAAGTGGCACCGAGTCGGT GC	30292
47	SpyCas 9-SpRY	+	ATAAGCAGTACTGTAGGCCCGTTTTAGAGCTAGAAATA GCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAA AAGTGGCACCGAGTCGGTGCttaacagtgataataactttt cactTGG GGCCTACAGTactg	30144	TGGGCTGTGATGTAGAAGGAGTTTTAGAGCTA GAAATAGCAAGTTAAAATAAGGCTAGTCCGT TATCAACTTGAAAAAGTGGCACCGAGTCGGT GC	30293
48	BlatCas 9	-	acagTGATAATAACTTTTCACTTGCTATAGTTCCTTACTG AAAGGTAAGTTGCTATAGTAAGGGCAACAGACCCGAG GCGTTGGGGATCGCCTAGCCCGTGTTTACGGGCTCTCC CCATATTCAAAATAATGACAGACGAGCACCTTGGAGC ATTTATCTCCGAGGTGCTtctctgataagcagtactgtaggccCCAAG TGAAAAGTtatt	30145	ctctGCCACGTAATAGAGGGGCTGCTATAGTTC CTTACTGAAAGGTAAGTTGCTATAGTAAGGGC AACAGACCCGAGGCGTTGGGGATCGCCTAGC CCGTGTTTACGGGCTCTCCCCATATTCAAAAT AATGACAGACGAGCACCTTGGAGCATTTATCT CCGAGGTGCT	30294
49	BlatCas 9	-	acagTGATAATAACTTTTCACTTGCTATAGTTCCTTACTG AAAGGTAAGTTGCTATAGTAAGGGCAACAGACCCGAG GCGTTGGGGATCGCCTAGCCCGTGTTTACGGGCTCTCC CCATATTCAAAATAATGACAGACGAGCACCTTGGAGC ATTTATCTCCGAGGTGCTtctctgataagcagtactgtaggccCCAAG TGAAAAGTtatt	30146	ctctGCCACGTAATAGAGGGGCTGCTATAGTTC CTTACTGAAAGGTAAGTTGCTATAGTAAGGGC AACAGACCCGAGGCGTTGGGGATCGCCTAGC CCGTGTTTACGGGCTCTCCCCATATTCAAAAT AATGACAGACGAGCACCTTGGAGCATTTATCT CCGAGGTGCT	30295
52	SauCas 9	-	aaCAGTGATAATAACTTTTCACTGTTTTAGTACTCTGGA AACAGAATCTACTAAAACAAGGCAAAATGCCGTGTTT ATCTCGTCAACTTGTTGGCGAGActctgataagcagtactgtaggcc CCAAGTGAAAAGTTatta	30147	tcTCTGCCACGTAATAGAGGGGCGTTTTAGTAC TCTGGAAACAGAATCTACTAAAACAAGGCAA AATGCCGTGTTTATCTCGTCAACTTGTTGGCG AGA	30296
53	SauCas 9KKH	-	CAGTGATAATAACTTTTCACTGTTTTAGTACTCTGGAA ACAGAATCTACTAAAACAAGGCAAAATGCCGTGTTTAT CTCGTCAACTTGTTGGCGAGActctgataagcagtactgtaggccCC AAGTGAAAAGTTatta	30148	TCTGCCACGTAATAGAGGGGCGTTTTAGTACT CTGGAAACAGAATCTACTAAAACAAGGCAAA ATGCCGTGTTTATCTCGTCAACTTGTTGGCGA GA	30297
54	SauCas 9KKH	+	TGATAAGCAGTACTGTAGGCCGTTTTAGTACTCTGGAA ACAGAATCTACTAAAACAAGGCAAAATGCCGTGTTTAT CTCGTCAACTTGTTGGCGAGAtaacagtgataataactttt cactTGG GGCCTACAGTActgc	30149	TGGGCTGTGATGTAGAAGGAAGTTTTAGTACT CTGGAAACAGAATCTACTAAAACAAGGCAAA ATGCCGTGTTTATCTCGTCAACTTGTTGGCGA GA	30298
55	SauCas 9KKH	+	TGATAAGCAGTACTGTAGGCCGTTTTAGTACTCTGGAA ACAGAATCTACTAAAACAAGGCAAAATGCCGTGTTTAT CTCGTCAACTTGTTGGCGAGAtaacagtgataataactttt cactTGG GGCCTACAGTActgc	30150	TGGGCTGTGATGTAGAAGGAAGTTTTAGTACT CTGGAAACAGAATCTACTAAAACAAGGCAAA ATGCCGTGTTTATCTCGTCAACTTGTTGGCGA GA	30299

58	SauriCas9	-	CAGTGATAATAACTTTTCACTGTTTTAGTACTCTGGAAACAGAATCTACTAAAACAAGGCAAAATGCCGTGTTTATCTCGTCAACTTGTTGGCGAGActctgataagcagtactgtaggccCCAAGTGAAAAGTTatta	30151	CTCTGCCACGTAATAGAGGGGGTTTTAGTACTCTGGAAACAGAATCTACTAAAACAAGGCAAAATGCCGTGTTTATCTCGTCAACTTGTTGGCGAGA	30300
59	SauriCas9-KKH	-	CAGTGATAATAACTTTTCACTGTTTTAGTACTCTGGAAACAGAATCTACTAAAACAAGGCAAAATGCCGTGTTTATCTCGTCAACTTGTTGGCGAGActctgataagcagtactgtaggccCCAAGTGAAAAGTTatta	30152	CTCTGCCACGTAATAGAGGGGGTTTTAGTACTCTGGAAACAGAATCTACTAAAACAAGGCAAAATGCCGTGTTTATCTCGTCAACTTGTTGGCGAGA	30301
62	ScaCas9-Sc++	-	AGTGATAATAACTTTTCACTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCctctgataagcagtactgtaggccCCAAGTGAAAAGTTatta	30153	CTGCCACGTAATAGAGGGGCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGC	30302
63	SpyCas9-SpRY	-	AGTGATAATAACTTTTCACTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCctctgataagcagtactgtaggccCCAAGTGAAAAGTTatta	30154	TGCCACGTAATAGAGGGGCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGC	30303
64	SpyCas9-SpRY	+	GATAAGCAGTACTGTAGGCCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCtaacagtgataataactttcactTGGGGCCTACAGTActgc	30155	GGGCTGTGATGTAGAAGGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGC	30304
67	SauCas9KKH	+	CTGATAAGCAGTACTGTAGGCGTTTTAGTACTCTGGAAACAGAATCTACTAAAACAAGGCAAAATGCCGTGTTTATCTCGTCAACTTGTTGGCGAGAaacagtgataataacttttcactTGGGGCCTACAGTACtgct	30156	GGGCTGTGATGTAGAAGGAATGTTTTAGTACTCTGGAAACAGAATCTACTAAAACAAGGCAAAATGCCGTGTTTATCTCGTCAACTTGTTGGCGAGA	30305
68	SauCas9KKH	-	ACAGTGATAATAACTTTTCACGTTTTAGTACTCTGGAAACAGAATCTACTAAAACAAGGCAAAATGCCGTGTTTATCTCGTCAACTTGTTGGCGAGAtctgataagcagtactgtaggccCCAAGTGAAAAGTTAttat	30157	TCTGCCACGTAATAGAGGGGCGTTTTAGTACTCTGGAAACAGAATCTACTAAAACAAGGCAAAATGCCGTGTTTATCTCGTCAACTTGTTGGCGAGA	30306
69	SauriCas9-KKH	-	ACAGTGATAATAACTTTTCACGTTTTAGTACTCTGGAAACAGAATCTACTAAAACAAGGCAAAATGCCGTGTTTATCTCGTCAACTTGTTGGCGAGAtctgataagcagtactgtaggccCCAAGTGAAAAGTTAttat	30158	CTCTGCCACGTAATAGAGGGGGTTTTAGTACTCTGGAAACAGAATCTACTAAAACAAGGCAAAATGCCGTGTTTATCTCGTCAACTTGTTGGCGAGA	30307
70	SpyCas9-SpRY	+	TGATAAGCAGTACTGTAGGCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCaacagtgataataacttttcactTGGGGCCTACAGTACtgct	30159	GGCTGTGATGTAGAAGGAATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGC	30308
71	SpyCas9-SpRY	-	CAGTGATAATAACTTTTCACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAA	30160	GCCACGTAATAGAGGGGCTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCG	30309

			AAGTGGCACCGAGTCGGTGCtctgataagcagtactgtaggccCCA AGTGAAAAGTTAttat		TTATCAACTTGAAAAAGTGGCACCGAGTCGGT GC	
74	SauCas 9KKH	-	AACAGTGATAATAACTTTTCAGTTTTAGTACTCTGGAA ACAGAATCTACTAAAACAAGGCAAAATGCCGTGTTTAT CTCGTCAACTTGTTGGCGAGActgataagcagtactgtaggccCCA AGTGAAAAGTTATtatc	30161	TCTGCCACGTAATAGAGGGGCGTTTTAGTACT CTGGAAACAGAATCTACTAAAACAAGGCAAA ATGCCGTGTTTATCTCGTCAACTTGTTGGCGA GA	30310
75	SpyCas 9-SpRY	+	CTGATAAGCAGTACTGTAGGGTTTTAGAGCTAGAAATA GCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAA AAGTGGCACCGAGTCGGTGCacagtgataataactttt cactTGGGG CCTACAGTACTgctt	30162	GCTGTGATGTAGAAGGAATCGTTTTAGAGCTA GAAATAGCAAGTTAAAATAAGGCTAGTCCGT TATCAACTTGAAAAAGTGGCACCGAGTCGGT GC	30311
76	SpyCas 9-SpRY	-	ACAGTGATAATAACTTTTCAGTTTTAGAGCTAGAAATA GCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAA AAGTGGCACCGAGTCGGTGCctgataagcagtactgtaggccCCAA GTGAAAAGTTATtatc	30163	CCACGTAATAGAGGGGCTGGGTTTTAGAGCT AGAAATAGCAAGTTAAAATAAGGCTAGTCCG TTATCAACTTGAAAAAGTGGCACCGAGTCGGT GC	30312
77	SpyCas 9-SpRY	+	TCTGATAAGCAGTACTGTAGGTTTTAGAGCTAGAAATA GCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAA AAGTGGCACCGAGTCGGTGCcagtgataataactttt cactTGGGG CCTACAGTACTGctta	30164	CTGTGATGTAGAAGGAATCGGTTTTAGAGCTA GAAATAGCAAGTTAAAATAAGGCTAGTCCGT TATCAACTTGAAAAAGTGGCACCGAGTCGGT GC	30313
78	SpyCas 9-SpRY	-	AACAGTGATAATAACTTTTCGTTTTAGAGCTAGAAATA GCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAA AAGTGGCACCGAGTCGGTGCtgataagcagtactgtaggccCCAA GTGAAAAGTTATTatca	30165	CACGTAATAGAGGGGCTGGAGTTTTAGAGCT AGAAATAGCAAGTTAAAATAAGGCTAGTCCG TTATCAACTTGAAAAAGTGGCACCGAGTCGGT GC	30314
79	SpyCas 9-NG	+	CTCTGATAAGCAGTACTGTAGTTTTAGAGCTAGAAATA GCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAA AAGTGGCACCGAGTCGGTGCagtgataataactttt cactTGGGGC CTACAGTACTGCttat	30166	TGTGATGTAGAAGGAATCGGGTTTTAGAGCTA GAAATAGCAAGTTAAAATAAGGCTAGTCCGT TATCAACTTGAAAAAGTGGCACCGAGTCGGT GC	30315
83	SpyCas 9-SpRY	+	CTCTGATAAGCAGTACTGTAGTTTTAGAGCTAGAAATA GCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAA AAGTGGCACCGAGTCGGTGCagtgataataactttt cactTGGGGC CTACAGTACTGCttat	30167	TGTGATGTAGAAGGAATCGGGTTTTAGAGCTA GAAATAGCAAGTTAAAATAAGGCTAGTCCGT TATCAACTTGAAAAAGTGGCACCGAGTCGGT GC	30316
84	SpyCas 9-SpRY	-	TAACAGTGATAATAACTTTTGTTTTAGAGCTAGAAATA GCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAA AAGTGGCACCGAGTCGGTGCgataagcagtactgtaggccCCAAG TGAAAAGTTATTAtcac	30168	ACGTAATAGAGGGGCTGGAAGTTTTAGAGCT AGAAATAGCAAGTTAAAATAAGGCTAGTCCG TTATCAACTTGAAAAAGTGGCACCGAGTCGGT GC	30317
85	BlatCas 9	+	cttcTCTGATAAGCAGTACTGTAGCTATAGTTCCTTACTG AAAGGTAAGTTGCTATAGTAAGGGCAACAGACCCGAG GCGTTGGGGATCGCCTAGCCCGTGTTTACGGGCTCTCC CCATATTCAAAATAATGACAGACGAGCACCTTGGAGC	30169	gcatTTGGGCTGTGATGTAGAAGGCTATAGTTC CTTACTGAAAGGTAAGTTGCTATAGTAAGGGC AACAGACCCGAGGCGTTGGGGATCGCCTAGC CCGTGTTTACGGGCTCTCCCCATATTCAAAAT	30318

			ATTTATCTCCGAGGTGCTagtgataataacttttcactTGGGGCCTACAGTACTGCttat		AATGACAGACGAGCACCTTGGAGCATTTATCTCCGAGGTGCT	
86	BlatCas9	+	cttcTCTGATAAGCAGTACTGTAGCTATAGTTCCTTACTGAAAGGTAAGTTGCTATAGTAAGGGCAACAGACCCGAGGCGTTGGGGATCGCCTAGCCCGTGTTTACGGGCTCTCCCCATATTCAAAATAATGACAGACGAGCACCTTGGAGCATTTATCTCCGAGGTGCTagtgataataacttttcactTGGGGCCTACAGTACTGCttat	30170	gcatTTGGGCTGTGATGTAGAAGGCTATAGTTCCTTACTGAAAGGTAAGTTGCTATAGTAAGGGCAACAGACCCGAGGCGTTGGGGATCGCCTAGCCCGTGTTTACGGGCTCTCCCCATATTCAAAATAATGACAGACGAGCACCTTGGAGCATTTATCTCCGAGGTGCT	30319
87	BlatCas9	+	cttcTCTGATAAGCAGTACTGTAGCTATAGTTCCTTACTGAAAGGTAAGTTGCTATAGTAAGGGCAACAGACCCGAGGCGTTGGGGATCGCCTAGCCCGTGTTTACGGGCTCTCCCCATATTCAAAATAATGACAGACGAGCACCTTGGAGCATTTATCTCCGAGGTGCTagtgataataacttttcactTGGGGCCTACAGTACTGCttat	30171	gcatTTGGGCTGTGATGTAGAAGGCTATAGTTCCTTACTGAAAGGTAAGTTGCTATAGTAAGGGCAACAGACCCGAGGCGTTGGGGATCGCCTAGCCCGTGTTTACGGGCTCTCCCCATATTCAAAATAATGACAGACGAGCACCTTGGAGCATTTATCTCCGAGGTGCT	30320
90	Nme2Cas9	+	ggCTTCTCTGATAAGCAGTACTGTGTTGTAGCTCCCTTTCTCATTTCGGAAACGAAATGAGAACCGTTGCTACAATAAGGCCGTCTGAAAAGATGTGCCGCAACGCTCTGCCCCTTAAAGCTTCTGCTTTAAGGGGCATCGTTTAgtgataataactttcactTGGGGCCTACAGTACTGCTtatc	30172	ggTGAGATGAGAGAAGGGGCACAAGTTGTAGCTCCCTTTCTCATTTCGGAAACGAAATGAGAACCGTTGCTACAATAAGGCCGTCTGAAAAGATGTGCCGCAACGCTCTGCCCCTTAAAGCTTCTGCTTTAAGGGGCATCGTTTA	30321
93	ScaCas9-Sc++	+	TCTCTGATAAGCAGTACTGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCgtgataataactttcactTGGGGCCTACAGTACTGCTtatc	30173	GTGATGTAGAAGGAATCGGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGC	30322
94	SpyCas9	+	TCTCTGATAAGCAGTACTGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCgtgataataactttcactTGGGGCCTACAGTACTGCTtatc	30174	CTGTGATGTAGAAGGAATCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTATCAACTTGAAAAAGTGGCACCGAGTCGGTGC	30323
97	SpyCas9-SpRY	+	TCTCTGATAAGCAGTACTGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCgtgataataactttcactTGGGGCCTACAGTACTGCTtatc	30175	GTGATGTAGAAGGAATCGGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGC	30324
98	SpyCas9-NG	+	TCTCTGATAAGCAGTACTGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCgtgataataactttcactTGGGGCCTACAGTACTGCTtatc	30176	TGTGATGTAGAAGGAATCGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTATCAACTTGAAAAAGTGGCACCGAGTCGGTGC	30325
101	SpyCas9-SpRY	-	TTAACAGTGATAATAACTTTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCataagcagtactgtaggccCCAAGTGAAAAGTTATTATcact	30177	CGTAATAGAGGGGCTGGAACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGC	30326

102	BlatCas9	+	gcttCTCTGATAAGCAGTACTGTGCTATAGTTCCTTACTGAAAGGTAAGTTGCTATAGTAAGGGCAACAGACCCGAGGCGTTGGGGATCGCCTAGCCCGTGTTTACGGGCTCTCCCCATATTCAAAATAATGACAGACGAGCACCTTGGAGCATTTATCTCCGAGGTGCTgtgataataacttttcactTGGGGCCTACAGTACTGCTtatc	30178	gcatTTGGGCTGTGATGTAGAAGGCTATAGTTCCTTACTGAAAGGTAAGTTGCTATAGTAAGGGCAACAGACCCGAGGCGTTGGGGATCGCCTAGCCCGTGTTTACGGGCTCTCCCCATATTCAAAATAATGACAGACGAGCACCTTGGAGCATTTATCTCCGAGGTGCT	30327
103	BlatCas9	+	gcttCTCTGATAAGCAGTACTGTGCTATAGTTCCTTACTGAAAGGTAAGTTGCTATAGTAAGGGCAACAGACCCGAGGCGTTGGGGATCGCCTAGCCCGTGTTTACGGGCTCTCCCCATATTCAAAATAATGACAGACGAGCACCTTGGAGCATTTATCTCCGAGGTGCTgtgataataacttttcactTGGGGCCTACAGTACTGCTtatc	30179	gcatTTGGGCTGTGATGTAGAAGGCTATAGTTCCTTACTGAAAGGTAAGTTGCTATAGTAAGGGCAACAGACCCGAGGCGTTGGGGATCGCCTAGCCCGTGTTTACGGGCTCTCCCCATATTCAAAATAATGACAGACGAGCACCTTGGAGCATTTATCTCCGAGGTGCT	30328
106	Nme2Cas9	+	tgGCTTCTCTGATAAGCAGTACTGGTTGTAGCTCCCTTTCTCATTTCGGAAACGAAATGAGAACCGTTGCTACAATAAGGCCGTCTGAAAAGATGTGCCGCAACGCTCTGCCCCTTTAAAGCTTCTGCTTTAAGGGGCATCGTTTAtgataataacttttcactTGGGGCCTACAGTACTGCTTatca	30180	ggTGAGATGAGAGAAGGGGCACAAGTTGTAGCTCCCTTTCTCATTTCGGAAACGAAATGAGAACCGTTGCTACAATAAGGCCGTCTGAAAAGATGTGCCGCAACGCTCTGCCCCTTAAAGCTTCTGCTTTAAGGGGCATCGTTTA	30329
107	SauriCas9	+	CTTCTCTGATAAGCAGTACTGGTTTTAGTACTCTGGAAACAGAATCTACTAAAACAAGGCAAAATGCCGTGTTTATCTCGTCAACTTGTTGGCGAGAtgataataacttttcactTGGGGCCTACAGTACTGCTTatca	30181	GGCTGTGATGTAGAAGGAATCGTTTTAGTACTCTGGAAACAGAATCTACTAAAACAAGGCAAAATGCCGTGTTTATCTCGTCAACTTGTTGGCGAGA	30330
108	SauriCas9-KKH	+	CTTCTCTGATAAGCAGTACTGGTTTTAGTACTCTGGAAACAGAATCTACTAAAACAAGGCAAAATGCCGTGTTTATCTCGTCAACTTGTTGGCGAGAtgataataacttttcactTGGGGCCTACAGTACTGCTTatca	30182	GTGATGTAGAAGGAATCGGGGGTTTTAGTACTCTGGAAACAGAATCTACTAAAACAAGGCAAAATGCCGTGTTTATCTCGTCAACTTGTTGGCGAGA	30331
111	ScaCas9-Sc++	+	TTCTCTGATAAGCAGTACTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCtgataataacttttcactTGGGGCCTACAGTACTGCTTatca	30183	GTGATGTAGAAGGAATCGGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGC	30332
112	SpyCas9-SpRY	+	TTCTCTGATAAGCAGTACTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCtgataataacttttcactTGGGGCCTACAGTACTGCTTatca	30184	TGATGTAGAAGGAATCGGGGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGC	30333
113	SpyCas9-SpRY	-	TTTAACAGTGATAATAACTTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCtaagcagtactgtaggccCCAAGTGAAAAGTTATTATCactg	30185	GTAATAGAGGGGCTGGAACTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGC	30334
114	BlatCas9	-	tgatTTAACAGTGATAATAACTTGCTATAGTTCCTTACTGAAAGGTAAGTTGCTATAGTAAGGGCAACAGACCCGAG	30186	cgtaATAGAGGGGCTGGAACTCCGCTATAGTTCCTTACTGAAAGGTAAGTTGCTATAGTAAGGGC	30335

			GCGTTGGGGATCGCCTAGCCCGTGTTTACGGGCTCTCC CCATATTCAAAATAATGACAGACGAGCACCTTGGAGC ATTTATCTCCGAGGTGCTtaagcagtactgtaggccCCAAGTGAA AAGTTATTATCactg		AACAGACCCGAGGCGTTGGGGATCGCCTAGC CCGTGTTTACGGGCTCTCCCCATATTCAAAAT AATGACAGACGAGCACCTTGGAGCATTTATCT CCGAGGTGCT	
115	BlatCas 9	+	ggctTCTCTGATAAGCAGTACTGGCTATAGTTCCTTACTG AAAGGTAAGTTGCTATAGTAAGGGCAACAGACCCGAG GCGTTGGGGATCGCCTAGCCCGTGTTTACGGGCTCTCC CCATATTCAAAATAATGACAGACGAGCACCTTGGAGC ATTTATCTCCGAGGTGCTtgataataacttttcactTGGGGCCTAC AGTACTGCTTatca	3018 7	gcatTTGGGCTGTGATGTAGAAGGCTATAGTTC CTTACTGAAAGGTAAGTTGCTATAGTAAGGGC AACAGACCCGAGGCGTTGGGGATCGCCTAGC CCGTGTTTACGGGCTCTCCCCATATTCAAAAT AATGACAGACGAGCACCTTGGAGCATTTATCT CCGAGGTGCT	30336
116	BlatCas 9	-	tgatTTAACAGTGATAATAACTTGCTATAGTTCCTTACTG AAAGGTAAGTTGCTATAGTAAGGGCAACAGACCCGAG GCGTTGGGGATCGCCTAGCCCGTGTTTACGGGCTCTCC CCATATTCAAAATAATGACAGACGAGCACCTTGGAGC ATTTATCTCCGAGGTGCTtaagcagtactgtaggccCCAAGTGAA AAGTTATTATCactg	3018 8	cgtaATAGAGGGGCTGGAACTCCGCTATAGTTC CTTACTGAAAGGTAAGTTGCTATAGTAAGGGC AACAGACCCGAGGCGTTGGGGATCGCCTAGC CCGTGTTTACGGGCTCTCCCCATATTCAAAAT AATGACAGACGAGCACCTTGGAGCATTTATCT CCGAGGTGCT	30337
119	SauCas 9KKH	+	GCTTCTCTGATAAGCAGTACTGTTTTAGTACTCTGGAA ACAGAATCTACTAAAACAAGGCAAAATGCCGTGTTTAT CTCGTCAACTTGTTGGCGAGAgataataacttttcactTGGGGCC TACAGTACTGCTTAtcag	3018 9	GTGATGTAGAAGGAATCGGGGGTTTTAGTACT CTGGAAACAGAATCTACTAAAACAAGGCAAA ATGCCGTGTTTATCTCGTCAACTTGTTGGCGA GA	30338
120	SauriCa s9-KKH	+	GCTTCTCTGATAAGCAGTACTGTTTTAGTACTCTGGAA ACAGAATCTACTAAAACAAGGCAAAATGCCGTGTTTAT CTCGTCAACTTGTTGGCGAGAgataataacttttcactTGGGGCC TACAGTACTGCTTAtcag	3019 0	GTGATGTAGAAGGAATCGGGGGTTTTAGTACT CTGGAAACAGAATCTACTAAAACAAGGCAAA ATGCCGTGTTTATCTCGTCAACTTGTTGGCGA GA	30339
121	SpyCas 9-SpRY	+	CTTCTCTGATAAGCAGTACTGTTTTAGAGCTAGAAATA GCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAA AAGTGGCACCGAGTCGGTGCgataataactttcactTGGGGCCT ACAGTACTGCTTAtcag	3019 1	GATGTAGAAGGAATCGGGGTGTTTTAGAGCT AGAAATAGCAAGTTAAAATAAGGCTAGTCCG TTATCAACTTGAAAAAGTGGCACCGAGTCGGT GC	30340
122	SpyCas 9-SpRY	-	ATTTAACAGTGATAATAACTGTTTTAGAGCTAGAAATA GCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAA AAGTGGCACCGAGTCGGTGCaagcagtactgtaggccCCAAGTG AAAAGTTATTATCActgt	3019 2	TAATAGAGGGGCTGGAACTCGTTTTAGAGCTA GAAATAGCAAGTTAAAATAAGGCTAGTCCGT TATCAACTTGAAAAAGTGGCACCGAGTCGGT GC	30341
125	SauCas 9KKH	+	GGCTTCTCTGATAAGCAGTACGTTTTAGTACTCTGGAA ACAGAATCTACTAAAACAAGGCAAAATGCCGTGTTTAT CTCGTCAACTTGTTGGCGAGAataataacttttcactTGGGGCCT ACAGTACTGCTTATcaga	3019 3	ATGTAGAAGGAATCGGGGTGAGTTTTAGTACT CTGGAAACAGAATCTACTAAAACAAGGCAAA ATGCCGTGTTTATCTCGTCAACTTGTTGGCGA GA	30342
126	SpyCas 9-NG	+	GCTTCTCTGATAAGCAGTACGTTTTAGAGCTAGAAATA GCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAA	3019 4	ATGTAGAAGGAATCGGGGTGGTTTTAGAGCT AGAAATAGCAAGTTAAAATAAGGCTAGTCCG	30343

			AAGTGGCACCGAGTCGGTGCataataacttttcactTGGGGCCTACAGTACTGCTTATcaga		TTATCAACTTGAAAAAGTGGCACCGAGTCGGTGC	
130	SpyCas9-SpRY	+	GCTTCTCTGATAAGCAGTACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCataataacttttcactTGGGGCCTACAGTACTGCTTATcaga	30195	ATGTAGAAGGAATCGGGGTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGC	30344
131	SpyCas9-SpRY	-	GATTTAACAGTGATAATAACGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCagcagtactgtaggccCCAAGTGAAAAGTTATTATCACtgtt	30196	AATAGAGGGGCTGGAACTCCGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGC	30345
132	BlatCas9	-	cctgATTTAACAGTGATAATAACGCTATAGTTCCTTACTGAAAGGTAAGTTGCTATAGTAAGGGCAACAGACCCGAGGCGTTGGGGATCGCCTAGCCCGTGTTTACGGGCTCTCCCCATATTCAAAATATTTATCTCCGAGGTGCTagcagtactgtaggccCCAAGTGAAAAGTTATTATCACtgtt	30197	cgtaATAGAGGGGCTGGAACTCCGCTATAGTTCCTTACTGAAAGGTAAGTTGCTATAGTAAGGGCAACAGACCCGAGGCGTTGGGGATCGCCTAGCCCGTGTTTACGGGCTCTCCCCATATTCAAAATAATGACAGACGAGCACCTTGGAGCATTTATCTCCGAGGTGCT	30346
136	ScaCas9-Sc++	+	GGCTTCTCTGATAAGCAGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCtaataacttttcactTGGGGCCTACAGTACTGCTTATCagag	30198	GTAGAAGGAATCGGGGTGAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGC	30347
137	SpyCas9-SpRY	+	GGCTTCTCTGATAAGCAGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCtaataacttttcactTGGGGCCTACAGTACTGCTTATCagag	30199	TGTAGAAGGAATCGGGGTGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGC	30348
138	SpyCas9-SpRY	-	TGATTTAACAGTGATAATAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCgcagtactgtaggccCCAAGTGAAAAGTTATTATCACTgtta	30200	ATAGAGGGGCTGGAACTCCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGC	30349
139	SpyCas9-SpRY	+	TGGCTTCTCTGATAAGCAGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCaataacttttcactTGGGGCCTACAGTACTGCTTATCAgaga	30201	GTAGAAGGAATCGGGGTGAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGC	30350
140	SpyCas9-SpRY	-	CTGATTTAACAGTGATAATAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAGTGGCACCGAGTCGGTGCcagtactgtaggccCCAAGTGAAAAGTTATTATCACTGttaa	30202	TAGAGGGGCTGGAACTCCGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGC	30351
141	SpyCas9-SpRY	+	TTGGCTTCTCTGATAAGCAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAA	30203	TAGAAGGAATCGGGGTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCG	30352

			AAGTGGCACCGAGTCGGTGCataacttttcactTGGGGCCTAC AGTACTGCTTATCAGagaa		TTATCAACTTGAAAAAGTGGCACCGAGTCGGT GC	
142	SpyCas 9-SpRY	-	CCTGATTTAACAGTGATAATGTTTTAGAGCTAGAAATA GCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAA AAGTGGCACCGAGTCGGTGCagtactgtaggccCCAAGTGAA AAGTTATTATCACTGTtaaa	3020 4	AGAGGGGCTGGAACTCCGTGGTTTTAGAGCT AGAAATAGCAAGTTAAAATAAGGCTAGTCCG TTATCAACTTGAAAAAGTGGCACCGAGTCGGT GC	30353
145	SpyCas 9-SpRY	-	TCCTGATTTAACAGTGATAAGTTTTAGAGCTAGAAATA GCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAA AAGTGGCACCGAGTCGGTGCgtactgtaggccCCAAGTGAAA AGTTATTATCACTGTTaaat	3020 5	GAGGGGCTGGAACTCCGTGAGTTTTAGAGCT AGAAATAGCAAGTTAAAATAAGGCTAGTCCG TTATCAACTTGAAAAAGTGGCACCGAGTCGGT GC	30354
146	SpyCas 9-SpRY	+	TTTGGCTTCTCTGATAAGCAGTTTTAGAGCTAGAAATA GCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAA AAGTGGCACCGAGTCGGTGCtaacttttcactTGGGGCCTACA GTACTGCTTATCAGAgaag	3020 6	AGAAGGAATCGGGGTGAGATGTTTTAGAGCT AGAAATAGCAAGTTAAAATAAGGCTAGTCCG TTATCAACTTGAAAAAGTGGCACCGAGTCGGT GC	30355
150	SpyCas 9-NG	+	CTTTGGCTTCTCTGATAAGCGTTTTAGAGCTAGAAATA GCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAA AAGTGGCACCGAGTCGGTGCaacttttcactTGGGGCCTACA GTACTGCTTATCAGAGaagc	3020 7	GAAGGAATCGGGGTGAGATGGTTTTAGAGCT AGAAATAGCAAGTTAAAATAAGGCTAGTCCG TTATCAACTTGAAAAAGTGGCACCGAGTCGGT GC	30356
154	SpyCas 9-SpRY	+	CTTTGGCTTCTCTGATAAGCGTTTTAGAGCTAGAAATA GCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAA AAGTGGCACCGAGTCGGTGCaacttttcactTGGGGCCTACA GTACTGCTTATCAGAGaagc	3020 8	GAAGGAATCGGGGTGAGATGGTTTTAGAGCT AGAAATAGCAAGTTAAAATAAGGCTAGTCCG TTATCAACTTGAAAAAGTGGCACCGAGTCGGT GC	30357
155	SpyCas 9-SpRY	-	ATCCTGATTTAACAGTGATAGTTTTAGAGCTAGAAATA GCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAA AAGTGGCACCGAGTCGGTGCtactgtaggccCCAAGTGAAA AGTTATTATCACTGTTAaatc	3020 9	AGGGGCTGGAACTCCGTGACGTTTTAGAGCTA GAAATAGCAAGTTAAAATAAGGCTAGTCCGT TATCAACTTGAAAAAGTGGCACCGAGTCGGT GC	30358
156	BlatCas 9	+	aagcTTTGGCTTCTCTGATAAGCGCTATAGTTCCTTACTG AAAGGTAAGTTGCTATAGTAAGGGCAACAGACCCGAG GCGTTGGGGATCGCCTAGCCCGTGTTTACGGGCTCTCC CCATATTCAAAATAATGACAGACGAGCACCTTGGAGC ATTTATCTCCGAGGTGCTaactttcactTGGGGCCTACAGTA CTGCTTATCAGAGaagc	3021 0	ggaaTCGGGGTGAGATGAGAGAAGCTATAGTTC CTTACTGAAAGGTAAGTTGCTATAGTAAGGGC AACAGACCCGAGGCGTTGGGGATCGCCTAGC CCGTGTTTACGGGCTCTCCCCATATTCAAAAT AATGACAGACGAGCACCTTGGAGCATTTATCT CCGAGGTGCT	30359
157	BlatCas 9	-	ctgaTCCTGATTTAACAGTGATAGCTATAGTTCCTTACTG AAAGGTAAGTTGCTATAGTAAGGGCAACAGACCCGAG GCGTTGGGGATCGCCTAGCCCGTGTTTACGGGCTCTCC CCATATTCAAAATAATGACAGACGAGCACCTTGGAGC ATTTATCTCCGAGGTGCTtactgtaggccCCAAGTGAAAAGT TATTATCACTGTTAaatc	3021 1	cgtaATAGAGGGGCTGGAACTCCGCTATAGTTC CTTACTGAAAGGTAAGTTGCTATAGTAAGGGC AACAGACCCGAGGCGTTGGGGATCGCCTAGC CCGTGTTTACGGGCTCTCCCCATATTCAAAAT AATGACAGACGAGCACCTTGGAGCATTTATCT CCGAGGTGCT	30360

158	BlatCas9	+	aagcTTTGGCTTCTCTGATAAGCGCTATAGTTCCTTACTGAAAGGTAAGTTGCTATAGTAAGGGCAACAGACCCGAGGCGTTGGGGATCGCCTAGCCCGTGTTTACGGGCTCTCCCCATATTCAAAATAATGACAGACGAGCACCTTGGAGCATTTATCTCCGAGGTGCTaacttttcactTGGGGCCTACAGTACTGCTTATCAGAGaagc	30212	ggaaTCGGGGTGAGATGAGAGAAGCTATAGTTCCTTACTGAAAGGTAAGTTGCTATAGTAAGGGCAACAGACCCGAGGCGTTGGGGATCGCCTAGCCCGTGTTTACGGGCTCTCCCCATATTCAAAATAATGACAGACGAGCACCTTGGAGCATTTATCTCCGAGGTGCT	30361
159	BlatCas9	-	ctgaTCCTGATTTAACAGTGATAGCTATAGTTCCTTACTGAAAGGTAAGTTGCTATAGTAAGGGCAACAGACCCGAGGCGTTGGGGATCGCCTAGCCCGTGTTTACGGGCTCTCCCCATATTCAAAATAATGACAGACGAGCACCTTGGAGCATTTATCTCCGAGGTGCTtactgtaggccCCAAGTGAAAAGTTATTATCACTGTTAaatc	30213	cgtaATAGAGGGGCTGGAACTCCGCTATAGTTCCTTACTGAAAGGTAAGTTGCTATAGTAAGGGCAACAGACCCGAGGCGTTGGGGATCGCCTAGCCCGTGTTTACGGGCTCTCCCCATATTCAAAATAATGACAGACGAGCACCTTGGAGCATTTATCTCCGAGGTGCT	30362
164	SauCas9KKH	-	TGATCCTGATTTAACAGTGATGTTTTAGTACTCTGGAAACAGAATCTACTAAAACAAGGCAAAATGCCGTGTTTATCTCGTCAACTTGTTGGCGAGAactgtaggccCCAAGTGAAAAGTTATTATCACTGTTAAatca	30214	GGGGCTGGAACTCCGTGACAGGTTTTAGTACTCTGGAAACAGAATCTACTAAAACAAGGCAAAATGCCGTGTTTATCTCGTCAACTTGTTGGCGAGA	30363
167	ScaCas9-Sc++	+	GCTTTGGCTTCTCTGATAAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCactttcactTGGGGCCTACAGTACTGCTTATCAGAGAagcc	30215	AAGGAATCGGGGTGAGATGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGC	30364
168	SpyCas9-SpRY	+	GCTTTGGCTTCTCTGATAAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCactttcactTGGGGCCTACAGTACTGCTTATCAGAGAagcc	30216	AAGGAATCGGGGTGAGATGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGC	30365
169	SpyCas9-SpRY	-	GATCCTGATTTAACAGTGATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCactgtaggccCCAAGTGAAAAGTTATTATCACTGTTAAatca	30217	GGGGCTGGAACTCCGTGACAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGC	30366
173	SauriCas9-KKH	+	AAGCTTTGGCTTCTCTGATAAGTTTTAGTACTCTGGAACAGAATCTACTAAAACAAGGCAAAATGCCGTGTTTATCTCGTCAACTTGTTGGCGAGActttcactTGGGGCCTACAGTACTGCTTATCAGAGAAgcca	30218	AGGAATCGGGGTGAGATGAGAGTTTTAGTACTCTGGAAACAGAATCTACTAAAACAAGGCAAAATGCCGTGTTTATCTCGTCAACTTGTTGGCGAGA	30367
174	SpyCas9-SpRY	-	TGATCCTGATTTAACAGTGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCctgtaggccCCAAGTGAAAAGTTATTATCACTGTTAAAtcag	30219	GGGCTGGAACTCCGTGACAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGC	30368
175	SpyCas9-SpRY	+	AGCTTTGGCTTCTCTGATAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAA	30220	AGGAATCGGGGTGAGATGAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCG	30369

			AAGTGGCACCGAGTCGGTGCcttttcactTGGGGCCTACAGT ACTGCTTATCAGAGAAgcca		TTATCAACTTGAAAAAGTGGCACCGAGTCGGT GC	
179	SauCas 9KKH	+	GAAGCTTTGGCTTCTCTGATAGTTTTAGTACTCTGGAA ACAGAATCTACTAAAACAAGGCAAAATGCCGTGTTTAT CTCGTCAACTTGTTGGCGAGAttttcactTGGGGCCTACAGT ACTGCTTATCAGAGAAGccaa	30221	AGGAATCGGGGTGAGATGAGAGTTTTAGTAC TCTGGAAACAGAATCTACTAAAACAAGGCAA AATGCCGTGTTTATCTCGTCAACTTGTTGGCG AGA	30370
180	SauCas 9KKH	+	GAAGCTTTGGCTTCTCTGATAGTTTTAGTACTCTGGAA ACAGAATCTACTAAAACAAGGCAAAATGCCGTGTTTAT CTCGTCAACTTGTTGGCGAGAttttcactTGGGGCCTACAGT ACTGCTTATCAGAGAAGccaa	30222	AGGAATCGGGGTGAGATGAGAGTTTTAGTAC TCTGGAAACAGAATCTACTAAAACAAGGCAA AATGCCGTGTTTATCTCGTCAACTTGTTGGCG AGA	30371
183	SpyCas 9-NG	+	AAGCTTTGGCTTCTCTGATAGTTTTAGAGCTAGAAATA GCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAA AAGTGGCACCGAGTCGGTGCttttcactTGGGGCCTACAGT ACTGCTTATCAGAGAAGccaa	30223	AGGAATCGGGGTGAGATGAGGTTTTAGAGCT AGAAATAGCAAGTTAAAATAAGGCTAGTCCG TTATCAACTTGAAAAAGTGGCACCGAGTCGGT GC	30372
187	SpyCas 9-SpRY	+	AAGCTTTGGCTTCTCTGATAGTTTTAGAGCTAGAAATA GCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAA AAGTGGCACCGAGTCGGTGCttttcactTGGGGCCTACAGT ACTGCTTATCAGAGAAGccaa	30224	GGAATCGGGGTGAGATGAGAGTTTTAGAGCT AGAAATAGCAAGTTAAAATAAGGCTAGTCCG TTATCAACTTGAAAAAGTGGCACCGAGTCGGT GC	30373
188	SpyCas 9-SpRY	-	CTGATCCTGATTTAACAGTGGTTTTAGAGCTAGAAATA GCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAA AAGTGGCACCGAGTCGGTGCtgtaggccCCAAGTGAAAAG TTATTATCACTGTTAAATcagg	30225	GGCTGGAACTCCGTGACAGTGTTTTAGAGCTA GAAATAGCAAGTTAAAATAAGGCTAGTCCGT TATCAACTTGAAAAAGTGGCACCGAGTCGGT GC	30374
191	SauCas 9KKH	-	TACTGATCCTGATTTAACAGTGTTTTAGTACTCTGGAA ACAGAATCTACTAAAACAAGGCAAAATGCCGTGTTTAT CTCGTCAACTTGTTGGCGAGAgtaggccCCAAGTGAAAAG TTATTATCACTGTTAAATCagga	30226	GGGGCTGGAACTCCGTGACAGGTTTTAGTACT CTGGAAACAGAATCTACTAAAACAAGGCAAA ATGCCGTGTTTATCTCGTCAACTTGTTGGCGA GA	30375
192	SauCas 9KKH	-	TACTGATCCTGATTTAACAGTGTTTTAGTACTCTGGAA ACAGAATCTACTAAAACAAGGCAAAATGCCGTGTTTAT CTCGTCAACTTGTTGGCGAGAgtaggccCCAAGTGAAAAG TTATTATCACTGTTAAATCagga	30227	GGGGCTGGAACTCCGTGACAGGTTTTAGTACT CTGGAAACAGAATCTACTAAAACAAGGCAAA ATGCCGTGTTTATCTCGTCAACTTGTTGGCGA GA	30376
195	ScaCas 9-Sc++	+	GAAGCTTTGGCTTCTCTGATGTTTTAGAGCTAGAAATA GCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAA AAGTGGCACCGAGTCGGTGCtttcactTGGGGCCTACAGTA CTGCTTATCAGAGAAGCcaaa	30228	GAATCGGGGTGAGATGAGAGGTTTTAGAGCT AGAAATAGCAAGTTAAAATAAGGCTAGTCCG TTATCAACTTGAAAAAGTGGCACCGAGTCGGT GC	30377
196	SpyCas 9-SpRY	+	GAAGCTTTGGCTTCTCTGATGTTTTAGAGCTAGAAATA GCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAA AAGTGGCACCGAGTCGGTGCtttcactTGGGGCCTACAGTA CTGCTTATCAGAGAAGCcaaa	30229	GAATCGGGGTGAGATGAGAGGTTTTAGAGCT AGAAATAGCAAGTTAAAATAAGGCTAGTCCG TTATCAACTTGAAAAAGTGGCACCGAGTCGGT GC	30378

197	SpyCas9-SpRY	-	ACTGATCCTGATTTAACAGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCgtaggccCCAAGTGAAAAGTTATTATCACTGTTAAATCagga	30230	GCTGGAACTCCGTGACAGTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGC	30379
201	SauriCas9-KKH	+	GAGAAGCTTTGGCTTCTCTGAGTTTTAGTACTCTGGAAACAGAATCTACTAAAACAAGGCAAAATGCCGTGTTTATCTCGTCAACTTGTTGGCGAGAttcactTGGGGCCTACAGTACTGCTTATCAGAGAAGCCaaag	30231	GAATCGGGGTGAGATGAGAGAGTTTTAGTACTCTGGAAACAGAATCTACTAAAACAAGGCAAAATGCCGTGTTTATCTCGTCAACTTGTTGGCGAGA	30380
204	SpyCas9-NG	-	TACTGATCCTGATTTAACAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCtaggccCCAAGTGAAAAGTTATTATCACTGTTAAATCAggat	30232	GGGCTGGAACTCCGTGACAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGC	30381
207	SpyCas9-SpRY	+	AGAAGCTTTGGCTTCTCTGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCttcactTGGGGCCTACAGTACTGCTTATCAGAGAAGCCaaag	30233	AATCGGGGTGAGATGAGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGC	30382
209	SpyCas9-SpRY	-	TACTGATCCTGATTTAACAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCtaggccCCAAGTGAAAAGTTATTATCACTGTTAAATCAggat	30234	CTGGAACTCCGTGACAGTGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGC	30383
210	BlatCas9	+	gggaGAAGCTTTGGCTTCTCTGAGCTATAGTTCCTTACTGAAAGGTAAGTTGCTATAGTAAGGGCAACAGACCCGAGGCGTTGGGGATCGCCTAGCCCGTGTTTACGGGCTCTCCCCATATTCAAAATAATGACAGACGAGCACCTTGGAGCATTTATCTCCGAGGTGCTttcactTGGGGCCTACAGTACTGCTTATCAGAGAAGCCaaag	30235	ggaaTCGGGGTGAGATGAGAGAAGCTATAGTTCCTTACTGAAAGGTAAGTTGCTATAGTAAGGGCAACAGACCCGAGGCGTTGGGGATCGCCTAGCCCGTGTTTACGGGCTCTCCCCATATTCAAAATAATGACAGACGAGCACCTTGGAGCATTTATCTCCGAGGTGCT	30384
211	BlatCas9	+	gggaGAAGCTTTGGCTTCTCTGAGCTATAGTTCCTTACTGAAAGGTAAGTTGCTATAGTAAGGGCAACAGACCCGAGGCGTTGGGGATCGCCTAGCCCGTGTTTACGGGCTCTCCCCATATTCAAAATAATGACAGACGAGCACCTTGGAGCATTTATCTCCGAGGTGCTttcactTGGGGCCTACAGTACTGCTTATCAGAGAAGCCaaag	30236	ggaaTCGGGGTGAGATGAGAGAAGCTATAGTTCCTTACTGAAAGGTAAGTTGCTATAGTAAGGGCAACAGACCCGAGGCGTTGGGGATCGCCTAGCCCGTGTTTACGGGCTCTCCCCATATTCAAAATAATGACAGACGAGCACCTTGGAGCATTTATCTCCGAGGTGCT	30385
215	SauCas9KKH	+	GGAGAAGCTTTGGCTTCTCTGGTTTTAGTACTCTGGAAACAGAATCTACTAAAACAAGGCAAAATGCCGTGTTTATCTCGTCAACTTGTTGGCGAGAtcactTGGGGCCTACAGTACTGCTTATCAGAGAAGCCAaagc	30237	GAATCGGGGTGAGATGAGAGAGTTTTAGTACTCTGGAAACAGAATCTACTAAAACAAGGCAAAATGCCGTGTTTATCTCGTCAACTTGTTGGCGAGA	30386
218	ScaCas9-Sc++	-	ATACTGATCCTGATTTAACAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAA	30238	AACTCCGTGACAGTGTAATTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGT	30387

			AAGTGGCACCGAGTCGGTGCaggccCCAAGTGAAAAGTT ATTATCACTGTTAAATCAGgatc		TATCAACTTGAAAAAGTGGCACCGAGTCGGT GC	
219	SpyCas 9-SpRY	-	ATACTGATCCTGATTTAACAGTTTTAGAGCTAGAAATA GCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAA AAGTGGCACCGAGTCGGTGCaggccCCAAGTGAAAAGTT ATTATCACTGTTAAATCAGgatc	30239	TGGAACTCCGTGACAGTGTAGTTTTAGAGCTA GAAATAGCAAGTTAAAATAAGGCTAGTCCGT TATCAACTTGAAAAAGTGGCACCGAGTCGGT GC	30388
220	SpyCas 9-SpRY	+	GAGAAGCTTTGGCTTCTCTGGTTTTAGAGCTAGAAATA GCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAA AAGTGGCACCGAGTCGGTGCtcactTGGGGCCTACAGTAC TGCTTATCAGAGAAGCCAaagc	30240	ATCGGGGTGAGATGAGAGAAGTTTTAGAGCT AGAAATAGCAAGTTAAAATAAGGCTAGTCCG TTATCAACTTGAAAAAGTGGCACCGAGTCGGT GC	30389
223	SauCas 9KKH	+	GGGAGAAGCTTTGGCTTCTCTGTTTTAGTACTCTGGAA ACAGAATCTACTAAAACAAGGCAAAATGCCGTGTTTAT CTCGTCAACTTGTTGGCGAGAcactTGGGGCCTACAGTA CTGCTTATCAGAGAAGCCAAagct	30241	GAATCGGGGTGAGATGAGAGAGTTTTAGTAC TCTGGAAACAGAATCTACTAAAACAAGGCAA AATGCCGTGTTTATCTCGTCAACTTGTTGGCG AGA	30390
224	SauCas 9KKH	-	GAATACTGATCCTGATTTAACGTTTTAGTACTCTGGAA ACAGAATCTACTAAAACAAGGCAAAATGCCGTGTTTAT CTCGTCAACTTGTTGGCGAGAggccCCAAGTGAAAAGTT ATTATCACTGTTAAATCAGGatca	30242	GGAACTCCGTGACAGTGTAATGTTTTAGTACT CTGGAAACAGAATCTACTAAAACAAGGCAAA ATGCCGTGTTTATCTCGTCAACTTGTTGGCGA GA	30391
225	SauCas 9KKH	-	GAATACTGATCCTGATTTAACGTTTTAGTACTCTGGAA ACAGAATCTACTAAAACAAGGCAAAATGCCGTGTTTAT CTCGTCAACTTGTTGGCGAGAggccCCAAGTGAAAAGTT ATTATCACTGTTAAATCAGGatca	30243	GGAACTCCGTGACAGTGTAATGTTTTAGTACT CTGGAAACAGAATCTACTAAAACAAGGCAAA ATGCCGTGTTTATCTCGTCAACTTGTTGGCGA GA	30392
226	SpyCas 9-NG	-	AATACTGATCCTGATTTAACGTTTTAGAGCTAGAAATA GCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAA AAGTGGCACCGAGTCGGTGCggccCCAAGTGAAAAGTT ATTATCACTGTTAAATCAGGatca	30244	ACTCCGTGACAGTGTAATTTGTTTTAGAGCTA GAAATAGCAAGTTAAAATAAGGCTAGTCCGT TATCAACTTGAAAAAGTGGCACCGAGTCGGT GC	30393
229	SpyCas 9-SpRY	+	GGAGAAGCTTTGGCTTCTCTGTTTTAGAGCTAGAAATA GCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAA AAGTGGCACCGAGTCGGTGCcactTGGGGCCTACAGTAC TGCTTATCAGAGAAGCCAAagct	30245	TCGGGGTGAGATGAGAGAAGGTTTTAGAGCT AGAAATAGCAAGTTAAAATAAGGCTAGTCCG TTATCAACTTGAAAAAGTGGCACCGAGTCGGT GC	30394
232	SpyCas 9-SpRY	-	AATACTGATCCTGATTTAACGTTTTAGAGCTAGAAATA GCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAA AAGTGGCACCGAGTCGGTGCggccCCAAGTGAAAAGTT ATTATCACTGTTAAATCAGGatca	30246	GGAACTCCGTGACAGTGTAAGTTTTAGAGCTA GAAATAGCAAGTTAAAATAAGGCTAGTCCGT TATCAACTTGAAAAAGTGGCACCGAGTCGGT GC	30395
236	ScaCas 9-Sc++	-	GAATACTGATCCTGATTTAAGTTTTAGAGCTAGAAATA GCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAA AAGTGGCACCGAGTCGGTGCgccCCAAGTGAAAAGTTA TTATCACTGTTAAATCAGGAtcag	30247	AACTCCGTGACAGTGTAATTGTTTTAGAGCTA GAAATAGCAAGTTAAAATAAGGCTAGTCCGT TATCAACTTGAAAAAGTGGCACCGAGTCGGT GC	30396

237	SpyCas 9-SpRY	-	GAATACTGATCCTGATTTAAGTTTTAGAGCTAGAAATA GCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAA AAGTGGCACCGAGTCGGTGCgccCCAAGTGAAAAGTTA TTATCACTGTTAAATCAGGAtcag	3024 8	GAACTCCGTGACAGTGTAATGTTTTAGAGCTA GAAATAGCAAGTTAAAATAAGGCTAGTCCGT TATCAACTTGAAAAAGTGGCACCGAGTCGGT GC	30397
238	SpyCas 9-NG	+	GGGAGAAGCTTTGGCTTCTCGTTTTAGAGCTAGAAATA GCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAA AAGTGGCACCGAGTCGGTGCactTGGGGCCTACAGTACT GCTTATCAGAGAAGCCAAAgctt	3024 9	CGGGGTGAGATGAGAGAAGGGTTTTAGAGCT AGAAATAGCAAGTTAAAATAAGGCTAGTCCG TTATCAACTTGAAAAAGTGGCACCGAGTCGGT GC	30398
242	SpyCas 9-SpRY	+	GGGAGAAGCTTTGGCTTCTCGTTTTAGAGCTAGAAATA GCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAA AAGTGGCACCGAGTCGGTGCactTGGGGCCTACAGTACT GCTTATCAGAGAAGCCAAAgctt	3025 0	CGGGGTGAGATGAGAGAAGGGTTTTAGAGCT AGAAATAGCAAGTTAAAATAAGGCTAGTCCG TTATCAACTTGAAAAAGTGGCACCGAGTCGGT GC	30399
247	SauriCa s9-KKH	-	GGGAATACTGATCCTGATTTAGTTTTAGTACTCTGGAA ACAGAATCTACTAAAACAAGGCAAAATGCCGTGTTTAT CTCGTCAACTTGTTGGCGAGAccCCAAGTGAAAAGTTA TTATCACTGTTAAATCAGGATcagt	3025 1	GAACTCCGTGACAGTGTAATTGTTTTAGTACT CTGGAAACAGAATCTACTAAAACAAGGCAAA ATGCCGTGTTTATCTCGTCAACTTGTTGGCGA GA	30400
250	ScaCas 9-Sc++	+	GGGGAGAAGCTTTGGCTTCTGTTTTAGAGCTAGAAATA GCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAA AAGTGGCACCGAGTCGGTGCctTGGGGCCTACAGTACT GCTTATCAGAGAAGCCAAAGcttc	3025 2	TCGGGGTGAGATGAGAGAAGGTTTTAGAGCT AGAAATAGCAAGTTAAAATAAGGCTAGTCCG TTATCAACTTGAAAAAGTGGCACCGAGTCGGT GC	30401
251	SpyCas 9-SpRY	+	GGGGAGAAGCTTTGGCTTCTGTTTTAGAGCTAGAAATA GCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAA AAGTGGCACCGAGTCGGTGCctTGGGGCCTACAGTACT GCTTATCAGAGAAGCCAAAGcttc	3025 3	GGGGTGAGATGAGAGAAGGGGTTTTAGAGCT AGAAATAGCAAGTTAAAATAAGGCTAGTCCG TTATCAACTTGAAAAAGTGGCACCGAGTCGGT GC	30402
252	SpyCas 9-SpRY	-	GGAATACTGATCCTGATTTAGTTTTAGAGCTAGAAATA GCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAA AAGTGGCACCGAGTCGGTGCccCCAAGTGAAAAGTTAT TATCACTGTTAAATCAGGATcagt	3025 4	AACTCCGTGACAGTGTAATTGTTTTAGAGCTA GAAATAGCAAGTTAAAATAAGGCTAGTCCGT TATCAACTTGAAAAAGTGGCACCGAGTCGGT GC	30403
255	SauCas 9KKH	+	AGGGGGAGAAGCTTTGGCTTCGTTTTAGTACTCTGGAA ACAGAATCTACTAAAACAAGGCAAAATGCCGTGTTTAT CTCGTCAACTTGTTGGCGAGAtTGGGGCCTACAGTACT GCTTATCAGAGAAGCCAAAGCttct	3025 5	GGGGTGAGATGAGAGAAGGGGGTTTTAGTAC TCTGGAAACAGAATCTACTAAAACAAGGCAA AATGCCGTGTTTATCTCGTCAACTTGTTGGCG AGA	30404
256	SauCas 9KKH	-	AGGGAATACTGATCCTGATTTGTTTTAGTACTCTGGAA ACAGAATCTACTAAAACAAGGCAAAATGCCGTGTTTAT CTCGTCAACTTGTTGGCGAGAcCCAAGTGAAAAGTTAT TATCACTGTTAAATCAGGATCagta	3025 6	GAACTCCGTGACAGTGTAATTGTTTTAGTACT CTGGAAACAGAATCTACTAAAACAAGGCAAA ATGCCGTGTTTATCTCGTCAACTTGTTGGCGA GA	30405
257	SauCas 9KKH	+	AGGGGGAGAAGCTTTGGCTTCGTTTTAGTACTCTGGAA ACAGAATCTACTAAAACAAGGCAAAATGCCGTGTTTAT	3025 7	GGGGTGAGATGAGAGAAGGGGGTTTTAGTAC TCTGGAAACAGAATCTACTAAAACAAGGCAA	30406

			CTCGTCAACTTGTTGGCGAGAtTGGGGCCTACAGTACT GCTTATCAGAGAAGCCAAAGCttct		AATGCCGTGTTTATCTCGTCAACTTGTTGGCG AGA	
258	SauCas 9KKH	-	AGGGAATACTGATCCTGATTTGTTTTAGTACTCTGGAA ACAGAATCTACTAAAACAAGGCAAAATGCCGTGTTTAT CTCGTCAACTTGTTGGCGAGAcCCAAGTGAAAAGTTAT TATCACTGTTAAATCAGGATCagta	30258	GAACTCCGTGACAGTGTAATTGTTTTAGTACT CTGGAAACAGAATCTACTAAAACAAGGCAAA ATGCCGTGTTTATCTCGTCAACTTGTTGGCGA GA	30407
261	SpyCas 9-SpRY	-	GGGAATACTGATCCTGATTTGTTTTAGAGCTAGAAATA GCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAA AAGTGGCACCGAGTCGGTGCcCCAAGTGAAAAGTTATT ATCACTGTTAAATCAGGATCagta	30259	ACTCCGTGACAGTGTAATTTGTTTTAGAGCTA GAAATAGCAAGTTAAAATAAGGCTAGTCCGT TATCAACTTGAAAAAGTGGCACCGAGTCGGT GC	30408
262	SpyCas 9-SpRY	+	GGGGGAGAAGCTTTGGCTTCGTTTTAGAGCTAGAAATA GCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAA AAGTGGCACCGAGTCGGTGCtTGGGGCCTACAGTACTG CTTATCAGAGAAGCCAAAGCttct	30260	GGGTGAGATGAGAGAAGGGGGTTTTAGAGCT AGAAATAGCAAGTTAAAATAAGGCTAGTCCG TTATCAACTTGAAAAAGTGGCACCGAGTCGGT GC	30409
264	SpyCas 9-SpRY	-	AGGGAATACTGATCCTGATTGTTTTAGAGCTAGAAATA GCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAA AAGTGGCACCGAGTCGGTGCCCAAGTGAAAAGTTATT ATCACTGTTAAATCAGGATCAgtat	30261	CTCCGTGACAGTGTAATTTTGTTTTAGAGCTA GAAATAGCAAGTTAAAATAAGGCTAGTCCGT TATCAACTTGAAAAAGTGGCACCGAGTCGGT GC	30410
265	SpyCas 9-SpRY	+	AGGGGGAGAAGCTTTGGCTTGTTTTAGAGCTAGAAATA GCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAA AAGTGGCACCGAGTCGGTGCTGGGGCCTACAGTACTG CTTATCAGAGAAGCCAAAGCTtctc	30262	GGTGAGATGAGAGAAGGGGCGTTTTAGAGCT AGAAATAGCAAGTTAAAATAAGGCTAGTCCG TTATCAACTTGAAAAAGTGGCACCGAGTCGGT GC	30411
269	SpyCas 9-SpRY	+	CAGGGGGAGAAGCTTTGGCTGTTTTAGAGCTAGAAAT AGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAA AAAGTGGCACCGAGTCGGTGCGGGGCCTACAGTACTG CTTATCAGAGAAGCCAAAGCTTctcc	30263	GTGAGATGAGAGAAGGGGCAGTTTTAGAGCT AGAAATAGCAAGTTAAAATAAGGCTAGTCCG TTATCAACTTGAAAAAGTGGCACCGAGTCGGT GC	30412
270	SpyCas 9-SpRY	-	CAGGGAATACTGATCCTGATGTTTTAGAGCTAGAAATA GCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAA AAGTGGCACCGAGTCGGTGCCAAGTGAAAAGTTATTA TCACTGTTAAATCAGGATCAGtatt	30264	TCCGTGACAGTGTAATTTTGGTTTTAGAGCTA GAAATAGCAAGTTAAAATAAGGCTAGTCCGT TATCAACTTGAAAAAGTGGCACCGAGTCGGT GC	30413
271	BlatCas 9	-	cagcAGGGAATACTGATCCTGATGCTATAGTTCCTTACT GAAAGGTAAGTTGCTATAGTAAGGGCAACAGACCCGA GGCGTTGGGGATCGCCTAGCCCGTGTTTACGGGCTCTC CCCATATTCAAAATAATGACAGACGAGCACCTTGGAG CATTTATCTCCGAGGTGCTCAAGTGAAAAGTTATTATC ACTGTTAAATCAGGATCAGtatt	30265	actcCGTGACAGTGTAATTTTGGGCTATAGTTCC TTACTGAAAGGTAAGTTGCTATAGTAAGGGC AACAGACCCGAGGCGTTGGGGATCGCCTAGC CCGTGTTTACGGGCTCTCCCCATATTCAAAAT AATGACAGACGAGCACCTTGGAGCATTTATCT CCGAGGTGCT	30414
272	BlatCas 9	-	cagcAGGGAATACTGATCCTGATGCTATAGTTCCTTACT GAAAGGTAAGTTGCTATAGTAAGGGCAACAGACCCGA GGCGTTGGGGATCGCCTAGCCCGTGTTTACGGGCTCTC	30266	actcCGTGACAGTGTAATTTTGGGCTATAGTTCC TTACTGAAAGGTAAGTTGCTATAGTAAGGGC AACAGACCCGAGGCGTTGGGGATCGCCTAGC	30415

			CCCATATTCAAAATAATGACAGACGAGCACCTTGGAG CATTTATCTCCGAGGTGCTCAAGTGAAAAGTTATTATC ACTGTTAAATCAGGATCAGtatt		CCGTGTTTACGGGCTCTCCCCATATTCAAAAT AATGACAGACGAGCACCTTGGAGCATTTATCT CCGAGGTGCT	
273	SauCas 9KKH	-	AGCAGGGAATACTGATCCTGAGTTTTAGTACTCTGGAA ACAGAATCTACTAAAACAAGGCAAAATGCCGTGTTTAT CTCGTCAACTTGTTGGCGAGAAAGTGAAAAGTTATTAT CACTGTTAAATCAGGATCAGTattc	30267	CTCCGTGACAGTGTAATTTTGGTTTTAGTACT CTGGAAACAGAATCTACTAAAACAAGGCAAA ATGCCGTGTTTATCTCGTCAACTTGTTGGCGA GA	30416
274	SpyCas 9-SpRY	+	CCAGGGGGAGAAGCTTTGGCGTTTTAGAGCTAGAAAT AGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAA AAAGTGGCACCGAGTCGGTGCGGGCCTACAGTACTGC TTATCAGAGAAGCCAAAGCTTCtccc	30268	TGAGATGAGAGAAGGGGCACGTTTTAGAGCT AGAAATAGCAAGTTAAAATAAGGCTAGTCCG TTATCAACTTGAAAAAGTGGCACCGAGTCGGT GC	30417
275	SpyCas 9-SpRY	-	GCAGGGAATACTGATCCTGAGTTTTAGAGCTAGAAATA GCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAA AAGTGGCACCGAGTCGGTGCAAGTGAAAAGTTATTAT CACTGTTAAATCAGGATCAGTattc	30269	CCGTGACAGTGTAATTTTGGGTTTTAGAGCTA GAAATAGCAAGTTAAAATAAGGCTAGTCCGT TATCAACTTGAAAAAGTGGCACCGAGTCGGT GC	30418
276	BlatCas 9	+	gctcCAGGGGGAGAAGCTTTGGCGCTATAGTTCCTTACT GAAAGGTAAGTTGCTATAGTAAGGGCAACAGACCCGA GGCGTTGGGGATCGCCTAGCCCGTGTTTACGGGCTCTC CCCATATTCAAAATAATGACAGACGAGCACCTTGGAG CATTTATCTCCGAGGTGCTGGGCCTACAGTACTGCTTA TCAGAGAAGCCAAAGCTTCtccc	30270	gtgaGATGAGAGAAGGGGCACAAGCTATAGTTC CTTACTGAAAGGTAAGTTGCTATAGTAAGGGC AACAGACCCGAGGCGTTGGGGATCGCCTAGC CCGTGTTTACGGGCTCTCCCCATATTCAAAAT AATGACAGACGAGCACCTTGGAGCATTTATCT CCGAGGTGCT	30419
277	BlatCas 9	+	gctcCAGGGGGAGAAGCTTTGGCGCTATAGTTCCTTACT GAAAGGTAAGTTGCTATAGTAAGGGCAACAGACCCGA GGCGTTGGGGATCGCCTAGCCCGTGTTTACGGGCTCTC CCCATATTCAAAATAATGACAGACGAGCACCTTGGAG CATTTATCTCCGAGGTGCTGGGCCTACAGTACTGCTTA TCAGAGAAGCCAAAGCTTCtccc	30271	gtgaGATGAGAGAAGGGGCACAAGCTATAGTTC CTTACTGAAAGGTAAGTTGCTATAGTAAGGGC AACAGACCCGAGGCGTTGGGGATCGCCTAGC CCGTGTTTACGGGCTCTCCCCATATTCAAAAT AATGACAGACGAGCACCTTGGAGCATTTATCT CCGAGGTGCT	30420

Capital letters indicate "core nucleotides" while lower case letters indicate "flanking nucleotides." Herein, when an RNA sequence (e.g., a template RNA sequence) is said to comprise a particular sequence (e.g., a sequence of Table 4A, Table 4B, Table 4C, or Table 4D or a portion thereof) that comprises thymine (T), it is of course understood that the RNA sequence may (and frequently does) comprise uracil (U) in place of T. For instance, the RNA sequence may comprise U at every position shown as T in the sequence in Table 4A, Table 4B, Table 4C, or Table 4D. More specifically, the present disclosure provides an RNA sequence

according to every template sequence shown in Table 4A, Table 4B, Table 4C, or Table 4D, wherein the RNA sequence has a U in place of each T in the sequence of Table 4A, Table 4B, Table 4C, or Table 4D.

In some embodiments, the systems and methods provided herein may comprise a template sequence listed in any of **Tables 5A-5F**. Tables 5A-5F provide exemplary template RNA sequences (column 2) designed to be paired with a gene modifying polypeptide to correct a mutation in the PAH gene. The templates in Tables 5A-5F are meant to exemplify the total sequence of: (1) gRNA spacer (e.g., for targeting for first strand nick), (2) gRNA scaffold, (3) RT (heterologous object sequence) sequence, and (4) PBS sequence (e.g., for initiating TPRT at first strand nick).

Table 5A. Exemplary template RNA sequences

Table 5A provides design of exemplary DNA components of gene modifying systems for correcting the pathogenic R408W mutation in PAH to the wild-type form. This table details the sequence of a complete template RNA for use in exemplary gene modifying systems comprising a gene modifying polypeptide. Templates in this table employ the hPKU1 spacer (ACCTCAATCCTTTGGGTGTA SEQ ID NO: 16355).

Name	tgRNA sequence	SEQ ID NO
hPKU1_P0R30	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCGGCCCTTCTCAGTTCGCTACGACCCATAC	31034
hPKU1_P0R31	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTCGGCCCTTCTCAGTTCGCTACGACCCATAC	31035
hPKU1_P0R32	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTCGGCCCTTCTCAGTTCGCTACGACCCATAC	31036
hPKU1_P0R33	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCCTCGGCCCTTCTCAGTTCGCTACGACCCATAC	31037
hPKU1_P0R34	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCACCTCGGCCCTTCTCAGTTCGCTACGACCCATAC	31038
hPKU1_P0R35	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTACCTCGGCCCTTCTCAGTTCGCTACGACCCATAC	31039

hPKU1_P0R36	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCAC CGAGTCGGTGCATACCTCGGCCCTTCTCAGTTCGCTACGACCCATAC	31040
hPKU1_P0R37	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCAC CGAGTCGGTGCAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATAC	31041
hPKU1_P0R38	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCAC CGAGTCGGTGCCAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATAC	31042
hPKU1_P0R39	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCAC CGAGTCGGTGCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATAC	31043
hPKU1_P0R40	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCAC CGAGTCGGTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATAC	31044
hPKU1_P0R41	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCAC CGAGTCGGTGCCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATAC	31045
hPKU1_P0R42	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCAC CGAGTCGGTGCGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATAC	31046
hPKU1_P0R43	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCAC CGAGTCGGTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATAC	31047
hPKU1_P0R44	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCAC CGAGTCGGTGCCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATAC	31048
hPKU1_P0R45	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCAC CGAGTCGGTGCGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATAC	31049
hPKU1_P0R46	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCAC CGAGTCGGTGCTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATAC	31050
hPKU1_P0R47	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCAC CGAGTCGGTGCTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATAC	31051
hPKU1_P0R48	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCAC CGAGTCGGTGCTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATAC	31052
hPKU1_P0R49	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCAC CGAGTCGGTGCCTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATAC	31053
hPKU1_P0R50	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCAC CGAGTCGGTGCACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATAC	31054
hPKU1_P0R51	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCAC CGAGTCGGTGCAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATAC	31055
hPKU1_P0R52	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCAC CGAGTCGGTGCGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATAC	31056

hPKU1_P0R53	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCAC CGAGTCGGTGCGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATAC	31057
hPKU1_P0R54	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCAC CGAGTCGGTGCAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATAC	31058
hPKU1_P0R55	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCAC CGAGTCGGTGCTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATAC	31059
hPKU1_P0R56	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCAC CGAGTCGGTGCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATAC	31060
hPKU1_P0R57	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCAC CGAGTCGGTGCCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATAC	31061
hPKU1_P0R58	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCAC CGAGTCGGTGCTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATAC	31062
hPKU1_P0R59	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCAC CGAGTCGGTGCGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATAC	31063
hPKU1_P0R60	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCAC CGAGTCGGTGCGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATAC	31064
hPKU1_P0R61	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCAC CGAGTCGGTGCTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATAC	31065
hPKU1_P0R62	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCAC CGAGTCGGTGCTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATAC	31066
hPKU1_P0R63	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCAC CGAGTCGGTGCTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATAC	31067
hPKU1_P0R64	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCAC CGAGTCGGTGCTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATAC	31068
hPKU1_P0R65	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCAC CGAGTCGGTGCGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATAC	31069
hPKU1_P0R66	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCAC CGAGTCGGTGCGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATAC	31070
hPKU1_P0R67	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCAC CGAGTCGGTGCTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATAC	31071
hPKU1_P0R68	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCAC CGAGTCGGTGCGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATAC	31072
hPKU1_P0R69	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCAC CGAGTCGGTGCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATAC	31073

hPKU1_P0R70	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATAC	31074
hPKU1_P0R71	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATAC	31075
hPKU1_P0R72	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATAC	31076
hPKU1_P0R73	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATAC	31077
hPKU1_P0R74	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATAC	31078
hPKU1_P0R75	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATAC	31079
hPKU1_P0R76	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATAC	31080
hPKU1_P0R77	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATAC	31081
hPKU1_P0R78	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCACTCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATAC	31082
hPKU1_P0R79	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCACTCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATAC	31083
hPKU1_P0R80	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTCACTCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATAC	31084
hPKU1_P10R30	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGA	31085
hPKU1_P10R31	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGA	31086
hPKU1_P10R32	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGA	31087

hPKU1_P10R33	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCAC CGAGTCGGTGCCCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGA	31088
hPKU1_P10R34	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCAC CGAGTCGGTGCACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGA	31089
hPKU1_P10R35	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCAC CGAGTCGGTGCTACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGA	31090
hPKU1_P10R36	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCAC CGAGTCGGTGCATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGA	31091
hPKU1_P10R37	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCAC CGAGTCGGTGCAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGA	31092
hPKU1_P10R38	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCAC CGAGTCGGTGCCAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGA	31093
hPKU1_P10R39	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCAC CGAGTCGGTGCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGA	31094
hPKU1_P10R40	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCAC CGAGTCGGTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGA	31095
hPKU1_P10R41	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCAC CGAGTCGGTGCCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGA	31096
hPKU1_P10R42	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCAC CGAGTCGGTGCGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGA	31097
hPKU1_P10R43	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCAC CGAGTCGGTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGA	31098
hPKU1_P10R44	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCAC CGAGTCGGTGCCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGA	31099
hPKU1_P10R45	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCAC CGAGTCGGTGCGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGA	31100
hPKU1_P10R46	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCAC CGAGTCGGTGCTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGA	31101
hPKU1_P10R47	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCAC CGAGTCGGTGCTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGA	31102
hPKU1_P10R48	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCAC CGAGTCGGTGCTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGA	31103
hPKU1_P10R49	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCAC CGAGTCGGTGCCTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGA	31104

hPKU1_P10R50	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGA	31105
hPKU1_P10R51	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGA	31106
hPKU1_P10R52	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGA	31107
hPKU1_P10R53	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGA	31108
hPKU1_P10R54	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGA	31109
hPKU1_P10R55	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGA	31110
hPKU1_P10R56	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGA	31111
hPKU1_P10R57	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGA	31112
hPKU1_P10R58	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGA	31113
hPKU1_P10R59	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGA	31114
hPKU1_P10R60	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGA	31115
hPKU1_P10R61	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGA	31116
hPKU1_P10R62	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGA	31117
hPKU1_P10R63	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGA	31118
hPKU1_P10R64	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGA	31119
hPKU1_P10R65	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGA	31120

hPKU1_P10R66	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGA	31121
hPKU1_P10R67	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGA	31122
hPKU1_P10R68	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGA	31123
hPKU1_P10R69	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGA	31124
hPKU1_P10R70	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGA	31125
hPKU1_P10R71	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGA	31126
hPKU1_P10R72	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGA	31127
hPKU1_P10R73	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGA	31128
hPKU1_P10R74	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGA	31129
hPKU1_P10R75	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGA	31130
hPKU1_P10R76	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGA	31131

hPKU1_P10R77	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGA	31132
hPKU1_P10R78	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCACTCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGA	31133
hPKU1_P10R79	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCACTCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGA	31134
hPKU1_P10R80	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTCACTCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGA	31135
hPKU1_P11R30	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGAT	31136
hPKU1_P11R31	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGAT	31137
hPKU1_P11R32	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGAT	31138
hPKU1_P11R33	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGAT	31139
hPKU1_P11R34	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGAT	31140
hPKU1_P11R35	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGAT	31141
hPKU1_P11R36	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGAT	31142
hPKU1_P11R37	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGAT	31143
hPKU1_P11R38	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGAT	31144
hPKU1_P11R39	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGAT	31145
hPKU1_P11R40	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGAT	31146

hPKU1_P11R41	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCAC CGAGTCGGTGCCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGAT	31147
hPKU1_P11R42	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCAC CGAGTCGGTGCGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGAT	31148
hPKU1_P11R43	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCAC CGAGTCGGTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGAT	31149
hPKU1_P11R44	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCAC CGAGTCGGTGCCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGAT	31150
hPKU1_P11R45	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCAC CGAGTCGGTGCGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGAT	31151
hPKU1_P11R46	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCAC CGAGTCGGTGCTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGAT	31152
hPKU1_P11R47	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCAC CGAGTCGGTGCTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGAT	31153
hPKU1_P11R48	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCAC CGAGTCGGTGCTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGAT	31154
hPKU1_P11R49	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCAC CGAGTCGGTGCCTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGAT	31155
hPKU1_P11R50	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCAC CGAGTCGGTGCACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGAT	31156
hPKU1_P11R51	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCAC CGAGTCGGTGCAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGAT	31157
hPKU1_P11R52	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCAC CGAGTCGGTGCGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGAT	31158
hPKU1_P11R53	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCAC CGAGTCGGTGCGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGAT	31159
hPKU1_P11R54	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCAC CGAGTCGGTGCAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGAT	31160
hPKU1_P11R55	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCAC CGAGTCGGTGCTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGAT	31161
hPKU1_P11R56	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCAC CGAGTCGGTGCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGAT	31162
hPKU1_P11R57	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCAC CGAGTCGGTGCCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGAT	31163

hPKU1_P11R58	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGAT	31164
hPKU1_P11R59	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGAT	31165
hPKU1_P11R60	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGAT	31166
hPKU1_P11R61	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGAT	31167
hPKU1_P11R62	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGAT	31168
hPKU1_P11R63	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGAT	31169
hPKU1_P11R64	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGAT	31170
hPKU1_P11R65	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGAT	31171
hPKU1_P11R66	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGAT	31172
hPKU1_P11R67	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGAT	31173
hPKU1_P11R68	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGAT	31174
hPKU1_P11R69	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGAT	31175
hPKU1_P11R70	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGAT	31176

hPKU1_P11R71	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGAT	31177
hPKU1_P11R72	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGAT	31178
hPKU1_P11R73	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGAT	31179
hPKU1_P11R74	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGAT	31180
hPKU1_P11R75	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGAT	31181
hPKU1_P11R76	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGAT	31182
hPKU1_P11R77	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGAT	31183
hPKU1_P11R78	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCACTCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGAT	31184
hPKU1_P11R79	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCACTCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGAT	31185
hPKU1_P11R80	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTCACTCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGAT	31186
hPKU1_P12R30	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATT	31187
hPKU1_P12R31	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATT	31188

hPKU1_P12R32	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATT	31189
hPKU1_P12R33	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATT	31190
hPKU1_P12R34	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATT	31191
hPKU1_P12R35	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATT	31192
hPKU1_P12R36	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATT	31193
hPKU1_P12R37	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATT	31194
hPKU1_P12R38	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATT	31195
hPKU1_P12R39	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATT	31196
hPKU1_P12R40	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATT	31197
hPKU1_P12R41	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATT	31198
hPKU1_P12R42	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATT	31199
hPKU1_P12R43	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATT	31200
hPKU1_P12R44	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATT	31201
hPKU1_P12R45	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATT	31202
hPKU1_P12R46	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATT	31203
hPKU1_P12R47	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATT	31204
hPKU1_P12R48	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATT	31205

hPKU1_P12R49	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATT	31206
hPKU1_P12R50	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATT	31207
hPKU1_P12R51	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATT	31208
hPKU1_P12R52	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATT	31209
hPKU1_P12R53	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATT	31210
hPKU1_P12R54	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATT	31211
hPKU1_P12R55	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATT	31212
hPKU1_P12R56	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATT	31213
hPKU1_P12R57	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATT	31214
hPKU1_P12R58	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATT	31215
hPKU1_P12R59	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATT	31216
hPKU1_P12R60	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATT	31217
hPKU1_P12R61	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATT	31218
hPKU1_P12R62	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATT	31219
hPKU1_P12R63	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATT	31220
hPKU1_P12R64	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATT	31221

hPKU1_P12R65	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATT	31222
hPKU1_P12R66	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATT	31223
hPKU1_P12R67	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATT	31224
hPKU1_P12R68	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATT	31225
hPKU1_P12R69	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATT	31226
hPKU1_P12R70	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATT	31227
hPKU1_P12R71	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATT	31228
hPKU1_P12R72	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATT	31229
hPKU1_P12R73	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATT	31230
hPKU1_P12R74	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATT	31231
hPKU1_P12R75	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATT	31232

hPKU1_P12R76	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATT	31233
hPKU1_P12R77	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATT	31234
hPKU1_P12R78	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCACTCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATT	31235
hPKU1_P12R79	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCACTCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATT	31236
hPKU1_P12R80	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTCACTCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATT	31237
hPKU1_P13R30	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTG	31238
hPKU1_P13R31	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTG	31239
hPKU1_P13R32	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTG	31240
hPKU1_P13R33	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTG	31241
hPKU1_P13R34	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTG	31242
hPKU1_P13R35	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTG	31243
hPKU1_P13R36	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTG	31244
hPKU1_P13R37	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTG	31245
hPKU1_P13R38	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTG	31246

hPKU1_P13R39	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTG	31247
hPKU1_P13R40	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTG	31248
hPKU1_P13R41	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTG	31249
hPKU1_P13R42	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTG	31250
hPKU1_P13R43	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTG	31251
hPKU1_P13R44	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTG	31252
hPKU1_P13R45	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTG	31253
hPKU1_P13R46	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTG	31254
hPKU1_P13R47	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTG	31255
hPKU1_P13R48	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTG	31256
hPKU1_P13R49	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTG	31257
hPKU1_P13R50	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTG	31258
hPKU1_P13R51	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTG	31259
hPKU1_P13R52	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTG	31260
hPKU1_P13R53	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTG	31261
hPKU1_P13R54	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTG	31262
hPKU1_P13R55	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTG	31263

hPKU1_P13R56	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTG	31264
hPKU1_P13R57	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTG	31265
hPKU1_P13R58	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTG	31266
hPKU1_P13R59	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTG	31267
hPKU1_P13R60	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTG	31268
hPKU1_P13R61	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTG	31269
hPKU1_P13R62	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTG	31270
hPKU1_P13R63	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTG	31271
hPKU1_P13R64	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTG	31272
hPKU1_P13R65	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTG	31273
hPKU1_P13R66	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTG	31274
hPKU1_P13R67	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTG	31275
hPKU1_P13R68	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTG	31276

hPKU1_P13R69	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTG	31277
hPKU1_P13R70	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTG	31278
hPKU1_P13R71	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTG	31279
hPKU1_P13R72	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTG	31280
hPKU1_P13R73	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTG	31281
hPKU1_P13R74	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTG	31282
hPKU1_P13R75	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTG	31283
hPKU1_P13R76	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTG	31284
hPKU1_P13R77	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTG	31285
hPKU1_P13R78	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCACTCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTG	31286
hPKU1_P13R79	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCACTCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTG	31287

hPKU1_P13R80	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTCACTCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTG	31288
hPKU1_P14R30	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTGA	31289
hPKU1_P14R31	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTGA	31290
hPKU1_P14R32	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTGA	31291
hPKU1_P14R33	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTGA	31292
hPKU1_P14R34	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTGA	31293
hPKU1_P14R35	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTGA	31294
hPKU1_P14R36	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTGA	31295
hPKU1_P14R37	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTGA	31296
hPKU1_P14R38	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTGA	31297
hPKU1_P14R39	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTGA	31298
hPKU1_P14R40	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTGA	31299
hPKU1_P14R41	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTGA	31300
hPKU1_P14R42	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTGA	31301
hPKU1_P14R43	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTGA	31302
hPKU1_P14R44	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTGA	31303

hPKU1_P14R45	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCAC CGAGTCGGTGCGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTGA	31304
hPKU1_P14R46	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCAC CGAGTCGGTGCTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTGA	31305
hPKU1_P14R47	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCAC CGAGTCGGTGCTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTGA	31306
hPKU1_P14R48	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCAC CGAGTCGGTGCTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTGA	31307
hPKU1_P14R49	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCAC CGAGTCGGTGCCTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTGA	31308
hPKU1_P14R50	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCAC CGAGTCGGTGCACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTGA	31309
hPKU1_P14R51	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCAC CGAGTCGGTGCAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTGA	31310
hPKU1_P14R52	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCAC CGAGTCGGTGCGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTGA	31311
hPKU1_P14R53	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCAC CGAGTCGGTGCGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTGA	31312
hPKU1_P14R54	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCAC CGAGTCGGTGCAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTGA	31313
hPKU1_P14R55	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCAC CGAGTCGGTGCTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTGA	31314
hPKU1_P14R56	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCAC CGAGTCGGTGCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTGA	31315
hPKU1_P14R57	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCAC CGAGTCGGTGCCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTGA	31316
hPKU1_P14R58	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCAC CGAGTCGGTGCTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTGA	31317
hPKU1_P14R59	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCAC CGAGTCGGTGCGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTGA	31318
hPKU1_P14R60	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCAC CGAGTCGGTGCGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTGA	31319

hPKU1_P14R61	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTGA	31320
hPKU1_P14R62	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTGA	31321
hPKU1_P14R63	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTGA	31322
hPKU1_P14R64	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTGA	31323
hPKU1_P14R65	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTGA	31324
hPKU1_P14R66	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTGA	31325
hPKU1_P14R67	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTGA	31326
hPKU1_P14R68	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTGA	31327
hPKU1_P14R69	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTGA	31328
hPKU1_P14R70	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTGA	31329
hPKU1_P14R71	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTGA	31330

hPKU1_P14R72	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTGA	31331
hPKU1_P14R73	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTGA	31332
hPKU1_P14R74	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTGA	31333
hPKU1_P14R75	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTGA	31334
hPKU1_P14R76	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTGA	31335
hPKU1_P14R77	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTGA	31336
hPKU1_P14R78	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCACTCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTGA	31337
hPKU1_P14R79	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCACTCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTGA	31338
hPKU1_P14R80	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTCACTCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTGA	31339
hPKU1_P15R30	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTGAG	31340
hPKU1_P15R31	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTGAG	31341
hPKU1_P15R32	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTGAG	31342

hPKU1_P15R33	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTGAG	31343
hPKU1_P15R34	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTGAG	31344
hPKU1_P15R35	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTGAG	31345
hPKU1_P15R36	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTGAG	31346
hPKU1_P15R37	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTGAG	31347
hPKU1_P15R38	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTGAG	31348
hPKU1_P15R39	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTGAG	31349
hPKU1_P15R40	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTGAG	31350
hPKU1_P15R41	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTGAG	31351
hPKU1_P15R42	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTGAG	31352
hPKU1_P15R43	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTGAG	31353
hPKU1_P15R44	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTGAG	31354
hPKU1_P15R45	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTGAG	31355
hPKU1_P15R46	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTGAG	31356
hPKU1_P15R47	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTGAG	31357
hPKU1_P15R48	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTGAG	31358
hPKU1_P15R49	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTGAG	31359

hPKU1_P15R50	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTGAG	31360
hPKU1_P15R51	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTGAG	31361
hPKU1_P15R52	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTGAG	31362
hPKU1_P15R53	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTGAG	31363
hPKU1_P15R54	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTGAG	31364
hPKU1_P15R55	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTGAG	31365
hPKU1_P15R56	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTGAG	31366
hPKU1_P15R57	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTGAG	31367
hPKU1_P15R58	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTGAG	31368
hPKU1_P15R59	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTGAG	31369
hPKU1_P15R60	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTGAG	31370
hPKU1_P15R61	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTGAG	31371
hPKU1_P15R62	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTGAG	31372
hPKU1_P15R63	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTGAG	31373

hPKU1_P15R64	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTGAG	31374
hPKU1_P15R65	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTGAG	31375
hPKU1_P15R66	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTGAG	31376
hPKU1_P15R67	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTGAG	31377
hPKU1_P15R68	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTGAG	31378
hPKU1_P15R69	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTGAG	31379
hPKU1_P15R70	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTGAG	31380
hPKU1_P15R71	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTGAG	31381
hPKU1_P15R72	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTGAG	31382
hPKU1_P15R73	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTGAG	31383
hPKU1_P15R74	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTGAG	31384

hPKU1_P15R75	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTGAG	31385
hPKU1_P15R76	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTGAG	31386
hPKU1_P15R77	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTGAG	31387
hPKU1_P15R78	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCACTCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTGAG	31388
hPKU1_P15R79	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCACTCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTGAG	31389
hPKU1_P15R80	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTCACTCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTGAG	31390
hPKU1_P16R30	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTGAGG	31391
hPKU1_P16R31	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTGAGG	31392
hPKU1_P16R32	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTGAGG	31393
hPKU1_P16R33	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTGAGG	31394
hPKU1_P16R34	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTGAGG	31395
hPKU1_P16R35	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTGAGG	31396
hPKU1_P16R36	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTGAGG	31397
hPKU1_P16R37	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTGAGG	31398

hPKU1_P16R38	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCAC CGAGTCGGTGCCAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTGAGG	31399
hPKU1_P16R39	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCAC CGAGTCGGTGCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTGAGG	31400
hPKU1_P16R40	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCAC CGAGTCGGTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTGAGG	31401
hPKU1_P16R41	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCAC CGAGTCGGTGCCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTGAGG	31402
hPKU1_P16R42	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCAC CGAGTCGGTGCGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTGAGG	31403
hPKU1_P16R43	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCAC CGAGTCGGTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTGAGG	31404
hPKU1_P16R44	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCAC CGAGTCGGTGCCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTGAGG	31405
hPKU1_P16R45	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCAC CGAGTCGGTGCGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTGAGG	31406
hPKU1_P16R46	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCAC CGAGTCGGTGCTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTGAGG	31407
hPKU1_P16R47	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCAC CGAGTCGGTGCTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTGAGG	31408
hPKU1_P16R48	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCAC CGAGTCGGTGCTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTGAGG	31409
hPKU1_P16R49	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCAC CGAGTCGGTGCCTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTGAGG	31410
hPKU1_P16R50	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCAC CGAGTCGGTGCACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTGAGG	31411
hPKU1_P16R51	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCAC CGAGTCGGTGCAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTGAGG	31412
hPKU1_P16R52	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCAC CGAGTCGGTGCGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTGAGG	31413
hPKU1_P16R53	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCAC CGAGTCGGTGCGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTGAGG	31414
hPKU1_P16R54	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCAC CGAGTCGGTGCAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTGAGG	31415

hPKU1_P16R55	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTGAGG	31416
hPKU1_P16R56	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTGAGG	31417
hPKU1_P16R57	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTGAGG	31418
hPKU1_P16R58	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTGAGG	31419
hPKU1_P16R59	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTGAGG	31420
hPKU1_P16R60	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTGAGG	31421
hPKU1_P16R61	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTGAGG	31422
hPKU1_P16R62	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTGAGG	31423
hPKU1_P16R63	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTGAGG	31424
hPKU1_P16R64	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTGAGG	31425
hPKU1_P16R65	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTGAGG	31426
hPKU1_P16R66	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTGAGG	31427

hPKU1_P16R67	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTGAGG	31428
hPKU1_P16R68	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTGAGG	31429
hPKU1_P16R69	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTGAGG	31430
hPKU1_P16R70	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTGAGG	31431
hPKU1_P16R71	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTGAGG	31432
hPKU1_P16R72	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTGAGG	31433
hPKU1_P16R73	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTGAGG	31434
hPKU1_P16R74	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTGAGG	31435
hPKU1_P16R75	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTGAGG	31436
hPKU1_P16R76	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTGAGG	31437
hPKU1_P16R77	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTGAGG	31438

hPKU1_P16R78	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCACTCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTGAGG	31439
hPKU1_P16R79	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCACTCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTGAGG	31440
hPKU1_P16R80	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTCACTCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTGAGG	31441
hPKU1_P17R30	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTGAGGT	31442
hPKU1_P17R31	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTGAGGT	31443
hPKU1_P17R32	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTGAGGT	31444
hPKU1_P17R33	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTGAGGT	31445
hPKU1_P17R34	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTGAGGT	31446
hPKU1_P17R35	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTGAGGT	31447
hPKU1_P17R36	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTGAGGT	31448
hPKU1_P17R37	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTGAGGT	31449
hPKU1_P17R38	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTGAGGT	31450
hPKU1_P17R39	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTGAGGT	31451
hPKU1_P17R40	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTGAGGT	31452
hPKU1_P17R41	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTGAGGT	31453

hPKU1_P17R42	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCAC CGAGTCGGTGCGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTGAGGT	31454
hPKU1_P17R43	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCAC CGAGTCGGTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTGAGGT	31455
hPKU1_P17R44	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCAC CGAGTCGGTGCCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTGAGGT	31456
hPKU1_P17R45	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCAC CGAGTCGGTGCGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTGAGGT	31457
hPKU1_P17R46	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCAC CGAGTCGGTGCTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTGAGGT	31458
hPKU1_P17R47	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCAC CGAGTCGGTGCTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTGAGGT	31459
hPKU1_P17R48	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCAC CGAGTCGGTGCTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTGAGGT	31460
hPKU1_P17R49	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCAC CGAGTCGGTGCCTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTGAGGT	31461
hPKU1_P17R50	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCAC CGAGTCGGTGCACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTGAGGT	31462
hPKU1_P17R51	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCAC CGAGTCGGTGCAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTGAGGT	31463
hPKU1_P17R52	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCAC CGAGTCGGTGCGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTGAGGT	31464
hPKU1_P17R53	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCAC CGAGTCGGTGCGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTGAGGT	31465
hPKU1_P17R54	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCAC CGAGTCGGTGCAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTGAGGT	31466
hPKU1_P17R55	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCAC CGAGTCGGTGCTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTGAGGT	31467
hPKU1_P17R56	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCAC CGAGTCGGTGCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTGAGGT	31468
hPKU1_P17R57	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCAC CGAGTCGGTGCCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTGAGGT	31469

hPKU1_P17R58	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTGAGGT	31470
hPKU1_P17R59	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTGAGGT	31471
hPKU1_P17R60	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTGAGGT	31472
hPKU1_P17R61	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTGAGGT	31473
hPKU1_P17R62	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTGAGGT	31474
hPKU1_P17R63	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTGAGGT	31475
hPKU1_P17R64	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTGAGGT	31476
hPKU1_P17R65	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTGAGGT	31477
hPKU1_P17R66	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTGAGGT	31478
hPKU1_P17R67	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTGAGGT	31479
hPKU1_P17R68	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTGAGGT	31480

hPKU1_P17R69	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTGAGGT	31481
hPKU1_P17R70	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTGAGGT	31482
hPKU1_P17R71	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTGAGGT	31483
hPKU1_P17R72	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTGAGGT	31484
hPKU1_P17R73	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTGAGGT	31485
hPKU1_P17R74	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTGAGGT	31486
hPKU1_P17R75	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTGAGGT	31487
hPKU1_P17R76	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTGAGGT	31488
hPKU1_P17R77	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTGAGGT	31489
hPKU1_P17R78	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCACTCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTGAGGT	31490
hPKU1_P17R79	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCACTCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTGAGGT	31491

hPKU1_P17R80	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTCACTCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTGAGGT	31492
hPKU1_P1R30	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCGGCCCTTCTCAGTTCGCTACGACCCATACA	31493
hPKU1_P1R31	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTCGGCCCTTCTCAGTTCGCTACGACCCATACA	31494
hPKU1_P1R32	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTCGGCCCTTCTCAGTTCGCTACGACCCATACA	31495
hPKU1_P1R33	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCCTCGGCCCTTCTCAGTTCGCTACGACCCATACA	31496
hPKU1_P1R34	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCACCTCGGCCCTTCTCAGTTCGCTACGACCCATACA	31497
hPKU1_P1R35	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTACCTCGGCCCTTCTCAGTTCGCTACGACCCATACA	31498
hPKU1_P1R36	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACA	31499
hPKU1_P1R37	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACA	31500
hPKU1_P1R38	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACA	31501
hPKU1_P1R39	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACA	31502
hPKU1_P1R40	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACA	31503
hPKU1_P1R41	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACA	31504
hPKU1_P1R42	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACA	31505
hPKU1_P1R43	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACA	31506
hPKU1_P1R44	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACA	31507

hPKU1_P1R45	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACA	31508
hPKU1_P1R46	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACA	31509
hPKU1_P1R47	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACA	31510
hPKU1_P1R48	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACA	31511
hPKU1_P1R49	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACA	31512
hPKU1_P1R50	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACA	31513
hPKU1_P1R51	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACA	31514
hPKU1_P1R52	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACA	31515
hPKU1_P1R53	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACA	31516
hPKU1_P1R54	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACA	31517
hPKU1_P1R55	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACA	31518
hPKU1_P1R56	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACA	31519
hPKU1_P1R57	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACA	31520
hPKU1_P1R58	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACA	31521
hPKU1_P1R59	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACA	31522
hPKU1_P1R60	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACA	31523
hPKU1_P1R61	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACA	31524

hPKU1_P1R62	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACA	31525
hPKU1_P1R63	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACA	31526
hPKU1_P1R64	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACA	31527
hPKU1_P1R65	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACA	31528
hPKU1_P1R66	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACA	31529
hPKU1_P1R67	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACA	31530
hPKU1_P1R68	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACA	31531
hPKU1_P1R69	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACA	31532
hPKU1_P1R70	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACA	31533
hPKU1_P1R71	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACA	31534
hPKU1_P1R72	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACA	31535
hPKU1_P1R73	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACA	31536
hPKU1_P1R74	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACA	31537
hPKU1_P1R75	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACA	31538
hPKU1_P1R76	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACA	31539

hPKU1_P1R77	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACA	31540
hPKU1_P1R78	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCACTCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACA	31541
hPKU1_P1R79	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCACTCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACA	31542
hPKU1_P1R80	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTCACTCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACA	31543
hPKU1_P2R30	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCGGCCCTTCTCAGTTCGCTACGACCCATACAC	31544
hPKU1_P2R31	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTCGGCCCTTCTCAGTTCGCTACGACCCATACAC	31545
hPKU1_P2R32	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTCGGCCCTTCTCAGTTCGCTACGACCCATACAC	31546
hPKU1_P2R33	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCCTCGGCCCTTCTCAGTTCGCTACGACCCATACAC	31547
hPKU1_P2R34	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCACCTCGGCCCTTCTCAGTTCGCTACGACCCATACAC	31548
hPKU1_P2R35	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTACCTCGGCCCTTCTCAGTTCGCTACGACCCATACAC	31549
hPKU1_P2R36	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACAC	31550
hPKU1_P2R37	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACAC	31551
hPKU1_P2R38	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACAC	31552
hPKU1_P2R39	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACAC	31553
hPKU1_P2R40	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACAC	31554

hPKU1_P2R41	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCAC CGAGTCGGTGCCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACAC	31555
hPKU1_P2R42	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCAC CGAGTCGGTGCGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACAC	31556
hPKU1_P2R43	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCAC CGAGTCGGTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACAC	31557
hPKU1_P2R44	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCAC CGAGTCGGTGCCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACAC	31558
hPKU1_P2R45	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCAC CGAGTCGGTGCGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACAC	31559
hPKU1_P2R46	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCAC CGAGTCGGTGCTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACAC	31560
hPKU1_P2R47	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCAC CGAGTCGGTGCTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACAC	31561
hPKU1_P2R48	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCAC CGAGTCGGTGCTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACAC	31562
hPKU1_P2R49	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCAC CGAGTCGGTGCCTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACAC	31563
hPKU1_P2R50	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCAC CGAGTCGGTGCACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACAC	31564
hPKU1_P2R51	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCAC CGAGTCGGTGCAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACAC	31565
hPKU1_P2R52	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCAC CGAGTCGGTGCGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACAC	31566
hPKU1_P2R53	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCAC CGAGTCGGTGCGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACAC	31567
hPKU1_P2R54	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCAC CGAGTCGGTGCAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACAC	31568
hPKU1_P2R55	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCAC CGAGTCGGTGCTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACAC	31569
hPKU1_P2R56	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCAC CGAGTCGGTGCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACAC	31570
hPKU1_P2R57	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCAC CGAGTCGGTGCCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACAC	31571

hPKU1_P2R58	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACAC	31572
hPKU1_P2R59	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACAC	31573
hPKU1_P2R60	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACAC	31574
hPKU1_P2R61	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACAC	31575
hPKU1_P2R62	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACAC	31576
hPKU1_P2R63	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACAC	31577
hPKU1_P2R64	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACAC	31578
hPKU1_P2R65	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACAC	31579
hPKU1_P2R66	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACAC	31580
hPKU1_P2R67	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACAC	31581
hPKU1_P2R68	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACAC	31582
hPKU1_P2R69	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACAC	31583
hPKU1_P2R70	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACAC	31584
hPKU1_P2R71	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACAC	31585
hPKU1_P2R72	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACAC	31586
hPKU1_P2R73	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACAC	31587

hPKU1_P2R74	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACAC	31588
hPKU1_P2R75	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACAC	31589
hPKU1_P2R76	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACAC	31590
hPKU1_P2R77	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACAC	31591
hPKU1_P2R78	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCACTCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACAC	31592
hPKU1_P2R79	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCACTCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACAC	31593
hPKU1_P2R80	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTCACTCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACAC	31594
hPKU1_P3R30	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCGGCCCTTCTCAGTTCGCTACGACCCATACACC	31595
hPKU1_P3R31	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTCGGCCCTTCTCAGTTCGCTACGACCCATACACC	31596
hPKU1_P3R32	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTCGGCCCTTCTCAGTTCGCTACGACCCATACACC	31597
hPKU1_P3R33	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCCTCGGCCCTTCTCAGTTCGCTACGACCCATACACC	31598
hPKU1_P3R34	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACC	31599
hPKU1_P3R35	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACC	31600

hPKU1_P3R36	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACC	31601
hPKU1_P3R37	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACC	31602
hPKU1_P3R38	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACC	31603
hPKU1_P3R39	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACC	31604
hPKU1_P3R40	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACC	31605
hPKU1_P3R41	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACC	31606
hPKU1_P3R42	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACC	31607
hPKU1_P3R43	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACC	31608
hPKU1_P3R44	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACC	31609
hPKU1_P3R45	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACC	31610
hPKU1_P3R46	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACC	31611
hPKU1_P3R47	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACC	31612
hPKU1_P3R48	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACC	31613
hPKU1_P3R49	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACC	31614
hPKU1_P3R50	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACC	31615
hPKU1_P3R51	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACC	31616
hPKU1_P3R52	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACC	31617

hPKU1_P3R53	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCAC CGAGTCGGTGCGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACC	31618
hPKU1_P3R54	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCAC CGAGTCGGTGCAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACC	31619
hPKU1_P3R55	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCAC CGAGTCGGTGCTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACC	31620
hPKU1_P3R56	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCAC CGAGTCGGTGCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACC	31621
hPKU1_P3R57	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCAC CGAGTCGGTGCCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACC	31622
hPKU1_P3R58	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCAC CGAGTCGGTGCTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACC	31623
hPKU1_P3R59	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCAC CGAGTCGGTGCGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACC	31624
hPKU1_P3R60	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCAC CGAGTCGGTGCGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACC	31625
hPKU1_P3R61	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCAC CGAGTCGGTGCTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACC	31626
hPKU1_P3R62	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCAC CGAGTCGGTGCTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACC	31627
hPKU1_P3R63	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCAC CGAGTCGGTGCTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACC	31628
hPKU1_P3R64	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCAC CGAGTCGGTGCTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACC	31629
hPKU1_P3R65	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCAC CGAGTCGGTGCGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACC	31630
hPKU1_P3R66	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCAC CGAGTCGGTGCGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACC	31631
hPKU1_P3R67	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCAC CGAGTCGGTGCTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACC	31632
hPKU1_P3R68	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCAC CGAGTCGGTGCGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACC	31633
hPKU1_P3R69	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCAC CGAGTCGGTGCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACC	31634

hPKU1_P3R70	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACC	31635
hPKU1_P3R71	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACC	31636
hPKU1_P3R72	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACC	31637
hPKU1_P3R73	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACC	31638
hPKU1_P3R74	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACC	31639
hPKU1_P3R75	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACC	31640
hPKU1_P3R76	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACC	31641
hPKU1_P3R77	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACC	31642
hPKU1_P3R78	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCACTCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACC	31643
hPKU1_P3R79	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCACTCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACC	31644
hPKU1_P3R80	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTCACTCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACC	31645
hPKU1_P4R30	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCGGCCCTTCTCAGTTCGCTACGACCCATACACCC	31646
hPKU1_P4R31	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCC	31647

hPKU1_P4R32	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCC	31648
hPKU1_P4R33	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCC	31649
hPKU1_P4R34	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCC	31650
hPKU1_P4R35	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCC	31651
hPKU1_P4R36	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCC	31652
hPKU1_P4R37	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCC	31653
hPKU1_P4R38	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCC	31654
hPKU1_P4R39	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCC	31655
hPKU1_P4R40	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCC	31656
hPKU1_P4R41	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCC	31657
hPKU1_P4R42	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCC	31658
hPKU1_P4R43	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCC	31659
hPKU1_P4R44	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCC	31660
hPKU1_P4R45	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCC	31661
hPKU1_P4R46	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCC	31662
hPKU1_P4R47	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCC	31663
hPKU1_P4R48	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCC	31664

hPKU1_P4R49	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCAC CGAGTCGGTGCCTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCC	31665
hPKU1_P4R50	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCAC CGAGTCGGTGCACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCC	31666
hPKU1_P4R51	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCAC CGAGTCGGTGCAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCC	31667
hPKU1_P4R52	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCAC CGAGTCGGTGCGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCC	31668
hPKU1_P4R53	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCAC CGAGTCGGTGCGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCC	31669
hPKU1_P4R54	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCAC CGAGTCGGTGCAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCC	31670
hPKU1_P4R55	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCAC CGAGTCGGTGCTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCC	31671
hPKU1_P4R56	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCAC CGAGTCGGTGCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCC	31672
hPKU1_P4R57	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCAC CGAGTCGGTGCCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCC	31673
hPKU1_P4R58	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCAC CGAGTCGGTGCTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCC	31674
hPKU1_P4R59	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCAC CGAGTCGGTGCGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCC	31675
hPKU1_P4R60	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCAC CGAGTCGGTGCGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCC	31676
hPKU1_P4R61	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCAC CGAGTCGGTGCTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCC	31677
hPKU1_P4R62	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCAC CGAGTCGGTGCTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCC	31678
hPKU1_P4R63	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCAC CGAGTCGGTGCTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCC	31679
hPKU1_P4R64	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCAC CGAGTCGGTGCTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCC	31680
hPKU1_P4R65	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCAC CGAGTCGGTGCGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCC	31681

hPKU1_P4R66	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCC	31682
hPKU1_P4R67	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCC	31683
hPKU1_P4R68	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCC	31684
hPKU1_P4R69	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCC	31685
hPKU1_P4R70	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCC	31686
hPKU1_P4R71	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCC	31687
hPKU1_P4R72	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCC	31688
hPKU1_P4R73	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCC	31689
hPKU1_P4R74	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCC	31690
hPKU1_P4R75	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCC	31691
hPKU1_P4R76	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCC	31692
hPKU1_P4R77	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCC	31693
hPKU1_P4R78	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCACTCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCC	31694

hPKU1_P4R79	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCACTCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCC	31695
hPKU1_P4R80	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTCACTCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCC	31696
hPKU1_P5R30	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCGGCCCTTCTCAGTTCGCTACGACCCATACACCCA	31697
hPKU1_P5R31	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCA	31698
hPKU1_P5R32	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCA	31699
hPKU1_P5R33	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCA	31700
hPKU1_P5R34	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCA	31701
hPKU1_P5R35	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCA	31702
hPKU1_P5R36	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCA	31703
hPKU1_P5R37	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCA	31704
hPKU1_P5R38	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCA	31705
hPKU1_P5R39	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCA	31706
hPKU1_P5R40	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCA	31707
hPKU1_P5R41	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCA	31708
hPKU1_P5R42	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCA	31709
hPKU1_P5R43	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCA	31710

hPKU1_P5R44	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCA	31711
hPKU1_P5R45	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCA	31712
hPKU1_P5R46	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCA	31713
hPKU1_P5R47	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCA	31714
hPKU1_P5R48	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCA	31715
hPKU1_P5R49	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCA	31716
hPKU1_P5R50	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCA	31717
hPKU1_P5R51	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCA	31718
hPKU1_P5R52	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCA	31719
hPKU1_P5R53	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCA	31720
hPKU1_P5R54	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCA	31721
hPKU1_P5R55	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCA	31722
hPKU1_P5R56	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCA	31723
hPKU1_P5R57	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCA	31724
hPKU1_P5R58	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCA	31725
hPKU1_P5R59	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCA	31726
hPKU1_P5R60	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCA	31727

hPKU1_P5R61	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCA	31728
hPKU1_P5R62	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCA	31729
hPKU1_P5R63	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCA	31730
hPKU1_P5R64	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCA	31731
hPKU1_P5R65	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCA	31732
hPKU1_P5R66	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCA	31733
hPKU1_P5R67	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCA	31734
hPKU1_P5R68	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCA	31735
hPKU1_P5R69	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCA	31736
hPKU1_P5R70	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCA	31737
hPKU1_P5R71	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCA	31738
hPKU1_P5R72	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCA	31739
hPKU1_P5R73	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCCA	31740
hPKU1_P5R74	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCA	31741

hPKU1_P5R75	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCA	31742
hPKU1_P5R76	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCA	31743
hPKU1_P5R77	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCA	31744
hPKU1_P5R78	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCACTCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCA	31745
hPKU1_P5R79	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCACTCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCA	31746
hPKU1_P5R80	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTCACTCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCA	31747
hPKU1_P6R30	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAA	31748
hPKU1_P6R31	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAA	31749
hPKU1_P6R32	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAA	31750
hPKU1_P6R33	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAA	31751
hPKU1_P6R34	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAA	31752
hPKU1_P6R35	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAA	31753
hPKU1_P6R36	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAA	31754
hPKU1_P6R37	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAA	31755

hPKU1_P6R38	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAA	31756
hPKU1_P6R39	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAA	31757
hPKU1_P6R40	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAA	31758
hPKU1_P6R41	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAA	31759
hPKU1_P6R42	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAA	31760
hPKU1_P6R43	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAA	31761
hPKU1_P6R44	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAA	31762
hPKU1_P6R45	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAA	31763
hPKU1_P6R46	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAA	31764
hPKU1_P6R47	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAA	31765
hPKU1_P6R48	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAA	31766
hPKU1_P6R49	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAA	31767
hPKU1_P6R50	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAA	31768
hPKU1_P6R51	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAA	31769
hPKU1_P6R52	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAA	31770
hPKU1_P6R53	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAA	31771
hPKU1_P6R54	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAA	31772

hPKU1_P6R55	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAA	31773
hPKU1_P6R56	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAA	31774
hPKU1_P6R57	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAA	31775
hPKU1_P6R58	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAA	31776
hPKU1_P6R59	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAA	31777
hPKU1_P6R60	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAA	31778
hPKU1_P6R61	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAA	31779
hPKU1_P6R62	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAA	31780
hPKU1_P6R63	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAA	31781
hPKU1_P6R64	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAA	31782
hPKU1_P6R65	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAA	31783
hPKU1_P6R66	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAA	31784
hPKU1_P6R67	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAA	31785
hPKU1_P6R68	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAA	31786
hPKU1_P6R69	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAA	31787
hPKU1_P6R70	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAA	31788

hPKU1_P6R71	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAA	31789
hPKU1_P6R72	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAA	31790
hPKU1_P6R73	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAA	31791
hPKU1_P6R74	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAA	31792
hPKU1_P6R75	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAA	31793
hPKU1_P6R76	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAA	31794
hPKU1_P6R77	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAA	31795
hPKU1_P6R78	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCACTCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAA	31796
hPKU1_P6R79	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCACTCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAA	31797
hPKU1_P6R80	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTCACTCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAA	31798
hPKU1_P7R30	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAA	31799
hPKU1_P7R31	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAA	31800

hPKU1_P7R32	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAA	31801
hPKU1_P7R33	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAA	31802
hPKU1_P7R34	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAA	31803
hPKU1_P7R35	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAA	31804
hPKU1_P7R36	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAA	31805
hPKU1_P7R37	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAA	31806
hPKU1_P7R38	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAA	31807
hPKU1_P7R39	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAA	31808
hPKU1_P7R40	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAA	31809
hPKU1_P7R41	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAA	31810
hPKU1_P7R42	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAA	31811
hPKU1_P7R43	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAA	31812
hPKU1_P7R44	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAA	31813
hPKU1_P7R45	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAA	31814
hPKU1_P7R46	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAA	31815
hPKU1_P7R47	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAA	31816
hPKU1_P7R48	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAA	31817

hPKU1_P7R49	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCAC CGAGTCGGTGCCTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAA	31818
hPKU1_P7R50	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCAC CGAGTCGGTGCACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAA	31819
hPKU1_P7R51	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCAC CGAGTCGGTGCAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAA	31820
hPKU1_P7R52	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCAC CGAGTCGGTGCGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAA	31821
hPKU1_P7R53	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCAC CGAGTCGGTGCGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAA	31822
hPKU1_P7R54	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCAC CGAGTCGGTGCAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAA	31823
hPKU1_P7R55	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCAC CGAGTCGGTGCTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAA	31824
hPKU1_P7R56	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCAC CGAGTCGGTGCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAA	31825
hPKU1_P7R57	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCAC CGAGTCGGTGCCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAA	31826
hPKU1_P7R58	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCAC CGAGTCGGTGCTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAA	31827
hPKU1_P7R59	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCAC CGAGTCGGTGCGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAA	31828
hPKU1_P7R60	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCAC CGAGTCGGTGCGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAA	31829
hPKU1_P7R61	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCAC CGAGTCGGTGCTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAA	31830
hPKU1_P7R62	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCAC CGAGTCGGTGCTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAA	31831
hPKU1_P7R63	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCAC CGAGTCGGTGCTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAA	31832
hPKU1_P7R64	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCAC CGAGTCGGTGCTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAA	31833
hPKU1_P7R65	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCAC CGAGTCGGTGCGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAA	31834

hPKU1_P7R66	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAA	31835
hPKU1_P7R67	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAA	31836
hPKU1_P7R68	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAA	31837
hPKU1_P7R69	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAA	31838
hPKU1_P7R70	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAA	31839
hPKU1_P7R71	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAA	31840
hPKU1_P7R72	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAA	31841
hPKU1_P7R73	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAA	31842
hPKU1_P7R74	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAA	31843
hPKU1_P7R75	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAA	31844
hPKU1_P7R76	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAA	31845
hPKU1_P7R77	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAA	31846

hPKU1_P7R78	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCACTCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAA	31847
hPKU1_P7R79	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCACTCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAA	31848
hPKU1_P7R80	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTCACTCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAA	31849
hPKU1_P8R30	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAG	31850
hPKU1_P8R31	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAG	31851
hPKU1_P8R32	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAG	31852
hPKU1_P8R33	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAG	31853
hPKU1_P8R34	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAG	31854
hPKU1_P8R35	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAG	31855
hPKU1_P8R36	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAG	31856
hPKU1_P8R37	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAG	31857
hPKU1_P8R38	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAG	31858
hPKU1_P8R39	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAG	31859
hPKU1_P8R40	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAG	31860
hPKU1_P8R41	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAG	31861

hPKU1_P8R42	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAG	31862
hPKU1_P8R43	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAG	31863
hPKU1_P8R44	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAG	31864
hPKU1_P8R45	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAG	31865
hPKU1_P8R46	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAG	31866
hPKU1_P8R47	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAG	31867
hPKU1_P8R48	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAG	31868
hPKU1_P8R49	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAG	31869
hPKU1_P8R50	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAG	31870
hPKU1_P8R51	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAG	31871
hPKU1_P8R52	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAG	31872
hPKU1_P8R53	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAG	31873
hPKU1_P8R54	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAG	31874
hPKU1_P8R55	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAG	31875
hPKU1_P8R56	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAG	31876
hPKU1_P8R57	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAG	31877
hPKU1_P8R58	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAG	31878

hPKU1_P8R59	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAG	31879
hPKU1_P8R60	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAG	31880
hPKU1_P8R61	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAG	31881
hPKU1_P8R62	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAG	31882
hPKU1_P8R63	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAG	31883
hPKU1_P8R64	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAG	31884
hPKU1_P8R65	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAG	31885
hPKU1_P8R66	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAG	31886
hPKU1_P8R67	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAG	31887
hPKU1_P8R68	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAG	31888
hPKU1_P8R69	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAG	31889
hPKU1_P8R70	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAG	31890
hPKU1_P8R71	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAG	31891
hPKU1_P8R72	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAG	31892

hPKU1_P8R73	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAG	31893
hPKU1_P8R74	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAG	31894
hPKU1_P8R75	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAG	31895
hPKU1_P8R76	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAG	31896
hPKU1_P8R77	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAG	31897
hPKU1_P8R78	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCACTCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAG	31898
hPKU1_P8R79	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCACTCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAG	31899
hPKU1_P8R80	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTCACTCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAG	31900
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hPKU1_P9R32	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGG	31903
hPKU1_P9R33	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGG	31904
hPKU1_P9R34	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGG	31905

hPKU1_P9R35	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCAC CGAGTCGGTGCTACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGG	31906
hPKU1_P9R36	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCAC CGAGTCGGTGCATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGG	31907
hPKU1_P9R37	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCAC CGAGTCGGTGCAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGG	31908
hPKU1_P9R38	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCAC CGAGTCGGTGCCAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGG	31909
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hPKU1_P9R42	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCAC CGAGTCGGTGCGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGG	31913
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hPKU1_P9R44	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCAC CGAGTCGGTGCCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGG	31915
hPKU1_P9R45	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCAC CGAGTCGGTGCGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGG	31916
hPKU1_P9R46	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCAC CGAGTCGGTGCTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGG	31917
hPKU1_P9R47	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCAC CGAGTCGGTGCTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGG	31918
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hPKU1_P9R51	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCAC CGAGTCGGTGCAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGG	31922

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hPKU1_P9R53	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGG	31924
hPKU1_P9R54	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGG	31925
hPKU1_P9R55	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGG	31926
hPKU1_P9R56	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGG	31927
hPKU1_P9R57	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGG	31928
hPKU1_P9R58	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGG	31929
hPKU1_P9R59	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGG	31930
hPKU1_P9R60	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGG	31931
hPKU1_P9R61	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGG	31932
hPKU1_P9R62	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGG	31933
hPKU1_P9R63	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGG	31934
hPKU1_P9R64	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGG	31935
hPKU1_P9R65	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGG	31936
hPKU1_P9R66	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGG	31937
hPKU1_P9R67	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGG	31938

hPKU1_P9R68	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGG	31939
hPKU1_P9R69	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGG	31940
hPKU1_P9R70	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGG	31941
hPKU1_P9R71	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGG	31942
hPKU1_P9R72	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGG	31943
hPKU1_P9R73	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGG	31944
hPKU1_P9R74	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGG	31945
hPKU1_P9R75	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGG	31946
hPKU1_P9R76	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGG	31947
hPKU1_P9R77	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGG	31948
hPKU1_P9R78	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCACTCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGG	31949

hPKU1_P9R79	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCACTCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGG	31950
hPKU1_P9R80	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTCACTCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGG	31951

Table 5B. Exemplary template RNA sequences

Table 5B provides design of exemplary DNA components of gene modifying systems for correcting the pathogenic R408W mutation in PAH to the wild-type form. This table details the sequence of a complete template RNA for use in exemplary gene modifying systems comprising a gene modifying polypeptide. Templates in this table employ the hPKU2 spacer CCTCAATCCTTTGGGTGTAT (SEQ ID NO: 16332).

Name	tgRNA sequence	SEQ ID NO
hPKU2_P0R29	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCGGCCCTTCTCAGTTCGCTACGACCCATA	31952
hPKU2_P0R30	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTCGGCCCTTCTCAGTTCGCTACGACCCATA	31953
hPKU2_P0R31	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTCGGCCCTTCTCAGTTCGCTACGACCCATA	31954
hPKU2_P0R32	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCCTCGGCCCTTCTCAGTTCGCTACGACCCATA	31955
hPKU2_P0R33	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCACCTCGGCCCTTCTCAGTTCGCTACGACCCATA	31956
hPKU2_P0R34	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTACCTCGGCCCTTCTCAGTTCGCTACGACCCATA	31957
hPKU2_P0R35	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCATACCTCGGCCCTTCTCAGTTCGCTACGACCCATA	31958
hPKU2_P0R36	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATA	31959

hPKU2_POR37	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATA	31960
hPKU2_POR38	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATA	31961
hPKU2_POR39	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATA	31962
hPKU2_POR40	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATA	31963
hPKU2_POR41	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATA	31964
hPKU2_POR42	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATA	31965
hPKU2_POR43	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATA	31966
hPKU2_POR44	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATA	31967
hPKU2_POR45	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATA	31968
hPKU2_POR46	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATA	31969
hPKU2_POR47	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATA	31970
hPKU2_POR48	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATA	31971
hPKU2_POR49	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATA	31972
hPKU2_POR50	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATA	31973
hPKU2_POR51	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATA	31974
hPKU2_POR52	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATA	31975
hPKU2_POR53	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATA	31976

hPKU2_POR54	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATA	31977
hPKU2_POR55	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATA	31978
hPKU2_POR56	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATA	31979
hPKU2_POR57	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATA	31980
hPKU2_POR58	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATA	31981
hPKU2_POR59	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATA	31982
hPKU2_POR60	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATA	31983
hPKU2_POR61	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATA	31984
hPKU2_POR62	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATA	31985
hPKU2_POR63	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATA	31986
hPKU2_POR64	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATA	31987
hPKU2_POR65	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATA	31988
hPKU2_POR66	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATA	31989
hPKU2_POR67	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATA	31990
hPKU2_POR68	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATA	31991
hPKU2_POR69	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATA	31992
hPKU2_POR70	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATA	31993

hPKU2_P0R71	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATA	31994
hPKU2_P0R72	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATA	31995
hPKU2_P0R73	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATA	31996
hPKU2_P0R74	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATA	31997
hPKU2_P0R75	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATA	31998
hPKU2_P0R76	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATA	31999
hPKU2_P0R77	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCACTCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATA	32000
hPKU2_P0R78	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCACTCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATA	32001
hPKU2_P0R79	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTCACTCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATA	32002
hPKU2_P10R29	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGG	32003
hPKU2_P10R30	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGG	32004
hPKU2_P10R31	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGG	32005
hPKU2_P10R32	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGG	32006
hPKU2_P10R33	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGG	32007
hPKU2_P10R34	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGG	32008
hPKU2_P10R35	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGG	32009
hPKU2_P10R36	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGG	32010

hPKU2_P10R37	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGG	32011
hPKU2_P10R38	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGG	32012
hPKU2_P10R39	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGG	32013
hPKU2_P10R40	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGG	32014
hPKU2_P10R41	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGG	32015
hPKU2_P10R42	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGG	32016
hPKU2_P10R43	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGG	32017
hPKU2_P10R44	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGG	32018
hPKU2_P10R45	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGG	32019
hPKU2_P10R46	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGG	32020
hPKU2_P10R47	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGG	32021
hPKU2_P10R48	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGG	32022
hPKU2_P10R49	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGG	32023
hPKU2_P10R50	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGG	32024
hPKU2_P10R51	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGG	32025
hPKU2_P10R52	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGG	32026
hPKU2_P10R53	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGG	32027

hPKU2_P10R54	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGG	32028
hPKU2_P10R55	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGG	32029
hPKU2_P10R56	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGG	32030
hPKU2_P10R57	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGG	32031
hPKU2_P10R58	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGG	32032
hPKU2_P10R59	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGG	32033
hPKU2_P10R60	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGG	32034
hPKU2_P10R61	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGG	32035
hPKU2_P10R62	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGG	32036
hPKU2_P10R63	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGG	32037
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hPKU2_P10R65	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGG	32039
hPKU2_P10R66	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGG	32040
hPKU2_P10R67	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGG	32041
hPKU2_P10R68	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGG	32042
hPKU2_P10R69	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGG	32043

hPKU2_P10R70	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGG	32044
hPKU2_P10R71	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGG	32045
hPKU2_P10R72	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGG	32046
hPKU2_P10R73	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGG	32047
hPKU2_P10R74	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGG	32048
hPKU2_P10R75	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGG	32049
hPKU2_P10R76	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGG	32050
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hPKU2_P10R79	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTCACTCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGG	32053
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hPKU2_P11R30	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGA	32055

hPKU2_P11R31	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGA	32056
hPKU2_P11R32	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGA	32057
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hPKU2_P11R37	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGA	32062
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hPKU2_P11R39	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGA	32064
hPKU2_P11R40	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGA	32065
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hPKU2_P11R44	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGA	32069
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hPKU2_P11R62	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGA	32087
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hPKU2_P12R30	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGAT	32106
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hPKU2_P12R34	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGAT	32110
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hPKU2_P12R43	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGAT	32119
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hPKU2_P12R46	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGAT	32122
hPKU2_P12R47	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGAT	32123
hPKU2_P12R48	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGAT	32124
hPKU2_P12R49	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGAT	32125
hPKU2_P12R50	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGAT	32126
hPKU2_P12R51	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGAT	32127
hPKU2_P12R52	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGAT	32128
hPKU2_P12R53	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGAT	32129
hPKU2_P12R54	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGAT	32130
hPKU2_P12R55	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGAT	32131
hPKU2_P12R56	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGAT	32132
hPKU2_P12R57	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGAT	32133

hPKU2_P12R58	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGAT	32134
hPKU2_P12R59	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGAT	32135
hPKU2_P12R60	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGAT	32136
hPKU2_P12R61	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGAT	32137
hPKU2_P12R62	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGAT	32138
hPKU2_P12R63	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGAT	32139
hPKU2_P12R64	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGAT	32140
hPKU2_P12R65	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGAT	32141
hPKU2_P12R66	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGAT	32142
hPKU2_P12R67	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGAT	32143
hPKU2_P12R68	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGAT	32144
hPKU2_P12R69	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGAT	32145
hPKU2_P12R70	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGAT	32146
hPKU2_P12R71	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGAT	32147

hPKU2_P12R72	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGAT	32148
hPKU2_P12R73	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGAT	32149
hPKU2_P12R74	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGAT	32150
hPKU2_P12R75	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGAT	32151
hPKU2_P12R76	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGAT	32152
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hPKU2_P12R78	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCACTCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGAT	32154
hPKU2_P12R79	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTCACTCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGAT	32155
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hPKU2_P13R30	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATT	32157
hPKU2_P13R31	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATT	32158
hPKU2_P13R32	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATT	32159
hPKU2_P13R33	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATT	32160

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hPKU2_P13R35	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATT	32162
hPKU2_P13R36	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATT	32163
hPKU2_P13R37	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATT	32164
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hPKU2_P13R40	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATT	32167
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hPKU2_P13R48	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATT	32175
hPKU2_P13R49	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATT	32176
hPKU2_P13R50	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATT	32177

hPKU2_P13 R51	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCG AGTCGGTGCGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATT	32178
hPKU2_P13 R52	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCG AGTCGGTGCGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATT	32179
hPKU2_P13 R53	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCG AGTCGGTGCAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATT	32180
hPKU2_P13 R54	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCG AGTCGGTGCTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATT	32181
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hPKU2_P13 R56	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCG AGTCGGTGCCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATT	32183
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hPKU2_P13 R60	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCG AGTCGGTGCTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATT	32187
hPKU2_P13 R61	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCG AGTCGGTGCTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATT	32188
hPKU2_P13 R62	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCG AGTCGGTGCTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATT	32189
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hPKU2_P13 R65	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCG AGTCGGTGCGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATT	32192
hPKU2_P13 R66	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCG AGTCGGTGCTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATT	32193

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hPKU2_P13R69	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATT	32196
hPKU2_P13R70	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATT	32197
hPKU2_P13R71	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATT	32198
hPKU2_P13R72	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATT	32199
hPKU2_P13R73	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATT	32200
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hPKU2_P13R75	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATT	32202
hPKU2_P13R76	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATT	32203
hPKU2_P13R77	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCACTCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATT	32204

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hPKU2_P14R29	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTG	32207
hPKU2_P14R30	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTG	32208
hPKU2_P14R31	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTG	32209
hPKU2_P14R32	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTG	32210
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hPKU2_P14R34	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTG	32212
hPKU2_P14R35	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTG	32213
hPKU2_P14R36	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTG	32214
hPKU2_P14R37	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTG	32215
hPKU2_P14R38	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTG	32216
hPKU2_P14R39	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTG	32217
hPKU2_P14R40	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTG	32218
hPKU2_P14R41	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTG	32219
hPKU2_P14R42	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTG	32220

hPKU2_P14 R43	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCG AGTCGGTGCCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTG	32221
hPKU2_P14 R44	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCG AGTCGGTGCGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTG	32222
hPKU2_P14 R45	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCG AGTCGGTGCTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTG	32223
hPKU2_P14 R46	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCG AGTCGGTGCTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTG	32224
hPKU2_P14 R47	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCG AGTCGGTGCTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTG	32225
hPKU2_P14 R48	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCG AGTCGGTGCCTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTG	32226
hPKU2_P14 R49	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCG AGTCGGTGCACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTG	32227
hPKU2_P14 R50	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCG AGTCGGTGCAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTG	32228
hPKU2_P14 R51	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCG AGTCGGTGCGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTG	32229
hPKU2_P14 R52	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCG AGTCGGTGCGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTG	32230
hPKU2_P14 R53	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCG AGTCGGTGCAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTG	32231
hPKU2_P14 R54	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCG AGTCGGTGCTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTG	32232
hPKU2_P14 R55	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCG AGTCGGTGCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTG	32233
hPKU2_P14 R56	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCG AGTCGGTGCCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTG	32234
hPKU2_P14 R57	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCG AGTCGGTGCTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTG	32235
hPKU2_P14 R58	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCG AGTCGGTGCGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTG	32236
hPKU2_P14 R59	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCG AGTCGGTGCGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTG	32237

hPKU2_P14R60	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTG	32238
hPKU2_P14R61	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTG	32239
hPKU2_P14R62	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTG	32240
hPKU2_P14R63	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTG	32241
hPKU2_P14R64	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTG	32242
hPKU2_P14R65	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTG	32243
hPKU2_P14R66	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTG	32244
hPKU2_P14R67	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTG	32245
hPKU2_P14R68	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTG	32246
hPKU2_P14R69	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTG	32247
hPKU2_P14R70	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTG	32248
hPKU2_P14R71	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTG	32249
hPKU2_P14R72	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTG	32250

hPKU2_P14R73	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTG	32251
hPKU2_P14R74	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTG	32252
hPKU2_P14R75	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTG	32253
hPKU2_P14R76	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTG	32254
hPKU2_P14R77	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCACTCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTG	32255
hPKU2_P14R78	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCACTCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTG	32256
hPKU2_P14R79	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTCACTCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTG	32257
hPKU2_P15R29	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTGA	32258
hPKU2_P15R30	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTGA	32259
hPKU2_P15R31	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTGA	32260
hPKU2_P15R32	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTGA	32261
hPKU2_P15R33	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTGA	32262
hPKU2_P15R34	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTGA	32263

hPKU2_P15R35	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTGA	32264
hPKU2_P15R36	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTGA	32265
hPKU2_P15R37	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTGA	32266
hPKU2_P15R38	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTGA	32267
hPKU2_P15R39	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTGA	32268
hPKU2_P15R40	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTGA	32269
hPKU2_P15R41	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTGA	32270
hPKU2_P15R42	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTGA	32271
hPKU2_P15R43	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTGA	32272
hPKU2_P15R44	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTGA	32273
hPKU2_P15R45	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTGA	32274
hPKU2_P15R46	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTGA	32275
hPKU2_P15R47	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTGA	32276
hPKU2_P15R48	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTGA	32277
hPKU2_P15R49	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTGA	32278
hPKU2_P15R50	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTGA	32279
hPKU2_P15R51	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTGA	32280

hPKU2_P15R52	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTGA	32281
hPKU2_P15R53	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTGA	32282
hPKU2_P15R54	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTGA	32283
hPKU2_P15R55	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTGA	32284
hPKU2_P15R56	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTGA	32285
hPKU2_P15R57	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTGA	32286
hPKU2_P15R58	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTGA	32287
hPKU2_P15R59	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTGA	32288
hPKU2_P15R60	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTGA	32289
hPKU2_P15R61	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTGA	32290
hPKU2_P15R62	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTGA	32291
hPKU2_P15R63	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTGA	32292
hPKU2_P15R64	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTGA	32293
hPKU2_P15R65	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTGA	32294
hPKU2_P15R66	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTGA	32295

hPKU2_P15R67	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTGA	32296
hPKU2_P15R68	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTGA	32297
hPKU2_P15R69	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTGA	32298
hPKU2_P15R70	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTGA	32299
hPKU2_P15R71	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTGA	32300
hPKU2_P15R72	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTGA	32301
hPKU2_P15R73	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTGA	32302
hPKU2_P15R74	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTGA	32303
hPKU2_P15R75	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTGA	32304
hPKU2_P15R76	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTGA	32305
hPKU2_P15R77	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCACTCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTGA	32306

hPKU2_P15R78	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCACTCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTGA	32307
hPKU2_P15R79	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTCACTCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTGA	32308
hPKU2_P16R29	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTGAG	32309
hPKU2_P16R30	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTGAG	32310
hPKU2_P16R31	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTGAG	32311
hPKU2_P16R32	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTGAG	32312
hPKU2_P16R33	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTGAG	32313
hPKU2_P16R34	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTGAG	32314
hPKU2_P16R35	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTGAG	32315
hPKU2_P16R36	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTGAG	32316
hPKU2_P16R37	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTGAG	32317
hPKU2_P16R38	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTGAG	32318
hPKU2_P16R39	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTGAG	32319
hPKU2_P16R40	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTGAG	32320
hPKU2_P16R41	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTGAG	32321
hPKU2_P16R42	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTGAG	32322

hPKU2_P16R43	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTGAG	32323
hPKU2_P16R44	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTGAG	32324
hPKU2_P16R45	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTGAG	32325
hPKU2_P16R46	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTGAG	32326
hPKU2_P16R47	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTGAG	32327
hPKU2_P16R48	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTGAG	32328
hPKU2_P16R49	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTGAG	32329
hPKU2_P16R50	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTGAG	32330
hPKU2_P16R51	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTGAG	32331
hPKU2_P16R52	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTGAG	32332
hPKU2_P16R53	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTGAG	32333
hPKU2_P16R54	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTGAG	32334
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hPKU2_P16R56	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTGAG	32336
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hPKU2_P16R61	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTGAG	32341
hPKU2_P16R62	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTGAG	32342
hPKU2_P16R63	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTGAG	32343
hPKU2_P16R64	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTGAG	32344
hPKU2_P16R65	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTGAG	32345
hPKU2_P16R66	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTGAG	32346
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hPKU2_P16R69	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTGAG	32349
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hPKU2_P16R73	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTGAG	32353
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hPKU2_P16R75	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTGAG	32355
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hPKU2_P16R77	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCACTCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTGAG	32357
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hPKU2_P17R29	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTGAGG	32360
hPKU2_P17R30	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTGAGG	32361
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hPKU2_P17R32	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTGAGG	32363
hPKU2_P17R33	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTGAGG	32364

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hPKU2_P17R35	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTGAGG	32366
hPKU2_P17R36	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTGAGG	32367
hPKU2_P17R37	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTGAGG	32368
hPKU2_P17R38	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTGAGG	32369
hPKU2_P17R39	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTGAGG	32370
hPKU2_P17R40	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTGAGG	32371
hPKU2_P17R41	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTGAGG	32372
hPKU2_P17R42	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTGAGG	32373
hPKU2_P17R43	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTGAGG	32374
hPKU2_P17R44	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTGAGG	32375
hPKU2_P17R45	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTGAGG	32376
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hPKU2_P17R47	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTGAGG	32378
hPKU2_P17R48	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTGAGG	32379
hPKU2_P17R49	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTGAGG	32380
hPKU2_P17R50	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTGAGG	32381

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hPKU2_P17R54	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTGAGG	32385
hPKU2_P17R55	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTGAGG	32386
hPKU2_P17R56	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTGAGG	32387
hPKU2_P17R57	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTGAGG	32388
hPKU2_P17R58	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTGAGG	32389
hPKU2_P17R59	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTGAGG	32390
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hPKU2_P17R62	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTGAGG	32393
hPKU2_P17R63	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTGAGG	32394
hPKU2_P17R64	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTGAGG	32395
hPKU2_P17R65	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTGAGG	32396

hPKU2_P17R66	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTGAGG	32397
hPKU2_P17R67	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTGAGG	32398
hPKU2_P17R68	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTGAGG	32399
hPKU2_P17R69	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTGAGG	32400
hPKU2_P17R70	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTGAGG	32401
hPKU2_P17R71	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTGAGG	32402
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hPKU2_P17R73	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTGAGG	32404
hPKU2_P17R74	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTGAGG	32405
hPKU2_P17R75	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTGAGG	32406
hPKU2_P17R76	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTGAGG	32407

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hPKU2_P17R78	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCACTCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTGAGG	32409
hPKU2_P17R79	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTCACTCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAGGATTGAGG	32410
hPKU2_P1R29	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCGGCCCTTCTCAGTTCGCTACGACCCATAC	32411
hPKU2_P1R30	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTCGGCCCTTCTCAGTTCGCTACGACCCATAC	32412
hPKU2_P1R31	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTCGGCCCTTCTCAGTTCGCTACGACCCATAC	32413
hPKU2_P1R32	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCCTCGGCCCTTCTCAGTTCGCTACGACCCATAC	32414
hPKU2_P1R33	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCACCTCGGCCCTTCTCAGTTCGCTACGACCCATAC	32415
hPKU2_P1R34	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTACCTCGGCCCTTCTCAGTTCGCTACGACCCATAC	32416
hPKU2_P1R35	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCATACCTCGGCCCTTCTCAGTTCGCTACGACCCATAC	32417
hPKU2_P1R36	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATAC	32418
hPKU2_P1R37	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATAC	32419
hPKU2_P1R38	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATAC	32420
hPKU2_P1R39	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATAC	32421
hPKU2_P1R40	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATAC	32422

hPKU2_P1R41	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATAC	32423
hPKU2_P1R42	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATAC	32424
hPKU2_P1R43	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATAC	32425
hPKU2_P1R44	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATAC	32426
hPKU2_P1R45	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATAC	32427
hPKU2_P1R46	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATAC	32428
hPKU2_P1R47	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATAC	32429
hPKU2_P1R48	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATAC	32430
hPKU2_P1R49	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATAC	32431
hPKU2_P1R50	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATAC	32432
hPKU2_P1R51	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATAC	32433
hPKU2_P1R52	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATAC	32434
hPKU2_P1R53	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATAC	32435
hPKU2_P1R54	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATAC	32436
hPKU2_P1R55	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATAC	32437
hPKU2_P1R56	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATAC	32438
hPKU2_P1R57	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATAC	32439

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hPKU2_P1R59	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATAC	32441
hPKU2_P1R60	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATAC	32442
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hPKU2_P1R62	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATAC	32444
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hPKU2_P1R64	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATAC	32446
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hPKU2_P1R67	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATAC	32449
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hPKU2_P1R79	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTCACTCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATAC	32461
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hPKU2_P2R32	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCCTCGGCCCTTCTCAGTTCGCTACGACCCATACA	32465
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hPKU2_P2R34	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTACCTCGGCCCTTCTCAGTTCGCTACGACCCATACA	32467
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hPKU2_P2R42	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACA	32475
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hPKU2_P2R47	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACA	32480
hPKU2_P2R48	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACA	32481
hPKU2_P2R49	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACA	32482
hPKU2_P2R50	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACA	32483
hPKU2_P2R51	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACA	32484
hPKU2_P2R52	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACA	32485
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hPKU2_P2R56	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACA	32489

hPKU2_P2R57	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACA	32490
hPKU2_P2R58	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACA	32491
hPKU2_P2R59	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACA	32492
hPKU2_P2R60	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACA	32493
hPKU2_P2R61	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACA	32494
hPKU2_P2R62	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACA	32495
hPKU2_P2R63	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACA	32496
hPKU2_P2R64	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACA	32497
hPKU2_P2R65	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACA	32498
hPKU2_P2R66	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACA	32499
hPKU2_P2R67	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACA	32500
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hPKU2_P2R69	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACA	32502
hPKU2_P2R70	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACA	32503
hPKU2_P2R71	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACA	32504
hPKU2_P2R72	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACA	32505
hPKU2_P2R73	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACA	32506

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hPKU2_P2R75	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACA	32508
hPKU2_P2R76	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACA	32509
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hPKU2_P2R78	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCACTCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACA	32511
hPKU2_P2R79	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTCACTCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACA	32512
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hPKU2_P3R31	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTCGGCCCTTCTCAGTTCGCTACGACCCATACAC	32515
hPKU2_P3R32	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCCTCGGCCCTTCTCAGTTCGCTACGACCCATACAC	32516
hPKU2_P3R33	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCACCTCGGCCCTTCTCAGTTCGCTACGACCCATACAC	32517
hPKU2_P3R34	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTACCTCGGCCCTTCTCAGTTCGCTACGACCCATACAC	32518
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hPKU2_P3R36	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACAC	32520
hPKU2_P3R37	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACAC	32521
hPKU2_P3R38	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACAC	32522

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hPKU2_P3R42	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACAC	32526
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hPKU2_P3R54	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACAC	32538
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hPKU2_P3R58	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACAC	32542
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hPKU2_P3R67	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACAC	32551
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hPKU2_P3R72	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACAC	32556

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hPKU2_P3R78	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCACTCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACAC	32562
hPKU2_P3R79	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTCACTCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACAC	32563
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hPKU2_P4R39	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACC	32574
hPKU2_P4R40	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACC	32575
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hPKU2_P4R42	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACC	32577
hPKU2_P4R43	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACC	32578
hPKU2_P4R44	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACC	32579
hPKU2_P4R45	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACC	32580
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hPKU2_P4R50	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACC	32585
hPKU2_P4R51	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACC	32586
hPKU2_P4R52	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACC	32587
hPKU2_P4R53	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACC	32588

hPKU2_P4R54	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACC	32589
hPKU2_P4R55	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACC	32590
hPKU2_P4R56	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACC	32591
hPKU2_P4R57	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACC	32592
hPKU2_P4R58	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACC	32593
hPKU2_P4R59	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACC	32594
hPKU2_P4R60	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACC	32595
hPKU2_P4R61	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACC	32596
hPKU2_P4R62	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACC	32597
hPKU2_P4R63	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACC	32598
hPKU2_P4R64	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACC	32599
hPKU2_P4R65	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACC	32600
hPKU2_P4R66	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACC	32601
hPKU2_P4R67	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACC	32602
hPKU2_P4R68	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACC	32603
hPKU2_P4R69	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACC	32604
hPKU2_P4R70	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACC	32605

hPKU2_P4R71	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACC	32606
hPKU2_P4R72	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACC	32607
hPKU2_P4R73	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACC	32608
hPKU2_P4R74	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACC	32609
hPKU2_P4R75	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACC	32610
hPKU2_P4R76	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACC	32611
hPKU2_P4R77	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCACTCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACC	32612
hPKU2_P4R78	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCACTCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACC	32613
hPKU2_P4R79	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTCACTCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACC	32614
hPKU2_P5R29	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCGGCCCTTCTCAGTTCGCTACGACCCATACACCC	32615
hPKU2_P5R30	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCC	32616
hPKU2_P5R31	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCC	32617
hPKU2_P5R32	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCC	32618
hPKU2_P5R33	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCC	32619
hPKU2_P5R34	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCC	32620

hPKU2_P5R35	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCC	32621
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hPKU2_P5R37	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCC	32623
hPKU2_P5R38	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCC	32624
hPKU2_P5R39	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCC	32625
hPKU2_P5R40	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCC	32626
hPKU2_P5R41	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCC	32627
hPKU2_P5R42	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCC	32628
hPKU2_P5R43	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCC	32629
hPKU2_P5R44	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCC	32630
hPKU2_P5R45	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCC	32631
hPKU2_P5R46	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCC	32632
hPKU2_P5R47	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCC	32633
hPKU2_P5R48	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCC	32634
hPKU2_P5R49	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCC	32635
hPKU2_P5R50	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCC	32636
hPKU2_P5R51	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCC	32637

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hPKU2_P5R53	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCC	32639
hPKU2_P5R54	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCC	32640
hPKU2_P5R55	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCC	32641
hPKU2_P5R56	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCC	32642
hPKU2_P5R57	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCC	32643
hPKU2_P5R58	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCC	32644
hPKU2_P5R59	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCC	32645
hPKU2_P5R60	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCC	32646
hPKU2_P5R61	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCC	32647
hPKU2_P5R62	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCC	32648
hPKU2_P5R63	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCC	32649
hPKU2_P5R64	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCC	32650
hPKU2_P5R65	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCC	32651
hPKU2_P5R66	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCC	32652
hPKU2_P5R67	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCC	32653
hPKU2_P5R68	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCC	32654

hPKU2_P5R69	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCC	32655
hPKU2_P5R70	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCC	32656
hPKU2_P5R71	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCC	32657
hPKU2_P5R72	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCC	32658
hPKU2_P5R73	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCC	32659
hPKU2_P5R74	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCC	32660
hPKU2_P5R75	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCC	32661
hPKU2_P5R76	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCC	32662
hPKU2_P5R77	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCACTCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCC	32663
hPKU2_P5R78	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCACTCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCC	32664
hPKU2_P5R79	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTCACTCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCC	32665
hPKU2_P6R29	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCGGCCCTTCTCAGTTCGCTACGACCCATACACCCA	32666
hPKU2_P6R30	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCA	32667
hPKU2_P6R31	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCA	32668

hPKU2_P6R32	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCA	32669
hPKU2_P6R33	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCA	32670
hPKU2_P6R34	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCA	32671
hPKU2_P6R35	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCA	32672
hPKU2_P6R36	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCA	32673
hPKU2_P6R37	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCA	32674
hPKU2_P6R38	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCA	32675
hPKU2_P6R39	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCA	32676
hPKU2_P6R40	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCA	32677
hPKU2_P6R41	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCA	32678
hPKU2_P6R42	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCA	32679
hPKU2_P6R43	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCA	32680
hPKU2_P6R44	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCA	32681
hPKU2_P6R45	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCA	32682
hPKU2_P6R46	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCA	32683
hPKU2_P6R47	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCA	32684
hPKU2_P6R48	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCA	32685

hPKU2_P6R49	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCA	32686
hPKU2_P6R50	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCA	32687
hPKU2_P6R51	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCA	32688
hPKU2_P6R52	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCA	32689
hPKU2_P6R53	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCA	32690
hPKU2_P6R54	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCA	32691
hPKU2_P6R55	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCA	32692
hPKU2_P6R56	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCA	32693
hPKU2_P6R57	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCA	32694
hPKU2_P6R58	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCA	32695
hPKU2_P6R59	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCA	32696
hPKU2_P6R60	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCA	32697
hPKU2_P6R61	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCA	32698
hPKU2_P6R62	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCA	32699
hPKU2_P6R63	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCA	32700
hPKU2_P6R64	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCA	32701
hPKU2_P6R65	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCA	32702

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hPKU2_P6R67	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCA	32704
hPKU2_P6R68	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCA	32705
hPKU2_P6R69	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCA	32706
hPKU2_P6R70	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCA	32707
hPKU2_P6R71	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCA	32708
hPKU2_P6R72	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCA	32709
hPKU2_P6R73	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCA	32710
hPKU2_P6R74	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCA	32711
hPKU2_P6R75	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCA	32712
hPKU2_P6R76	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCA	32713
hPKU2_P6R77	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCACTCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCA	32714
hPKU2_P6R78	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCACTCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCA	32715
hPKU2_P6R79	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTCACTCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCA	32716

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hPKU2_P7R30	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAA	32718
hPKU2_P7R31	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAA	32719
hPKU2_P7R32	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAA	32720
hPKU2_P7R33	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAA	32721
hPKU2_P7R34	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAA	32722
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hPKU2_P7R37	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAA	32725
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hPKU2_P7R39	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAA	32727
hPKU2_P7R40	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAA	32728
hPKU2_P7R41	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAA	32729
hPKU2_P7R42	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAA	32730
hPKU2_P7R43	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAA	32731
hPKU2_P7R44	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAA	32732
hPKU2_P7R45	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAA	32733

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hPKU2_P7R49	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAA	32737
hPKU2_P7R50	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAA	32738
hPKU2_P7R51	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAA	32739
hPKU2_P7R52	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAA	32740
hPKU2_P7R53	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAA	32741
hPKU2_P7R54	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAA	32742
hPKU2_P7R55	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAA	32743
hPKU2_P7R56	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAA	32744
hPKU2_P7R57	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAA	32745
hPKU2_P7R58	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAA	32746
hPKU2_P7R59	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAA	32747
hPKU2_P7R60	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAA	32748
hPKU2_P7R61	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAA	32749
hPKU2_P7R62	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAA	32750

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hPKU2_P7R64	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAA	32752
hPKU2_P7R65	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAA	32753
hPKU2_P7R66	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAA	32754
hPKU2_P7R67	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAA	32755
hPKU2_P7R68	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAA	32756
hPKU2_P7R69	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAA	32757
hPKU2_P7R70	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAA	32758
hPKU2_P7R71	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAA	32759
hPKU2_P7R72	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAA	32760
hPKU2_P7R73	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAA	32761
hPKU2_P7R74	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAA	32762
hPKU2_P7R75	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAA	32763
hPKU2_P7R76	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAA	32764

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hPKU2_P7R78	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCACTCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAA	32766
hPKU2_P7R79	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTCACTCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAA	32767
hPKU2_P8R29	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAA	32768
hPKU2_P8R30	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAA	32769
hPKU2_P8R31	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAA	32770
hPKU2_P8R32	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAA	32771
hPKU2_P8R33	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAA	32772
hPKU2_P8R34	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAA	32773
hPKU2_P8R35	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAA	32774
hPKU2_P8R36	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAA	32775
hPKU2_P8R37	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAA	32776
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hPKU2_P8R42	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAA	32781
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hPKU2_P9R77	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCACTCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAG	32867
hPKU2_P9R78	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCACTCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAG	32868
hPKU2_P9R79	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTCACTCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCATACACCCAAAG	32869

Table 5C. Exemplary template RNA sequences

Table 5C provides design of exemplary DNA components of gene modifying systems for correcting the pathogenic R408W mutation in PAH to the wild-type form. This table details the sequence of a complete template RNA for use in exemplary gene modifying systems comprising a gene modifying polypeptide. Templates in this table employ the hPKU33 spacer TGGGTCGTAGCGAACTGAGA (SEQ ID NO: 16102).

Name	tgRNA sequence	SEQ ID NO
hPKU3_P0R10	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCGGCCCTTCT	32870
hPKU3_P0R11	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTCGGCCCTTCT	32871
hPKU3_P0R12	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTCGGCCCTTCT	32872
hPKU3_P0R13	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCCTCGGCCCTTCT	32873
hPKU3_P0R14	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCACCTCGGCCCTTCT	32874
hPKU3_P0R15	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTACCTCGGCCCTTCT	32875
hPKU3_P0R16	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCATACCTCGGCCCTTCT	32876
hPKU3_P0R17	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAATACCTCGGCCCTTCT	32877
hPKU3_P0R18	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCAATACCTCGGCCCTTCT	32878
hPKU3_P0R19	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCACAATACCTCGGCCCTTCT	32879
hPKU3_P0R20	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCACAATACCTCGGCCCTTCT	32880
hPKU3_P0R21	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCCACAATACCTCGGCCCTTCT	32881

hPKU3_P0R22	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGCGCCACAATACCTCGGCCCTTCT	32882
hPKU3_P0R23	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGCTGCCACAATACCTCGGCCCTTCT	32883
hPKU3_P0R24	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGCCTGCCACAATACCTCGGCCCTTCT	32884
hPKU3_P0R25	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGCGCTGCCACAATACCTCGGCCCTTCT	32885
hPKU3_P0R26	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGCTGCTGCCACAATACCTCGGCCCTTCT	32886
hPKU3_P0R27	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGCTTGCTGCCACAATACCTCGGCCCTTCT	32887
hPKU3_P0R28	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGCTTTGCTGCCACAATACCTCGGCCCTTCT	32888
hPKU3_P0R29	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGCCTTTGCTGCCACAATACCTCGGCCCTTCT	32889
hPKU3_P0R30	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGCACTTTGCTGCCACAATACCTCGGCCCTTCT	32890
hPKU3_P0R31	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGCAACTTTGCTGCCACAATACCTCGGCCCTTCT	32891
hPKU3_P0R32	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGCGAACTTTGCTGCCACAATACCTCGGCCCTTCT	32892
hPKU3_P0R33	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGCGGAACTTTGCTGCCACAATACCTCGGCCCTTCT	32893
hPKU3_P0R34	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGCAGGAACTTTGCTGCCACAATACCTCGGCCCTTCT	32894
hPKU3_P0R35	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGCTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCT	32895
hPKU3_P0R36	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCT	32896
hPKU3_P0R37	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGCCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCT	32897
hPKU3_P0R38	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGCTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCT	32898

hPKU3_P0R39	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGCGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCT	32899
hPKU3_P0R40	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGCGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCT	32900
hPKU3_P0R41	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGCTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCT	32901
hPKU3_P0R42	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGCTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCT	32902
hPKU3_P0R43	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGCTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCT	32903
hPKU3_P0R44	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGCTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCT	32904
hPKU3_P0R45	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGCGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCT	32905
hPKU3_P0R46	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGCGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCT	32906
hPKU3_P0R47	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGCTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCT	32907
hPKU3_P0R48	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGCGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCT	32908
hPKU3_P0R49	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCT	32909
hPKU3_P0R50	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCT	32910
hPKU3_P0R51	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGCCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCT	32911
hPKU3_P0R52	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGCGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCT	32912
hPKU3_P0R53	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGCAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCT	32913
hPKU3_P0R54	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCT	32914
hPKU3_P0R55	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGCCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCT	32915

hPKU3_P0R56	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGCTCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCT	32916
hPKU3_P0R57	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGCCTCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCT	32917
hPKU3_P0R58	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGCACTCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCT	32918
hPKU3_P0R59	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGCCACTCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCT	32919
hPKU3_P0R60	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGCTCACTCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCT	32920
hPKU3_P10R10	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGCCGGCCCTTCTCAGTTCGCTA	32921
hPKU3_P10R11	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGCTCGGCCCTTCTCAGTTCGCTA	32922
hPKU3_P10R12	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGCCTCGGCCCTTCTCAGTTCGCTA	32923
hPKU3_P10R13	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGCCCTCGGCCCTTCTCAGTTCGCTA	32924
hPKU3_P10R14	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGCACCTCGGCCCTTCTCAGTTCGCTA	32925
hPKU3_P10R15	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGCTACCTCGGCCCTTCTCAGTTCGCTA	32926
hPKU3_P10R16	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGCATACCTCGGCCCTTCTCAGTTCGCTA	32927
hPKU3_P10R17	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGCAATACCTCGGCCCTTCTCAGTTCGCTA	32928
hPKU3_P10R18	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGCCAATACCTCGGCCCTTCTCAGTTCGCTA	32929
hPKU3_P10R19	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGCACAATACCTCGGCCCTTCTCAGTTCGCTA	32930
hPKU3_P10R20	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGCCACAATACCTCGGCCCTTCTCAGTTCGCTA	32931
hPKU3_P10R21	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGCCCACAATACCTCGGCCCTTCTCAGTTCGCTA	32932

hPKU3_P10R22	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGCCACAATACCTCGGCCCTTCTCAGTTCGCTA	32933
hPKU3_P10R23	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTA	32934
hPKU3_P10R24	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTA	32935
hPKU3_P10R25	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTA	32936
hPKU3_P10R26	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTA	32937
hPKU3_P10R27	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTA	32938
hPKU3_P10R28	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTA	32939
hPKU3_P10R29	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTA	32940
hPKU3_P10R30	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTA	32941
hPKU3_P10R31	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTA	32942
hPKU3_P10R32	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTA	32943
hPKU3_P10R33	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTA	32944
hPKU3_P10R34	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTA	32945
hPKU3_P10R35	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTA	32946
hPKU3_P10R36	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTA	32947
hPKU3_P10R37	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTA	32948
hPKU3_P10R38	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTA	32949

hPKU3_P10R39	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTA	32950
hPKU3_P10R40	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTA	32951
hPKU3_P10R41	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTA	32952
hPKU3_P10R42	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTA	32953
hPKU3_P10R43	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTA	32954
hPKU3_P10R44	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTA	32955
hPKU3_P10R45	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTA	32956
hPKU3_P10R46	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTA	32957
hPKU3_P10R47	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTA	32958
hPKU3_P10R48	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTA	32959
hPKU3_P10R49	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTA	32960
hPKU3_P10R50	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTA	32961
hPKU3_P10R51	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTA	32962
hPKU3_P10R52	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTA	32963
hPKU3_P10R53	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTA	32964
hPKU3_P10R54	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTA	32965
hPKU3_P10R55	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTA	32966

hPKU3_P10R56	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTA	32967
hPKU3_P10R57	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTA	32968
hPKU3_P10R58	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCACTCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTA	32969
hPKU3_P10R59	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCACTCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTA	32970
hPKU3_P10R60	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTCACTCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTA	32971
hPKU3_P11R10	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCGGCCCTTCTCAGTTCGCTAC	32972
hPKU3_P11R11	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTCGGCCCTTCTCAGTTCGCTAC	32973
hPKU3_P11R12	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTCGGCCCTTCTCAGTTCGCTAC	32974
hPKU3_P11R13	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCCTCGGCCCTTCTCAGTTCGCTAC	32975
hPKU3_P11R14	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCACCTCGGCCCTTCTCAGTTCGCTAC	32976
hPKU3_P11R15	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTACCTCGGCCCTTCTCAGTTCGCTAC	32977
hPKU3_P11R16	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCATACCTCGGCCCTTCTCAGTTCGCTAC	32978
hPKU3_P11R17	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAATACCTCGGCCCTTCTCAGTTCGCTAC	32979
hPKU3_P11R18	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCAATACCTCGGCCCTTCTCAGTTCGCTAC	32980
hPKU3_P11R19	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCACAATACCTCGGCCCTTCTCAGTTCGCTAC	32981
hPKU3_P11R20	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCACAATACCTCGGCCCTTCTCAGTTCGCTAC	32982
hPKU3_P11R21	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCCACAATACCTCGGCCCTTCTCAGTTCGCTAC	32983

hPKU3_P11R22	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGCCACAATACCTCGGCCCTTCTCAGTTCGCTAC	32984
hPKU3_P11R23	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTAC	32985
hPKU3_P11R24	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTAC	32986
hPKU3_P11R25	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTAC	32987
hPKU3_P11R26	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTAC	32988
hPKU3_P11R27	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTAC	32989
hPKU3_P11R28	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTAC	32990
hPKU3_P11R29	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTAC	32991
hPKU3_P11R30	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTAC	32992
hPKU3_P11R31	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTAC	32993
hPKU3_P11R32	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTAC	32994
hPKU3_P11R33	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTAC	32995
hPKU3_P11R34	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTAC	32996
hPKU3_P11R35	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTAC	32997
hPKU3_P11R36	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTAC	32998
hPKU3_P11R37	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTAC	32999
hPKU3_P11R38	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTAC	33000

hPKU3_P11R39	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTAC	33001
hPKU3_P11R40	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTAC	33002
hPKU3_P11R41	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTAC	33003
hPKU3_P11R42	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTAC	33004
hPKU3_P11R43	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTAC	33005
hPKU3_P11R44	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTAC	33006
hPKU3_P11R45	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTAC	33007
hPKU3_P11R46	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTAC	33008
hPKU3_P11R47	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTAC	33009
hPKU3_P11R48	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTAC	33010
hPKU3_P11R49	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTAC	33011
hPKU3_P11R50	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTAC	33012
hPKU3_P11R51	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTAC	33013
hPKU3_P11R52	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTAC	33014
hPKU3_P11R53	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTAC	33015
hPKU3_P11R54	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTAC	33016
hPKU3_P11R55	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTAC	33017

hPKU3_P11R56	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTAC	33018
hPKU3_P11R57	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTAC	33019
hPKU3_P11R58	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCACTCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTAC	33020
hPKU3_P11R59	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCACTCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTAC	33021
hPKU3_P11R60	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTCACTCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTAC	33022
hPKU3_P12R10	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCGGCCCTTCTCAGTTCGCTACG	33023
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hPKU3_P12R14	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCACCTCGGCCCTTCTCAGTTCGCTACG	33027
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hPKU3_P12R16	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCATACCTCGGCCCTTCTCAGTTCGCTACG	33029
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hPKU3_P12R18	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCAATACCTCGGCCCTTCTCAGTTCGCTACG	33031
hPKU3_P12R19	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCACAATACCTCGGCCCTTCTCAGTTCGCTACG	33032
hPKU3_P12R20	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACG	33033
hPKU3_P12R21	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCCACAATACCTCGGCCCTTCTCAGTTCGCTACG	33034

hPKU3_P12R22	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGCCACAATACCTCGGCCCTTCTCAGTTCGCTACG	33035
hPKU3_P12R23	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACG	33036
hPKU3_P12R24	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACG	33037
hPKU3_P12R25	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACG	33038
hPKU3_P12R26	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACG	33039
hPKU3_P12R27	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACG	33040
hPKU3_P12R28	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACG	33041
hPKU3_P12R29	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACG	33042
hPKU3_P12R30	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACG	33043
hPKU3_P12R31	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACG	33044
hPKU3_P12R32	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACG	33045
hPKU3_P12R33	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACG	33046
hPKU3_P12R34	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACG	33047
hPKU3_P12R35	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACG	33048
hPKU3_P12R36	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACG	33049
hPKU3_P12R37	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACG	33050
hPKU3_P12R38	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACG	33051

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hPKU3_P12R40	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACG	33053
hPKU3_P12R41	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACG	33054
hPKU3_P12R42	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACG	33055
hPKU3_P12R43	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACG	33056
hPKU3_P12R44	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACG	33057
hPKU3_P12R45	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACG	33058
hPKU3_P12R46	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACG	33059
hPKU3_P12R47	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACG	33060
hPKU3_P12R48	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACG	33061
hPKU3_P12R49	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACG	33062
hPKU3_P12R50	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACG	33063
hPKU3_P12R51	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACG	33064
hPKU3_P12R52	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACG	33065
hPKU3_P12R53	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACG	33066
hPKU3_P12R54	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACG	33067
hPKU3_P12R55	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACG	33068

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hPKU3_P12R57	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACG	33070
hPKU3_P12R58	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCACTCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACG	33071
hPKU3_P12R59	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCACTCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACG	33072
hPKU3_P12R60	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTCACTCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACG	33073
hPKU3_P13R10	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCGGCCCTTCTCAGTTCGCTACGA	33074
hPKU3_P13R11	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTCGGCCCTTCTCAGTTCGCTACGA	33075
hPKU3_P13R12	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTCGGCCCTTCTCAGTTCGCTACGA	33076
hPKU3_P13R13	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCCTCGGCCCTTCTCAGTTCGCTACGA	33077
hPKU3_P13R14	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCACCTCGGCCCTTCTCAGTTCGCTACGA	33078
hPKU3_P13R15	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTACCTCGGCCCTTCTCAGTTCGCTACGA	33079
hPKU3_P13R16	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCATACCTCGGCCCTTCTCAGTTCGCTACGA	33080
hPKU3_P13R17	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAATACCTCGGCCCTTCTCAGTTCGCTACGA	33081
hPKU3_P13R18	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCAATACCTCGGCCCTTCTCAGTTCGCTACGA	33082
hPKU3_P13R19	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCACAATACCTCGGCCCTTCTCAGTTCGCTACGA	33083
hPKU3_P13R20	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGA	33084
hPKU3_P13R21	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCCACAATACCTCGGCCCTTCTCAGTTCGCTACGA	33085

hPKU3_P13R22	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGA	33086
hPKU3_P13R23	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGA	33087
hPKU3_P13R24	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGA	33088
hPKU3_P13R25	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGA	33089
hPKU3_P13R26	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGA	33090
hPKU3_P13R27	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGA	33091
hPKU3_P13R28	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGA	33092
hPKU3_P13R29	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGA	33093
hPKU3_P13R30	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGA	33094
hPKU3_P13R31	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGA	33095
hPKU3_P13R32	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGA	33096
hPKU3_P13R33	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGA	33097
hPKU3_P13R34	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGA	33098
hPKU3_P13R35	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGA	33099
hPKU3_P13R36	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGA	33100
hPKU3_P13R37	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGA	33101
hPKU3_P13R38	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGA	33102

hPKU3_P13R39	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGA	33103
hPKU3_P13R40	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGA	33104
hPKU3_P13R41	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGA	33105
hPKU3_P13R42	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGA	33106
hPKU3_P13R43	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGA	33107
hPKU3_P13R44	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGA	33108
hPKU3_P13R45	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGA	33109
hPKU3_P13R46	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGA	33110
hPKU3_P13R47	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGA	33111
hPKU3_P13R48	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGA	33112
hPKU3_P13R49	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGA	33113
hPKU3_P13R50	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGA	33114
hPKU3_P13R51	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGA	33115
hPKU3_P13R52	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGA	33116
hPKU3_P13R53	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGA	33117
hPKU3_P13R54	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGA	33118
hPKU3_P13R55	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGA	33119

hPKU3_P13R56	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGA	33120
hPKU3_P13R57	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGA	33121
hPKU3_P13R58	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCACTCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGA	33122
hPKU3_P13R59	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCACTCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGA	33123
hPKU3_P13R60	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTCACTCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGA	33124
hPKU3_P14R10	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCGGCCCTTCTCAGTTCGCTACGAC	33125
hPKU3_P14R11	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTCGGCCCTTCTCAGTTCGCTACGAC	33126
hPKU3_P14R12	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTCGGCCCTTCTCAGTTCGCTACGAC	33127
hPKU3_P14R13	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCCTCGGCCCTTCTCAGTTCGCTACGAC	33128
hPKU3_P14R14	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCACCTCGGCCCTTCTCAGTTCGCTACGAC	33129
hPKU3_P14R15	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTACCTCGGCCCTTCTCAGTTCGCTACGAC	33130
hPKU3_P14R16	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCATACCTCGGCCCTTCTCAGTTCGCTACGAC	33131
hPKU3_P14R17	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAATACCTCGGCCCTTCTCAGTTCGCTACGAC	33132
hPKU3_P14R18	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCAATACCTCGGCCCTTCTCAGTTCGCTACGAC	33133
hPKU3_P14R19	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCACAATACCTCGGCCCTTCTCAGTTCGCTACGAC	33134
hPKU3_P14R20	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGAC	33135

hPKU3_P14R21	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCCACAATACCTCGGCCCTTCTCAGTTCGCTACGAC	33136
hPKU3_P14R22	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGAC	33137
hPKU3_P14R23	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGAC	33138
hPKU3_P14R24	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGAC	33139
hPKU3_P14R25	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGAC	33140
hPKU3_P14R26	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGAC	33141
hPKU3_P14R27	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGAC	33142
hPKU3_P14R28	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGAC	33143
hPKU3_P14R29	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGAC	33144
hPKU3_P14R30	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGAC	33145
hPKU3_P14R31	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGAC	33146
hPKU3_P14R32	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGAC	33147
hPKU3_P14R33	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGAC	33148
hPKU3_P14R34	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGAC	33149
hPKU3_P14R35	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGAC	33150
hPKU3_P14R36	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGAC	33151
hPKU3_P14R37	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGAC	33152

hPKU3_P14R38	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGAC	33153
hPKU3_P14R39	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGAC	33154
hPKU3_P14R40	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGAC	33155
hPKU3_P14R41	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGAC	33156
hPKU3_P14R42	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGAC	33157
hPKU3_P14R43	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGAC	33158
hPKU3_P14R44	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGAC	33159
hPKU3_P14R45	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGAC	33160
hPKU3_P14R46	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGAC	33161
hPKU3_P14R47	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGAC	33162
hPKU3_P14R48	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGAC	33163
hPKU3_P14R49	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGAC	33164
hPKU3_P14R50	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGAC	33165
hPKU3_P14R51	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGAC	33166
hPKU3_P14R52	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGAC	33167
hPKU3_P14R53	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGAC	33168
hPKU3_P14R54	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGAC	33169

hPKU3_P14R55	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGAC	33170
hPKU3_P14R56	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGAC	33171
hPKU3_P14R57	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGAC	33172
hPKU3_P14R58	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCACTCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGAC	33173
hPKU3_P14R59	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCACTCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGAC	33174
hPKU3_P14R60	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTCACTCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGAC	33175
hPKU3_P15R10	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCGGCCCTTCTCAGTTCGCTACGACC	33176
hPKU3_P15R11	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTCGGCCCTTCTCAGTTCGCTACGACC	33177
hPKU3_P15R12	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTCGGCCCTTCTCAGTTCGCTACGACC	33178
hPKU3_P15R13	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCCTCGGCCCTTCTCAGTTCGCTACGACC	33179
hPKU3_P15R14	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCACCTCGGCCCTTCTCAGTTCGCTACGACC	33180
hPKU3_P15R15	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTACCTCGGCCCTTCTCAGTTCGCTACGACC	33181
hPKU3_P15R16	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCATACCTCGGCCCTTCTCAGTTCGCTACGACC	33182
hPKU3_P15R17	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAATACCTCGGCCCTTCTCAGTTCGCTACGACC	33183
hPKU3_P15R18	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCAATACCTCGGCCCTTCTCAGTTCGCTACGACC	33184
hPKU3_P15R19	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCACAATACCTCGGCCCTTCTCAGTTCGCTACGACC	33185

hPKU3_P15R20	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACC	33186
hPKU3_P15R21	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACC	33187
hPKU3_P15R22	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACC	33188
hPKU3_P15R23	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACC	33189
hPKU3_P15R24	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACC	33190
hPKU3_P15R25	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACC	33191
hPKU3_P15R26	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACC	33192
hPKU3_P15R27	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACC	33193
hPKU3_P15R28	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACC	33194
hPKU3_P15R29	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACC	33195
hPKU3_P15R30	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACC	33196
hPKU3_P15R31	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACC	33197
hPKU3_P15R32	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACC	33198
hPKU3_P15R33	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACC	33199
hPKU3_P15R34	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACC	33200
hPKU3_P15R35	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACC	33201
hPKU3_P15R36	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACC	33202

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hPKU3_P15R38	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACC	33204
hPKU3_P15R39	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACC	33205
hPKU3_P15R40	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACC	33206
hPKU3_P15R41	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACC	33207
hPKU3_P15R42	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACC	33208
hPKU3_P15R43	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACC	33209
hPKU3_P15R44	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACC	33210
hPKU3_P15R45	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACC	33211
hPKU3_P15R46	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACC	33212
hPKU3_P15R47	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACC	33213
hPKU3_P15R48	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACC	33214
hPKU3_P15R49	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACC	33215
hPKU3_P15R50	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACC	33216
hPKU3_P15R51	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACC	33217
hPKU3_P15R52	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACC	33218
hPKU3_P15R53	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACC	33219

hPKU3_P15R54	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACC	33220
hPKU3_P15R55	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACC	33221
hPKU3_P15R56	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACC	33222
hPKU3_P15R57	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACC	33223
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hPKU3_P15R59	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCACTCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACC	33225
hPKU3_P15R60	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTCACTCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACC	33226
hPKU3_P16R10	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCGGCCCTTCTCAGTTCGCTACGACCC	33227
hPKU3_P16R11	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTCGGCCCTTCTCAGTTCGCTACGACCC	33228
hPKU3_P16R12	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTCGGCCCTTCTCAGTTCGCTACGACCC	33229
hPKU3_P16R13	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCCTCGGCCCTTCTCAGTTCGCTACGACCC	33230
hPKU3_P16R14	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCACCTCGGCCCTTCTCAGTTCGCTACGACCC	33231
hPKU3_P16R15	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTACCTCGGCCCTTCTCAGTTCGCTACGACCC	33232
hPKU3_P16R16	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCATACCTCGGCCCTTCTCAGTTCGCTACGACCC	33233
hPKU3_P16R17	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAATACCTCGGCCCTTCTCAGTTCGCTACGACCC	33234

hPKU3_P16R18	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCAATACCTCGGCCCTTCTCAGTTCGCTACGACCC	33235
hPKU3_P16R19	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCC	33236
hPKU3_P16R20	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCC	33237
hPKU3_P16R21	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCC	33238
hPKU3_P16R22	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCC	33239
hPKU3_P16R23	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCC	33240
hPKU3_P16R24	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCC	33241
hPKU3_P16R25	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCC	33242
hPKU3_P16R26	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCC	33243
hPKU3_P16R27	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCC	33244
hPKU3_P16R28	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCC	33245
hPKU3_P16R29	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCC	33246
hPKU3_P16R30	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCC	33247
hPKU3_P16R31	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCC	33248
hPKU3_P16R32	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCC	33249
hPKU3_P16R33	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCC	33250
hPKU3_P16R34	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCC	33251

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hPKU3_P16R36	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCC	33253
hPKU3_P16R37	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCC	33254
hPKU3_P16R38	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCC	33255
hPKU3_P16R39	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCC	33256
hPKU3_P16R40	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCC	33257
hPKU3_P16R41	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCC	33258
hPKU3_P16R42	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCC	33259
hPKU3_P16R43	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCC	33260
hPKU3_P16R44	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCC	33261
hPKU3_P16R45	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCC	33262
hPKU3_P16R46	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCC	33263
hPKU3_P16R47	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCC	33264
hPKU3_P16R48	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCC	33265
hPKU3_P16R49	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCC	33266
hPKU3_P16R50	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCC	33267
hPKU3_P16R51	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCC	33268

hPKU3_P16R52	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCC	33269
hPKU3_P16R53	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCC	33270
hPKU3_P16R54	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCC	33271
hPKU3_P16R55	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCC	33272
hPKU3_P16R56	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCC	33273
hPKU3_P16R57	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCC	33274
hPKU3_P16R58	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCACTCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCC	33275
hPKU3_P16R59	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCACTCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCC	33276
hPKU3_P16R60	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTCACTCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCC	33277
hPKU3_P17R10	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCGGCCCTTCTCAGTTCGCTACGACCCA	33278
hPKU3_P17R11	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTCGGCCCTTCTCAGTTCGCTACGACCCA	33279
hPKU3_P17R12	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTCGGCCCTTCTCAGTTCGCTACGACCCA	33280
hPKU3_P17R13	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCCTCGGCCCTTCTCAGTTCGCTACGACCCA	33281
hPKU3_P17R14	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCACCTCGGCCCTTCTCAGTTCGCTACGACCCA	33282
hPKU3_P17R15	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTACCTCGGCCCTTCTCAGTTCGCTACGACCCA	33283

hPKU3_P17R16	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCATACCTCGGCCCTTCTCAGTTCGCTACGACCCA	33284
hPKU3_P17R17	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAATACCTCGGCCCTTCTCAGTTCGCTACGACCCA	33285
hPKU3_P17R18	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCAATACCTCGGCCCTTCTCAGTTCGCTACGACCCA	33286
hPKU3_P17R19	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCA	33287
hPKU3_P17R20	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCA	33288
hPKU3_P17R21	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCA	33289
hPKU3_P17R22	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCA	33290
hPKU3_P17R23	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCA	33291
hPKU3_P17R24	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCA	33292
hPKU3_P17R25	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCA	33293
hPKU3_P17R26	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCA	33294
hPKU3_P17R27	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCA	33295
hPKU3_P17R28	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCA	33296
hPKU3_P17R29	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCA	33297
hPKU3_P17R30	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCA	33298
hPKU3_P17R31	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCA	33299
hPKU3_P17R32	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCA	33300

hPKU3_P17R33	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCA	33301
hPKU3_P17R34	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCA	33302
hPKU3_P17R35	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCA	33303
hPKU3_P17R36	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCA	33304
hPKU3_P17R37	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCA	33305
hPKU3_P17R38	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCA	33306
hPKU3_P17R39	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCA	33307
hPKU3_P17R40	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCA	33308
hPKU3_P17R41	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCA	33309
hPKU3_P17R42	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCA	33310
hPKU3_P17R43	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCA	33311
hPKU3_P17R44	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCA	33312
hPKU3_P17R45	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCA	33313
hPKU3_P17R46	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCA	33314
hPKU3_P17R47	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCA	33315
hPKU3_P17R48	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCA	33316
hPKU3_P17R49	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCA	33317

hPKU3_P17R50	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCA	33318
hPKU3_P17R51	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCA	33319
hPKU3_P17R52	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCA	33320
hPKU3_P17R53	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCA	33321
hPKU3_P17R54	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCA	33322
hPKU3_P17R55	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCA	33323
hPKU3_P17R56	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCA	33324
hPKU3_P17R57	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCA	33325
hPKU3_P17R58	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCACTCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCA	33326
hPKU3_P17R59	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCACTCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCCA	33327
hPKU3_P17R60	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTCACTCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCCA	33328
hPKU3_P1R10	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCGGCCCTTCTC	33329
hPKU3_P1R11	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTCGGCCCTTCTC	33330
hPKU3_P1R12	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTCGGCCCTTCTC	33331

hPKU3_P1R13	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGCCCTCGGCCCTTCTC	33332
hPKU3_P1R14	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGCACCTCGGCCCTTCTC	33333
hPKU3_P1R15	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGCTACCTCGGCCCTTCTC	33334
hPKU3_P1R16	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGCATACCTCGGCCCTTCTC	33335
hPKU3_P1R17	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGCAATACCTCGGCCCTTCTC	33336
hPKU3_P1R18	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGCCAATACCTCGGCCCTTCTC	33337
hPKU3_P1R19	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGCACAATACCTCGGCCCTTCTC	33338
hPKU3_P1R20	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGCCACAATACCTCGGCCCTTCTC	33339
hPKU3_P1R21	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGCCCACAATACCTCGGCCCTTCTC	33340
hPKU3_P1R22	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGCGCCACAATACCTCGGCCCTTCTC	33341
hPKU3_P1R23	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGCTGCCACAATACCTCGGCCCTTCTC	33342
hPKU3_P1R24	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGCCTGCCACAATACCTCGGCCCTTCTC	33343
hPKU3_P1R25	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGCGCTGCCACAATACCTCGGCCCTTCTC	33344
hPKU3_P1R26	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGCTGCTGCCACAATACCTCGGCCCTTCTC	33345
hPKU3_P1R27	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGCTTGCTGCCACAATACCTCGGCCCTTCTC	33346
hPKU3_P1R28	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGCTTTGCTGCCACAATACCTCGGCCCTTCTC	33347
hPKU3_P1R29	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGCCTTTGCTGCCACAATACCTCGGCCCTTCTC	33348

hPKU3_P1R30	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGCACTTTGCTGCCACAATACCTCGGCCCTTCTC	33349
hPKU3_P1R31	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGCAACTTTGCTGCCACAATACCTCGGCCCTTCTC	33350
hPKU3_P1R32	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGCGAACTTTGCTGCCACAATACCTCGGCCCTTCTC	33351
hPKU3_P1R33	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGCGGAACTTTGCTGCCACAATACCTCGGCCCTTCTC	33352
hPKU3_P1R34	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGCAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTC	33353
hPKU3_P1R35	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGCTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTC	33354
hPKU3_P1R36	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTC	33355
hPKU3_P1R37	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGCCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTC	33356
hPKU3_P1R38	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGCTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTC	33357
hPKU3_P1R39	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGCGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTC	33358
hPKU3_P1R40	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGCGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTC	33359
hPKU3_P1R41	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGCTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTC	33360
hPKU3_P1R42	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGCTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTC	33361
hPKU3_P1R43	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGCTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTC	33362
hPKU3_P1R44	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGCTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTC	33363
hPKU3_P1R45	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGCGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTC	33364
hPKU3_P1R46	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGCGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTC	33365

hPKU3_P1R47	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGCTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTC	33366
hPKU3_P1R48	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGCGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTC	33367
hPKU3_P1R49	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTC	33368
hPKU3_P1R50	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTC	33369
hPKU3_P1R51	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGCCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTC	33370
hPKU3_P1R52	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGCGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTC	33371
hPKU3_P1R53	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGCAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTC	33372
hPKU3_P1R54	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTC	33373
hPKU3_P1R55	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGCCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTC	33374
hPKU3_P1R56	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGCTCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTC	33375
hPKU3_P1R57	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGCCTCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTC	33376
hPKU3_P1R58	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGCACTCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTC	33377
hPKU3_P1R59	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGCCACTCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTC	33378
hPKU3_P1R60	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGCTCACTCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTC	33379
hPKU3_P2R10	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGCCGGCCCTTCTCA	33380
hPKU3_P2R11	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGCTCGGCCCTTCTCA	33381
hPKU3_P2R12	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGCCTCGGCCCTTCTCA	33382

hPKU3_P2R13	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGCCCTCGGCCCTTCTCA	33383
hPKU3_P2R14	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGCACCTCGGCCCTTCTCA	33384
hPKU3_P2R15	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGCTACCTCGGCCCTTCTCA	33385
hPKU3_P2R16	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGCATACCTCGGCCCTTCTCA	33386
hPKU3_P2R17	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGCAATACCTCGGCCCTTCTCA	33387
hPKU3_P2R18	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGCCAATACCTCGGCCCTTCTCA	33388
hPKU3_P2R19	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGCACAATACCTCGGCCCTTCTCA	33389
hPKU3_P2R20	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGCCACAATACCTCGGCCCTTCTCA	33390
hPKU3_P2R21	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGCCCACAATACCTCGGCCCTTCTCA	33391
hPKU3_P2R22	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGCGCCACAATACCTCGGCCCTTCTCA	33392
hPKU3_P2R23	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGCTGCCACAATACCTCGGCCCTTCTCA	33393
hPKU3_P2R24	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGCCTGCCACAATACCTCGGCCCTTCTCA	33394
hPKU3_P2R25	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGCGCTGCCACAATACCTCGGCCCTTCTCA	33395
hPKU3_P2R26	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGCTGCTGCCACAATACCTCGGCCCTTCTCA	33396
hPKU3_P2R27	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGCTTGCTGCCACAATACCTCGGCCCTTCTCA	33397
hPKU3_P2R28	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGCTTTGCTGCCACAATACCTCGGCCCTTCTCA	33398
hPKU3_P2R29	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGCCTTTGCTGCCACAATACCTCGGCCCTTCTCA	33399

hPKU3_P2R30	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGCACTTTGCTGCCACAATACCTCGGCCCTTCTCA	33400
hPKU3_P2R31	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGCAACTTTGCTGCCACAATACCTCGGCCCTTCTCA	33401
hPKU3_P2R32	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGCGAACTTTGCTGCCACAATACCTCGGCCCTTCTCA	33402
hPKU3_P2R33	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGCGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCA	33403
hPKU3_P2R34	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGCAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCA	33404
hPKU3_P2R35	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGCTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCA	33405
hPKU3_P2R36	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCA	33406
hPKU3_P2R37	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGCCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCA	33407
hPKU3_P2R38	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGCTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCA	33408
hPKU3_P2R39	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGCGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCA	33409
hPKU3_P2R40	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGCGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCA	33410
hPKU3_P2R41	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGCTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCA	33411
hPKU3_P2R42	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGCTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCA	33412
hPKU3_P2R43	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGCTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCA	33413
hPKU3_P2R44	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGCTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCA	33414
hPKU3_P2R45	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGCGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCA	33415
hPKU3_P2R46	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGCGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCA	33416

hPKU3_P2R47	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGCTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCA	33417
hPKU3_P2R48	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGCGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCA	33418
hPKU3_P2R49	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCA	33419
hPKU3_P2R50	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCA	33420
hPKU3_P2R51	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGCCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCA	33421
hPKU3_P2R52	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGCGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCA	33422
hPKU3_P2R53	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGCAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCA	33423
hPKU3_P2R54	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCA	33424
hPKU3_P2R55	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGCCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCA	33425
hPKU3_P2R56	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGCTCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCA	33426
hPKU3_P2R57	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGCCTCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCA	33427
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hPKU3_P2R59	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGCCACTCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCA	33429
hPKU3_P2R60	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGCTCACTCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCA	33430
hPKU3_P3R10	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGCCGGCCCTTCTCAG	33431
hPKU3_P3R11	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGCTCGGCCCTTCTCAG	33432
hPKU3_P3R12	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGCCTCGGCCCTTCTCAG	33433

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hPKU3_P3R14	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGCACCTCGGCCCTTCTCAG	33435
hPKU3_P3R15	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGCTACCTCGGCCCTTCTCAG	33436
hPKU3_P3R16	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGCATACCTCGGCCCTTCTCAG	33437
hPKU3_P3R17	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGCAATACCTCGGCCCTTCTCAG	33438
hPKU3_P3R18	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGCCAATACCTCGGCCCTTCTCAG	33439
hPKU3_P3R19	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGCACAATACCTCGGCCCTTCTCAG	33440
hPKU3_P3R20	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGCCACAATACCTCGGCCCTTCTCAG	33441
hPKU3_P3R21	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGCCCACAATACCTCGGCCCTTCTCAG	33442
hPKU3_P3R22	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGCGCCACAATACCTCGGCCCTTCTCAG	33443
hPKU3_P3R23	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGCTGCCACAATACCTCGGCCCTTCTCAG	33444
hPKU3_P3R24	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGCCTGCCACAATACCTCGGCCCTTCTCAG	33445
hPKU3_P3R25	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGCGCTGCCACAATACCTCGGCCCTTCTCAG	33446
hPKU3_P3R26	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGCTGCTGCCACAATACCTCGGCCCTTCTCAG	33447
hPKU3_P3R27	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGCTTGCTGCCACAATACCTCGGCCCTTCTCAG	33448
hPKU3_P3R28	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGCTTTGCTGCCACAATACCTCGGCCCTTCTCAG	33449
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hPKU3_P3R31	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGCAACTTTGCTGCCACAATACCTCGGCCCTTCTCAG	33452
hPKU3_P3R32	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGCGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAG	33453
hPKU3_P3R33	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGCGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAG	33454
hPKU3_P3R34	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGCAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAG	33455
hPKU3_P3R35	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGCTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAG	33456
hPKU3_P3R36	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAG	33457
hPKU3_P3R37	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGCCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAG	33458
hPKU3_P3R38	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGCTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAG	33459
hPKU3_P3R39	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGCGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAG	33460
hPKU3_P3R40	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGCGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAG	33461
hPKU3_P3R41	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGCTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAG	33462
hPKU3_P3R42	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGCTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAG	33463
hPKU3_P3R43	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGCTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAG	33464
hPKU3_P3R44	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGCTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAG	33465
hPKU3_P3R45	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGCGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAG	33466
hPKU3_P3R46	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGCGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAG	33467

hPKU3_P3R47	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGCTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAG	33468
hPKU3_P3R48	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGCGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAG	33469
hPKU3_P3R49	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAG	33470
hPKU3_P3R50	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAG	33471
hPKU3_P3R51	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGCCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAG	33472
hPKU3_P3R52	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGCGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAG	33473
hPKU3_P3R53	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGCAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAG	33474
hPKU3_P3R54	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAG	33475
hPKU3_P3R55	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGCCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAG	33476
hPKU3_P3R56	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGCTCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAG	33477
hPKU3_P3R57	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGCCTCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAG	33478
hPKU3_P3R58	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGCACTCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAG	33479
hPKU3_P3R59	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGCCACTCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAG	33480
hPKU3_P3R60	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGCTCACTCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAG	33481
hPKU3_P4R10	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGCCGGCCCTTCTCAGT	33482
hPKU3_P4R11	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGCTCGGCCCTTCTCAGT	33483
hPKU3_P4R12	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGCCTCGGCCCTTCTCAGT	33484

hPKU3_P4R13	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGCCCTCGGCCCTTCTCAGT	33485
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hPKU3_P4R15	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGCTACCTCGGCCCTTCTCAGT	33487
hPKU3_P4R16	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGCATACCTCGGCCCTTCTCAGT	33488
hPKU3_P4R17	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGCAATACCTCGGCCCTTCTCAGT	33489
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hPKU3_P4R21	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGCCCACAATACCTCGGCCCTTCTCAGT	33493
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hPKU3_P4R24	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGCCTGCCACAATACCTCGGCCCTTCTCAGT	33496
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hPKU3_P4R32	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGCGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGT	33504
hPKU3_P4R33	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGCGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGT	33505
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hPKU3_P4R39	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGCGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGT	33511
hPKU3_P4R40	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGCGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGT	33512
hPKU3_P4R41	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGCTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGT	33513
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hPKU3_P4R43	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGCTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGT	33515
hPKU3_P4R44	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGCTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGT	33516
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hPKU3_P5R25	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGCGCTGCCACAATACCTCGGCCCTTCTCAGTT	33548
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hPKU3_P5R32	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGCGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTT	33555
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hPKU3_P5R36	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTT	33559
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hPKU3_P5R41	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGCTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTT	33564
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hPKU3_P5R43	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGCTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTT	33566
hPKU3_P5R44	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGCTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTT	33567
hPKU3_P5R45	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGCGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTT	33568
hPKU3_P5R46	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGCGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTT	33569

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hPKU3_P5R49	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTT	33572
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hPKU3_P5R52	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGCGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTT	33575
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hPKU3_P6R10	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGCCGGCCCTTCTCAGTTC	33584
hPKU3_P6R11	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGCTCGGCCCTTCTCAGTTC	33585
hPKU3_P6R12	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGCCTCGGCCCTTCTCAGTTC	33586

hPKU3_P6R13	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGCCCTCGGCCCTTCTCAGTTC	33587
hPKU3_P6R14	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGCACCTCGGCCCTTCTCAGTTC	33588
hPKU3_P6R15	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGCTACCTCGGCCCTTCTCAGTTC	33589
hPKU3_P6R16	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGCATACCTCGGCCCTTCTCAGTTC	33590
hPKU3_P6R17	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGCAATACCTCGGCCCTTCTCAGTTC	33591
hPKU3_P6R18	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGCCAATACCTCGGCCCTTCTCAGTTC	33592
hPKU3_P6R19	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGCACAATACCTCGGCCCTTCTCAGTTC	33593
hPKU3_P6R20	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGCCACAATACCTCGGCCCTTCTCAGTTC	33594
hPKU3_P6R21	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGCCCACAATACCTCGGCCCTTCTCAGTTC	33595
hPKU3_P6R22	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGCGCCACAATACCTCGGCCCTTCTCAGTTC	33596
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hPKU3_P6R24	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGCCTGCCACAATACCTCGGCCCTTCTCAGTTC	33598
hPKU3_P6R25	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGCGCTGCCACAATACCTCGGCCCTTCTCAGTTC	33599
hPKU3_P6R26	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGCTGCTGCCACAATACCTCGGCCCTTCTCAGTTC	33600
hPKU3_P6R27	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGCTTGCTGCCACAATACCTCGGCCCTTCTCAGTTC	33601
hPKU3_P6R28	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGCTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTC	33602
hPKU3_P6R29	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGCCTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTC	33603

hPKU3_P6R30	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGCACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTC	33604
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hPKU3_P6R32	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGCGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTC	33606
hPKU3_P6R33	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGCGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTC	33607
hPKU3_P6R34	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGCAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTC	33608
hPKU3_P6R35	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGCTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTC	33609
hPKU3_P6R36	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTC	33610
hPKU3_P6R37	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGCCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTC	33611
hPKU3_P6R38	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGCTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTC	33612
hPKU3_P6R39	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGCGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTC	33613
hPKU3_P6R40	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGCGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTC	33614
hPKU3_P6R41	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGCTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTC	33615
hPKU3_P6R42	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGCTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTC	33616
hPKU3_P6R43	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGCTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTC	33617
hPKU3_P6R44	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGCTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTC	33618
hPKU3_P6R45	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGCGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTC	33619
hPKU3_P6R46	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGCGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTC	33620

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hPKU3_P6R48	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGCGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTC	33622
hPKU3_P6R49	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTC	33623
hPKU3_P6R50	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTC	33624
hPKU3_P6R51	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGCCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTC	33625
hPKU3_P6R52	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGCGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTC	33626
hPKU3_P6R53	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGCAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTC	33627
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hPKU3_P7R12	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGCCTCGGCCCTTCTCAGTTCG	33637

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hPKU3_P7R15	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTACCTCGGCCCTTCTCAGTTCG	33640
hPKU3_P7R16	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCATACCTCGGCCCTTCTCAGTTCG	33641
hPKU3_P7R17	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAATACCTCGGCCCTTCTCAGTTCG	33642
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hPKU3_P7R21	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCCACAATACCTCGGCCCTTCTCAGTTCG	33646
hPKU3_P7R22	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGCCACAATACCTCGGCCCTTCTCAGTTCG	33647
hPKU3_P7R23	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGCCACAATACCTCGGCCCTTCTCAGTTCG	33648
hPKU3_P7R24	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTGCCACAATACCTCGGCCCTTCTCAGTTCG	33649
hPKU3_P7R25	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGCTGCCACAATACCTCGGCCCTTCTCAGTTCG	33650
hPKU3_P7R26	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGCTGCCACAATACCTCGGCCCTTCTCAGTTCG	33651
hPKU3_P7R27	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCG	33652
hPKU3_P7R28	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCG	33653
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hPKU3_P7R31	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCG	33656
hPKU3_P7R32	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCG	33657
hPKU3_P7R33	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCG	33658
hPKU3_P7R34	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCG	33659
hPKU3_P7R35	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCG	33660
hPKU3_P7R36	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCG	33661
hPKU3_P7R37	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCG	33662
hPKU3_P7R38	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCG	33663
hPKU3_P7R39	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCG	33664
hPKU3_P7R40	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCG	33665
hPKU3_P7R41	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCG	33666
hPKU3_P7R42	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCG	33667
hPKU3_P7R43	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCG	33668
hPKU3_P7R44	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCG	33669
hPKU3_P7R45	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCG	33670
hPKU3_P7R46	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCG	33671

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hPKU3_P7R48	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGCGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCG	33673
hPKU3_P7R49	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCG	33674
hPKU3_P7R50	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCG	33675
hPKU3_P7R51	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGCCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCG	33676
hPKU3_P7R52	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGCGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCG	33677
hPKU3_P7R53	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGCAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCG	33678
hPKU3_P7R54	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCG	33679
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hPKU3_P8R11	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGCTCGGCCCTTCTCAGTTCGC	33687
hPKU3_P8R12	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGCCTCGGCCCTTCTCAGTTCGC	33688

hPKU3_P8R13	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGCCCTCGGCCCTTCTCAGTTCGC	33689
hPKU3_P8R14	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGCACCTCGGCCCTTCTCAGTTCGC	33690
hPKU3_P8R15	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGCTACCTCGGCCCTTCTCAGTTCGC	33691
hPKU3_P8R16	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGCATACCTCGGCCCTTCTCAGTTCGC	33692
hPKU3_P8R17	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGCAATACCTCGGCCCTTCTCAGTTCGC	33693
hPKU3_P8R18	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGCCAATACCTCGGCCCTTCTCAGTTCGC	33694
hPKU3_P8R19	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGCACAATACCTCGGCCCTTCTCAGTTCGC	33695
hPKU3_P8R20	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGCCACAATACCTCGGCCCTTCTCAGTTCGC	33696
hPKU3_P8R21	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGCCCACAATACCTCGGCCCTTCTCAGTTCGC	33697
hPKU3_P8R22	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGCGCCACAATACCTCGGCCCTTCTCAGTTCGC	33698
hPKU3_P8R23	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGC	33699
hPKU3_P8R24	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGCCTGCCACAATACCTCGGCCCTTCTCAGTTCGC	33700
hPKU3_P8R25	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGCGCTGCCACAATACCTCGGCCCTTCTCAGTTCGC	33701
hPKU3_P8R26	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGCTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGC	33702
hPKU3_P8R27	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGCTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGC	33703
hPKU3_P8R28	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGCTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGC	33704
hPKU3_P8R29	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGCCTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGC	33705

hPKU3_P8R30	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGCACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGC	33706
hPKU3_P8R31	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGCAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGC	33707
hPKU3_P8R32	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGCGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGC	33708
hPKU3_P8R33	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGCGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGC	33709
hPKU3_P8R34	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGCAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGC	33710
hPKU3_P8R35	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGCTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGC	33711
hPKU3_P8R36	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGC	33712
hPKU3_P8R37	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGCCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGC	33713
hPKU3_P8R38	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGCTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGC	33714
hPKU3_P8R39	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGCGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGC	33715
hPKU3_P8R40	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGCGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGC	33716
hPKU3_P8R41	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGCTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGC	33717
hPKU3_P8R42	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGCTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGC	33718
hPKU3_P8R43	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGCTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGC	33719
hPKU3_P8R44	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGCTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGC	33720
hPKU3_P8R45	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGCGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGC	33721
hPKU3_P8R46	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGCGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGC	33722

hPKU3_P8R47	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGCTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGC	33723
hPKU3_P8R48	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGCGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGC	33724
hPKU3_P8R49	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGC	33725
hPKU3_P8R50	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGC	33726
hPKU3_P8R51	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGCCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGC	33727
hPKU3_P8R52	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGCGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGC	33728
hPKU3_P8R53	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGCAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGC	33729
hPKU3_P8R54	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGC	33730
hPKU3_P8R55	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGCCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGC	33731
hPKU3_P8R56	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGCTCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGC	33732
hPKU3_P8R57	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGCCTCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGC	33733
hPKU3_P8R58	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGCACTCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGC	33734
hPKU3_P8R59	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGCCACTCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGC	33735
hPKU3_P8R60	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGCTCACTCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGC	33736
hPKU3_P9R10	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGCCGGCCCTTCTCAGTTCGCT	33737
hPKU3_P9R11	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGCTCGGCCCTTCTCAGTTCGCT	33738
hPKU3_P9R12	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGCCTCGGCCCTTCTCAGTTCGCT	33739

hPKU3_P9R13	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCCTCGGCCCTTCTCAGTTCGCT	33740
hPKU3_P9R14	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCACCTCGGCCCTTCTCAGTTCGCT	33741
hPKU3_P9R15	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTACCTCGGCCCTTCTCAGTTCGCT	33742
hPKU3_P9R16	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCATACCTCGGCCCTTCTCAGTTCGCT	33743
hPKU3_P9R17	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAATACCTCGGCCCTTCTCAGTTCGCT	33744
hPKU3_P9R18	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCAATACCTCGGCCCTTCTCAGTTCGCT	33745
hPKU3_P9R19	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCACAATACCTCGGCCCTTCTCAGTTCGCT	33746
hPKU3_P9R20	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCACAATACCTCGGCCCTTCTCAGTTCGCT	33747
hPKU3_P9R21	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCCACAATACCTCGGCCCTTCTCAGTTCGCT	33748
hPKU3_P9R22	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGCCACAATACCTCGGCCCTTCTCAGTTCGCT	33749
hPKU3_P9R23	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCT	33750
hPKU3_P9R24	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTGCCACAATACCTCGGCCCTTCTCAGTTCGCT	33751
hPKU3_P9R25	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCT	33752
hPKU3_P9R26	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCT	33753
hPKU3_P9R27	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCT	33754
hPKU3_P9R28	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCT	33755
hPKU3_P9R29	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCT	33756

hPKU3_P9R30	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGCACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCT	33757
hPKU3_P9R31	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGCAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCT	33758
hPKU3_P9R32	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGCGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCT	33759
hPKU3_P9R33	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGCGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCT	33760
hPKU3_P9R34	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGCAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCT	33761
hPKU3_P9R35	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGCTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCT	33762
hPKU3_P9R36	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCT	33763
hPKU3_P9R37	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGCCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCT	33764
hPKU3_P9R38	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGCTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCT	33765
hPKU3_P9R39	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGCGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCT	33766
hPKU3_P9R40	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGCGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCT	33767
hPKU3_P9R41	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGCTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCT	33768
hPKU3_P9R42	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGCTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCT	33769
hPKU3_P9R43	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGCTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCT	33770
hPKU3_P9R44	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGCTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCT	33771
hPKU3_P9R45	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGCGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCT	33772
hPKU3_P9R46	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGCGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCT	33773

hPKU3_P9R47	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGCTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCT	33774
hPKU3_P9R48	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGCGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCT	33775
hPKU3_P9R49	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCT	33776
hPKU3_P9R50	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCT	33777
hPKU3_P9R51	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGCCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCT	33778
hPKU3_P9R52	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGCGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCT	33779
hPKU3_P9R53	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGCAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCT	33780
hPKU3_P9R54	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCT	33781
hPKU3_P9R55	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGCCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCT	33782
hPKU3_P9R56	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGCTCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCT	33783
hPKU3_P9R57	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGCCTCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCT	33784
hPKU3_P9R58	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGCACTCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCT	33785
hPKU3_P9R59	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGCCACTCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCT	33786
hPKU3_P9R60	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGC ACCGAGTCGGTGCTCACTCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCT	33787

Table 5D. Exemplary template RNA sequences

Table 5D provides design of exemplary DNA components of gene modifying systems for correcting the pathogenic R408W mutation in PAH to the wild-type form. This table details the sequence of a complete template RNA for use in exemplary gene modifying systems comprising a gene modifying polypeptide. Templates in this table employ the hPKU4 spacer GGGTCGTAGCGAACTGAGAA (SEQ ID NO:16084).

Name	tgRNA sequence	SEQ ID NO
hPKU4_P0R10	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTCGGCCCTTC	33788
hPKU4_P0R11	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTCGGCCCTTC	33789
hPKU4_P0R12	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCCTCGGCCCTTC	33790
hPKU4_P0R13	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCACCTCGGCCCTTC	33791
hPKU4_P0R14	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTACCTCGGCCCTTC	33792
hPKU4_P0R15	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCATACCTCGGCCCTTC	33793
hPKU4_P0R16	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAATACCTCGGCCCTTC	33794
hPKU4_P0R17	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCAATACCTCGGCCCTTC	33795
hPKU4_P0R18	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCACAATACCTCGGCCCTTC	33796
hPKU4_P0R19	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCACAATACCTCGGCCCTTC	33797
hPKU4_P0R20	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCCACAATACCTCGGCCCTTC	33798
hPKU4_P0R21	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGCCACAATACCTCGGCCCTTC	33799

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hPKU4_P0R24	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGCTGCCACAATACCTCGGCCCTTC	33802
hPKU4_P0R25	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGCTGCCACAATACCTCGGCCCTTC	33803
hPKU4_P0R26	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTGCTGCCACAATACCTCGGCCCTTC	33804
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hPKU4_P0R35	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTC	33813
hPKU4_P0R36	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTC	33814
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hPKU4_P0R38	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTC	33816

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hPKU4_P0R44	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTC	33822
hPKU4_P0R45	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTC	33823
hPKU4_P0R46	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTC	33824
hPKU4_P0R47	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTC	33825
hPKU4_P0R48	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTC	33826
hPKU4_P0R49	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTC	33827
hPKU4_P0R50	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTC	33828
hPKU4_P0R51	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTC	33829
hPKU4_P0R52	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTC	33830
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hPKU4_P0R54	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTC	33832
hPKU4_P0R55	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTC	33833

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hPKU4_P10R24	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCT	33853
hPKU4_P10R25	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCT	33854
hPKU4_P10R26	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCT	33855
hPKU4_P10R27	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCT	33856
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hPKU4_P10R33	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCT	33862
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hPKU4_P10R35	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCT	33864
hPKU4_P10R36	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCT	33865
hPKU4_P10R37	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCT	33866
hPKU4_P10R38	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCT	33867

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hPKU4_P10R41	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCT	33870
hPKU4_P10R42	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCT	33871
hPKU4_P10R43	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCT	33872
hPKU4_P10R44	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCT	33873
hPKU4_P10R45	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCT	33874
hPKU4_P10R46	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCT	33875
hPKU4_P10R47	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCT	33876
hPKU4_P10R48	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCT	33877
hPKU4_P10R49	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCT	33878
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hPKU4_P10R51	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCT	33880
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hPKU4_P10R54	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCT	33883
hPKU4_P10R55	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCT	33884

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hPKU4_P10R57	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCACTCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCT	33886
hPKU4_P10R58	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCACTCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCT	33887
hPKU4_P10R59	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTCACTCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCT	33888
hPKU4_P10R9	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCGGCCCTTCTCAGTTCGCT	33889
hPKU4_P11R10	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTCGGCCCTTCTCAGTTCGCTA	33890
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hPKU4_P11R15	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCATACCTCGGCCCTTCTCAGTTCGCTA	33895
hPKU4_P11R16	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAATACCTCGGCCCTTCTCAGTTCGCTA	33896
hPKU4_P11R17	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCAATACCTCGGCCCTTCTCAGTTCGCTA	33897
hPKU4_P11R18	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCACAATACCTCGGCCCTTCTCAGTTCGCTA	33898
hPKU4_P11R19	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCACAATACCTCGGCCCTTCTCAGTTCGCTA	33899

hPKU4_P11R20	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCCACAATACCTCGGCCCTTCTCAGTTCGCTA	33900
hPKU4_P11R21	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGCCACAATACCTCGGCCCTTCTCAGTTCGCTA	33901
hPKU4_P11R22	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTA	33902
hPKU4_P11R23	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTA	33903
hPKU4_P11R24	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTA	33904
hPKU4_P11R25	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTA	33905
hPKU4_P11R26	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTA	33906
hPKU4_P11R27	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTA	33907
hPKU4_P11R28	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTA	33908
hPKU4_P11R29	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTA	33909
hPKU4_P11R30	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTA	33910
hPKU4_P11R31	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTA	33911
hPKU4_P11R32	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTA	33912
hPKU4_P11R33	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTA	33913
hPKU4_P11R34	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTA	33914
hPKU4_P11R35	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTA	33915
hPKU4_P11R36	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTA	33916

hPKU4_P11R37	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTA	33917
hPKU4_P11R38	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTA	33918
hPKU4_P11R39	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTA	33919
hPKU4_P11R40	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTA	33920
hPKU4_P11R41	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTA	33921
hPKU4_P11R42	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTA	33922
hPKU4_P11R43	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTA	33923
hPKU4_P11R44	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTA	33924
hPKU4_P11R45	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTA	33925
hPKU4_P11R46	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTA	33926
hPKU4_P11R47	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTA	33927
hPKU4_P11R48	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTA	33928
hPKU4_P11R49	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTA	33929
hPKU4_P11R50	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTA	33930
hPKU4_P11R51	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTA	33931
hPKU4_P11R52	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTA	33932
hPKU4_P11R53	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTA	33933

hPKU4_P11R54	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTA	33934
hPKU4_P11R55	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTA	33935
hPKU4_P11R56	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTA	33936
hPKU4_P11R57	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCACTCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTA	33937
hPKU4_P11R58	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCACTCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTA	33938
hPKU4_P11R59	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTCACTCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTA	33939
hPKU4_P11R9	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCGGCCCTTCTCAGTTCGCTA	33940
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hPKU4_P12R11	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTCGGCCCTTCTCAGTTCGCTAC	33942
hPKU4_P12R12	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCCTCGGCCCTTCTCAGTTCGCTAC	33943
hPKU4_P12R13	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCACCTCGGCCCTTCTCAGTTCGCTAC	33944
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hPKU4_P12R15	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCATACCTCGGCCCTTCTCAGTTCGCTAC	33946
hPKU4_P12R16	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAATACCTCGGCCCTTCTCAGTTCGCTAC	33947
hPKU4_P12R17	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCAATACCTCGGCCCTTCTCAGTTCGCTAC	33948

hPKU4_P12R18	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCACAATACCTCGGCCCTTCTCAGTTCGCTAC	33949
hPKU4_P12R19	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCACAATACCTCGGCCCTTCTCAGTTCGCTAC	33950
hPKU4_P12R20	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCCACAATACCTCGGCCCTTCTCAGTTCGCTAC	33951
hPKU4_P12R21	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGCCACAATACCTCGGCCCTTCTCAGTTCGCTAC	33952
hPKU4_P12R22	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTAC	33953
hPKU4_P12R23	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTAC	33954
hPKU4_P12R24	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTAC	33955
hPKU4_P12R25	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTAC	33956
hPKU4_P12R26	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTAC	33957
hPKU4_P12R27	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTAC	33958
hPKU4_P12R28	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTAC	33959
hPKU4_P12R29	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTAC	33960
hPKU4_P12R30	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTAC	33961
hPKU4_P12R31	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTAC	33962
hPKU4_P12R32	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTAC	33963
hPKU4_P12R33	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTAC	33964
hPKU4_P12R34	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTAC	33965

hPKU4_P12R35	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTAC	33966
hPKU4_P12R36	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTAC	33967
hPKU4_P12R37	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTAC	33968
hPKU4_P12R38	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTAC	33969
hPKU4_P12R39	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTAC	33970
hPKU4_P12R40	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTAC	33971
hPKU4_P12R41	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTAC	33972
hPKU4_P12R42	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTAC	33973
hPKU4_P12R43	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTAC	33974
hPKU4_P12R44	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTAC	33975
hPKU4_P12R45	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTAC	33976
hPKU4_P12R46	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTAC	33977
hPKU4_P12R47	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTAC	33978
hPKU4_P12R48	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTAC	33979
hPKU4_P12R49	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTAC	33980
hPKU4_P12R50	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTAC	33981
hPKU4_P12R51	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTAC	33982

hPKU4_P12R52	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTAC	33983
hPKU4_P12R53	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTAC	33984
hPKU4_P12R54	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTAC	33985
hPKU4_P12R55	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTAC	33986
hPKU4_P12R56	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTAC	33987
hPKU4_P12R57	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCACTCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTAC	33988
hPKU4_P12R58	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCACTCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTAC	33989
hPKU4_P12R59	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTCACTCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTAC	33990
hPKU4_P12R9	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCGGCCCTTCTCAGTTCGCTAC	33991
hPKU4_P13R10	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTCGGCCCTTCTCAGTTCGCTACG	33992
hPKU4_P13R11	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTCGGCCCTTCTCAGTTCGCTACG	33993
hPKU4_P13R12	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCCTCGGCCCTTCTCAGTTCGCTACG	33994
hPKU4_P13R13	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCACCTCGGCCCTTCTCAGTTCGCTACG	33995
hPKU4_P13R14	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTACCTCGGCCCTTCTCAGTTCGCTACG	33996

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hPKU4_P13R16	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAATACCTCGGCCCTTCTCAGTTCGCTACG	33998
hPKU4_P13R17	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCAATACCTCGGCCCTTCTCAGTTCGCTACG	33999
hPKU4_P13R18	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCACAATACCTCGGCCCTTCTCAGTTCGCTACG	34000
hPKU4_P13R19	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACG	34001
hPKU4_P13R20	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCCACAATACCTCGGCCCTTCTCAGTTCGCTACG	34002
hPKU4_P13R21	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGCCACAATACCTCGGCCCTTCTCAGTTCGCTACG	34003
hPKU4_P13R22	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACG	34004
hPKU4_P13R23	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACG	34005
hPKU4_P13R24	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACG	34006
hPKU4_P13R25	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACG	34007
hPKU4_P13R26	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACG	34008
hPKU4_P13R27	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACG	34009
hPKU4_P13R28	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACG	34010
hPKU4_P13R29	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACG	34011
hPKU4_P13R30	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACG	34012
hPKU4_P13R31	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACG	34013

hPKU4_P13R32	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACG	34014
hPKU4_P13R33	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACG	34015
hPKU4_P13R34	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACG	34016
hPKU4_P13R35	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACG	34017
hPKU4_P13R36	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACG	34018
hPKU4_P13R37	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACG	34019
hPKU4_P13R38	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACG	34020
hPKU4_P13R39	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACG	34021
hPKU4_P13R40	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACG	34022
hPKU4_P13R41	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACG	34023
hPKU4_P13R42	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACG	34024
hPKU4_P13R43	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACG	34025
hPKU4_P13R44	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACG	34026
hPKU4_P13R45	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACG	34027
hPKU4_P13R46	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACG	34028
hPKU4_P13R47	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACG	34029
hPKU4_P13R48	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACG	34030

hPKU4_P13R49	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACG	34031
hPKU4_P13R50	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACG	34032
hPKU4_P13R51	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACG	34033
hPKU4_P13R52	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACG	34034
hPKU4_P13R53	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACG	34035
hPKU4_P13R54	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACG	34036
hPKU4_P13R55	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACG	34037
hPKU4_P13R56	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACG	34038
hPKU4_P13R57	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCACTCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACG	34039
hPKU4_P13R58	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCACTCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACG	34040
hPKU4_P13R59	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTCACTCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACG	34041
hPKU4_P13R9	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCGGCCCTTCTCAGTTCGCTACG	34042
hPKU4_P14R10	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTCGGCCCTTCTCAGTTCGCTACGA	34043
hPKU4_P14R11	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTCGGCCCTTCTCAGTTCGCTACGA	34044

hPKU4_P14R 12	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGT GGCACCGAGTCGGTGCCCTCGGCCCTTCTCAGTTCGCTACGA	34045
hPKU4_P14R 13	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGT GGCACCGAGTCGGTGCACCTCGGCCCTTCTCAGTTCGCTACGA	34046
hPKU4_P14R 14	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGT GGCACCGAGTCGGTGCTACCTCGGCCCTTCTCAGTTCGCTACGA	34047
hPKU4_P14R 15	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGT GGCACCGAGTCGGTGCATACCTCGGCCCTTCTCAGTTCGCTACGA	34048
hPKU4_P14R 16	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGT GGCACCGAGTCGGTGCAATACCTCGGCCCTTCTCAGTTCGCTACGA	34049
hPKU4_P14R 17	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGT GGCACCGAGTCGGTGCCAATACCTCGGCCCTTCTCAGTTCGCTACGA	34050
hPKU4_P14R 18	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGT GGCACCGAGTCGGTGCACAATACCTCGGCCCTTCTCAGTTCGCTACGA	34051
hPKU4_P14R 19	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGT GGCACCGAGTCGGTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGA	34052
hPKU4_P14R 20	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGT GGCACCGAGTCGGTGCCCACAATACCTCGGCCCTTCTCAGTTCGCTACGA	34053
hPKU4_P14R 21	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGT GGCACCGAGTCGGTGCGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGA	34054
hPKU4_P14R 22	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGT GGCACCGAGTCGGTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGA	34055
hPKU4_P14R 23	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGT GGCACCGAGTCGGTGCCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGA	34056
hPKU4_P14R 24	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGT GGCACCGAGTCGGTGCGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGA	34057
hPKU4_P14R 25	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGT GGCACCGAGTCGGTGCTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGA	34058
hPKU4_P14R 26	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGT GGCACCGAGTCGGTGCTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGA	34059
hPKU4_P14R 27	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGT GGCACCGAGTCGGTGCTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGA	34060
hPKU4_P14R 28	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGT GGCACCGAGTCGGTGCCTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGA	34061

hPKU4_P14R29	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGA	34062
hPKU4_P14R30	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGA	34063
hPKU4_P14R31	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGA	34064
hPKU4_P14R32	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGA	34065
hPKU4_P14R33	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGA	34066
hPKU4_P14R34	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGA	34067
hPKU4_P14R35	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGA	34068
hPKU4_P14R36	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGA	34069
hPKU4_P14R37	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGA	34070
hPKU4_P14R38	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGA	34071
hPKU4_P14R39	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGA	34072
hPKU4_P14R40	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGA	34073
hPKU4_P14R41	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGA	34074
hPKU4_P14R42	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGA	34075
hPKU4_P14R43	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGA	34076
hPKU4_P14R44	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGA	34077
hPKU4_P14R45	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGA	34078

hPKU4_P14R46	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGA	34079
hPKU4_P14R47	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGA	34080
hPKU4_P14R48	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGA	34081
hPKU4_P14R49	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGA	34082
hPKU4_P14R50	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGA	34083
hPKU4_P14R51	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGA	34084
hPKU4_P14R52	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGA	34085
hPKU4_P14R53	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGA	34086
hPKU4_P14R54	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGA	34087
hPKU4_P14R55	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGA	34088
hPKU4_P14R56	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGA	34089
hPKU4_P14R57	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCACTCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGA	34090
hPKU4_P14R58	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCACTCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGA	34091

hPKU4_P14R59	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTCACTCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGA	34092
hPKU4_P14R9	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCGGCCCTTCTCAGTTCGCTACGA	34093
hPKU4_P15R10	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTCGGCCCTTCTCAGTTCGCTACGAC	34094
hPKU4_P15R11	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTCGGCCCTTCTCAGTTCGCTACGAC	34095
hPKU4_P15R12	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCCTCGGCCCTTCTCAGTTCGCTACGAC	34096
hPKU4_P15R13	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCACCTCGGCCCTTCTCAGTTCGCTACGAC	34097
hPKU4_P15R14	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTACCTCGGCCCTTCTCAGTTCGCTACGAC	34098
hPKU4_P15R15	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCATACCTCGGCCCTTCTCAGTTCGCTACGAC	34099
hPKU4_P15R16	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAATACCTCGGCCCTTCTCAGTTCGCTACGAC	34100
hPKU4_P15R17	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCAATACCTCGGCCCTTCTCAGTTCGCTACGAC	34101
hPKU4_P15R18	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCACAATACCTCGGCCCTTCTCAGTTCGCTACGAC	34102
hPKU4_P15R19	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGAC	34103
hPKU4_P15R20	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCCACAATACCTCGGCCCTTCTCAGTTCGCTACGAC	34104
hPKU4_P15R21	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGAC	34105
hPKU4_P15R22	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGAC	34106
hPKU4_P15R23	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGAC	34107

hPKU4_P15R24	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGAC	34108
hPKU4_P15R25	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGAC	34109
hPKU4_P15R26	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGAC	34110
hPKU4_P15R27	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGAC	34111
hPKU4_P15R28	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGAC	34112
hPKU4_P15R29	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGAC	34113
hPKU4_P15R30	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGAC	34114
hPKU4_P15R31	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGAC	34115
hPKU4_P15R32	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGAC	34116
hPKU4_P15R33	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGAC	34117
hPKU4_P15R34	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGAC	34118
hPKU4_P15R35	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGAC	34119
hPKU4_P15R36	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGAC	34120
hPKU4_P15R37	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGAC	34121
hPKU4_P15R38	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGAC	34122
hPKU4_P15R39	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGAC	34123
hPKU4_P15R40	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGAC	34124

hPKU4_P15R41	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGAC	34125
hPKU4_P15R42	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGAC	34126
hPKU4_P15R43	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGAC	34127
hPKU4_P15R44	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGAC	34128
hPKU4_P15R45	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGAC	34129
hPKU4_P15R46	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGAC	34130
hPKU4_P15R47	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGAC	34131
hPKU4_P15R48	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGAC	34132
hPKU4_P15R49	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGAC	34133
hPKU4_P15R50	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGAC	34134
hPKU4_P15R51	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGAC	34135
hPKU4_P15R52	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGAC	34136
hPKU4_P15R53	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGAC	34137
hPKU4_P15R54	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGAC	34138
hPKU4_P15R55	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGAC	34139

hPKU4_P15R56	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGAC	34140
hPKU4_P15R57	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCACTCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGAC	34141
hPKU4_P15R58	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCACTCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGAC	34142
hPKU4_P15R59	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTCACTCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGAC	34143
hPKU4_P15R9	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCGGCCCTTCTCAGTTCGCTACGAC	34144
hPKU4_P16R10	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTCGGCCCTTCTCAGTTCGCTACGACC	34145
hPKU4_P16R11	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTCGGCCCTTCTCAGTTCGCTACGACC	34146
hPKU4_P16R12	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCCTCGGCCCTTCTCAGTTCGCTACGACC	34147
hPKU4_P16R13	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCACCTCGGCCCTTCTCAGTTCGCTACGACC	34148
hPKU4_P16R14	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTACCTCGGCCCTTCTCAGTTCGCTACGACC	34149
hPKU4_P16R15	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCATACCTCGGCCCTTCTCAGTTCGCTACGACC	34150
hPKU4_P16R16	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAATACCTCGGCCCTTCTCAGTTCGCTACGACC	34151
hPKU4_P16R17	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCAATACCTCGGCCCTTCTCAGTTCGCTACGACC	34152
hPKU4_P16R18	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCACAATACCTCGGCCCTTCTCAGTTCGCTACGACC	34153
hPKU4_P16R19	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACC	34154

hPKU4_P16R20	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACC	34155
hPKU4_P16R21	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACC	34156
hPKU4_P16R22	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACC	34157
hPKU4_P16R23	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACC	34158
hPKU4_P16R24	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACC	34159
hPKU4_P16R25	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACC	34160
hPKU4_P16R26	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACC	34161
hPKU4_P16R27	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACC	34162
hPKU4_P16R28	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACC	34163
hPKU4_P16R29	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACC	34164
hPKU4_P16R30	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACC	34165
hPKU4_P16R31	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACC	34166
hPKU4_P16R32	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACC	34167
hPKU4_P16R33	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACC	34168
hPKU4_P16R34	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACC	34169
hPKU4_P16R35	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACC	34170
hPKU4_P16R36	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACC	34171

hPKU4_P16R37	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACC	34172
hPKU4_P16R38	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACC	34173
hPKU4_P16R39	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACC	34174
hPKU4_P16R40	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACC	34175
hPKU4_P16R41	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACC	34176
hPKU4_P16R42	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACC	34177
hPKU4_P16R43	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACC	34178
hPKU4_P16R44	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACC	34179
hPKU4_P16R45	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACC	34180
hPKU4_P16R46	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACC	34181
hPKU4_P16R47	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACC	34182
hPKU4_P16R48	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACC	34183
hPKU4_P16R49	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACC	34184
hPKU4_P16R50	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACC	34185
hPKU4_P16R51	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACC	34186
hPKU4_P16R52	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACC	34187

hPKU4_P16R53	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACC	34188
hPKU4_P16R54	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACC	34189
hPKU4_P16R55	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACC	34190
hPKU4_P16R56	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACC	34191
hPKU4_P16R57	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCACTCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACC	34192
hPKU4_P16R58	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCACTCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACC	34193
hPKU4_P16R59	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTCACTCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACC	34194
hPKU4_P16R9	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCGGCCCTTCTCAGTTCGCTACGACC	34195
hPKU4_P17R10	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTCGGCCCTTCTCAGTTCGCTACGACCC	34196
hPKU4_P17R11	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTCGGCCCTTCTCAGTTCGCTACGACCC	34197
hPKU4_P17R12	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCCTCGGCCCTTCTCAGTTCGCTACGACCC	34198
hPKU4_P17R13	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCACCTCGGCCCTTCTCAGTTCGCTACGACCC	34199
hPKU4_P17R14	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTACCTCGGCCCTTCTCAGTTCGCTACGACCC	34200

hPKU4_P17R15	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCATACCTCGGCCCTTCTCAGTTCGCTACGACCC	34201
hPKU4_P17R16	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAATACCTCGGCCCTTCTCAGTTCGCTACGACCC	34202
hPKU4_P17R17	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCAATACCTCGGCCCTTCTCAGTTCGCTACGACCC	34203
hPKU4_P17R18	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCC	34204
hPKU4_P17R19	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCC	34205
hPKU4_P17R20	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCC	34206
hPKU4_P17R21	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCC	34207
hPKU4_P17R22	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCC	34208
hPKU4_P17R23	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCC	34209
hPKU4_P17R24	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCC	34210
hPKU4_P17R25	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCC	34211
hPKU4_P17R26	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCC	34212
hPKU4_P17R27	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCC	34213
hPKU4_P17R28	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCC	34214
hPKU4_P17R29	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCC	34215
hPKU4_P17R30	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCC	34216
hPKU4_P17R31	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCC	34217

hPKU4_P17R32	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCC	34218
hPKU4_P17R33	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCC	34219
hPKU4_P17R34	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCC	34220
hPKU4_P17R35	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCC	34221
hPKU4_P17R36	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCC	34222
hPKU4_P17R37	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCC	34223
hPKU4_P17R38	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCC	34224
hPKU4_P17R39	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCC	34225
hPKU4_P17R40	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCC	34226
hPKU4_P17R41	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCC	34227
hPKU4_P17R42	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCC	34228
hPKU4_P17R43	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCC	34229
hPKU4_P17R44	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCC	34230
hPKU4_P17R45	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCC	34231
hPKU4_P17R46	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCC	34232
hPKU4_P17R47	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCC	34233
hPKU4_P17R48	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCC	34234

hPKU4_P17R49	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCC	34235
hPKU4_P17R50	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCC	34236
hPKU4_P17R51	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCC	34237
hPKU4_P17R52	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCC	34238
hPKU4_P17R53	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCC	34239
hPKU4_P17R54	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCC	34240
hPKU4_P17R55	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCC	34241
hPKU4_P17R56	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCC	34242
hPKU4_P17R57	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCACTCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCC	34243
hPKU4_P17R58	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCACTCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCC	34244
hPKU4_P17R59	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTCACTCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTACGACCC	34245
hPKU4_P17R9	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCGGCCCTTCTCAGTTCGCTACGACCC	34246

hPKU4_P1R10	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTCGGCCCTTCT	34247
hPKU4_P1R11	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTCGGCCCTTCT	34248
hPKU4_P1R12	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCCTCGGCCCTTCT	34249
hPKU4_P1R13	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCACCTCGGCCCTTCT	34250
hPKU4_P1R14	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTACCTCGGCCCTTCT	34251
hPKU4_P1R15	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCATACCTCGGCCCTTCT	34252
hPKU4_P1R16	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAATACCTCGGCCCTTCT	34253
hPKU4_P1R17	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCAATACCTCGGCCCTTCT	34254
hPKU4_P1R18	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCACAATACCTCGGCCCTTCT	34255
hPKU4_P1R19	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCACAATACCTCGGCCCTTCT	34256
hPKU4_P1R20	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCCACAATACCTCGGCCCTTCT	34257
hPKU4_P1R21	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGCCACAATACCTCGGCCCTTCT	34258
hPKU4_P1R22	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGCCACAATACCTCGGCCCTTCT	34259
hPKU4_P1R23	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTGCCACAATACCTCGGCCCTTCT	34260
hPKU4_P1R24	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGCTGCCACAATACCTCGGCCCTTCT	34261
hPKU4_P1R25	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGCTGCCACAATACCTCGGCCCTTCT	34262
hPKU4_P1R26	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTGCTGCCACAATACCTCGGCCCTTCT	34263

hPKU4_P1R27	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTTGCTGCCACAATACCTCGGCCCTTCT	34264
hPKU4_P1R28	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTTTGCTGCCACAATACCTCGGCCCTTCT	34265
hPKU4_P1R29	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCACTTTGCTGCCACAATACCTCGGCCCTTCT	34266
hPKU4_P1R30	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAACTTTGCTGCCACAATACCTCGGCCCTTCT	34267
hPKU4_P1R31	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGAACTTTGCTGCCACAATACCTCGGCCCTTCT	34268
hPKU4_P1R32	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGGAACTTTGCTGCCACAATACCTCGGCCCTTCT	34269
hPKU4_P1R33	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAGGAACTTTGCTGCCACAATACCTCGGCCCTTCT	34270
hPKU4_P1R34	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCT	34271
hPKU4_P1R35	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCT	34272
hPKU4_P1R36	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCT	34273
hPKU4_P1R37	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCT	34274
hPKU4_P1R38	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCT	34275
hPKU4_P1R39	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCT	34276
hPKU4_P1R40	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCT	34277
hPKU4_P1R41	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCT	34278
hPKU4_P1R42	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCT	34279
hPKU4_P1R43	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCT	34280

hPKU4_P1R44	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCT	34281
hPKU4_P1R45	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCT	34282
hPKU4_P1R46	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCT	34283
hPKU4_P1R47	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCT	34284
hPKU4_P1R48	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCT	34285
hPKU4_P1R49	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCT	34286
hPKU4_P1R50	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCT	34287
hPKU4_P1R51	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCT	34288
hPKU4_P1R52	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCT	34289
hPKU4_P1R53	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCT	34290
hPKU4_P1R54	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCT	34291
hPKU4_P1R55	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCT	34292
hPKU4_P1R56	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCT	34293
hPKU4_P1R57	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCACTCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCT	34294
hPKU4_P1R58	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCACTCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCT	34295
hPKU4_P1R59	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTCACTCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCT	34296
hPKU4_P1R9	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCGGCCCTTCT	34297

hPKU4_P2R10	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTCGGCCCTTCTC	34298
hPKU4_P2R11	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTCGGCCCTTCTC	34299
hPKU4_P2R12	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCCTCGGCCCTTCTC	34300
hPKU4_P2R13	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCACCTCGGCCCTTCTC	34301
hPKU4_P2R14	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTACCTCGGCCCTTCTC	34302
hPKU4_P2R15	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCATACCTCGGCCCTTCTC	34303
hPKU4_P2R16	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAATACCTCGGCCCTTCTC	34304
hPKU4_P2R17	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCAATACCTCGGCCCTTCTC	34305
hPKU4_P2R18	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCACAATACCTCGGCCCTTCTC	34306
hPKU4_P2R19	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCACAATACCTCGGCCCTTCTC	34307
hPKU4_P2R20	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCCACAATACCTCGGCCCTTCTC	34308
hPKU4_P2R21	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGCCACAATACCTCGGCCCTTCTC	34309
hPKU4_P2R22	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGCCACAATACCTCGGCCCTTCTC	34310
hPKU4_P2R23	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTGCCACAATACCTCGGCCCTTCTC	34311
hPKU4_P2R24	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGCTGCCACAATACCTCGGCCCTTCTC	34312
hPKU4_P2R25	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGCTGCCACAATACCTCGGCCCTTCTC	34313
hPKU4_P2R26	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTGCTGCCACAATACCTCGGCCCTTCTC	34314

hPKU4_P2R27	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTTGCTGCCACAATACCTCGGCCCTTCTC	34315
hPKU4_P2R28	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTTTGCTGCCACAATACCTCGGCCCTTCTC	34316
hPKU4_P2R29	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCACTTTGCTGCCACAATACCTCGGCCCTTCTC	34317
hPKU4_P2R30	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAACTTTGCTGCCACAATACCTCGGCCCTTCTC	34318
hPKU4_P2R31	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGAACTTTGCTGCCACAATACCTCGGCCCTTCTC	34319
hPKU4_P2R32	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGGAACTTTGCTGCCACAATACCTCGGCCCTTCTC	34320
hPKU4_P2R33	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTC	34321
hPKU4_P2R34	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTC	34322
hPKU4_P2R35	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTC	34323
hPKU4_P2R36	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTC	34324
hPKU4_P2R37	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTC	34325
hPKU4_P2R38	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTC	34326
hPKU4_P2R39	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTC	34327
hPKU4_P2R40	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTC	34328
hPKU4_P2R41	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTC	34329
hPKU4_P2R42	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTC	34330
hPKU4_P2R43	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTC	34331

hPKU4_P2R44	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTC	34332
hPKU4_P2R45	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTC	34333
hPKU4_P2R46	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTC	34334
hPKU4_P2R47	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTC	34335
hPKU4_P2R48	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTC	34336
hPKU4_P2R49	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTC	34337
hPKU4_P2R50	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTC	34338
hPKU4_P2R51	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTC	34339
hPKU4_P2R52	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTC	34340
hPKU4_P2R53	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTC	34341
hPKU4_P2R54	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTC	34342
hPKU4_P2R55	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTC	34343
hPKU4_P2R56	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTC	34344
hPKU4_P2R57	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCACTCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTC	34345
hPKU4_P2R58	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCACTCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTC	34346
hPKU4_P2R59	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTCACTCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTC	34347
hPKU4_P2R9	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCGGCCCTTCTC	34348

hPKU4_P3R10	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTCGGCCCTTCTCA	34349
hPKU4_P3R11	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTCGGCCCTTCTCA	34350
hPKU4_P3R12	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCCTCGGCCCTTCTCA	34351
hPKU4_P3R13	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCACCTCGGCCCTTCTCA	34352
hPKU4_P3R14	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTACCTCGGCCCTTCTCA	34353
hPKU4_P3R15	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCATACCTCGGCCCTTCTCA	34354
hPKU4_P3R16	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAATACCTCGGCCCTTCTCA	34355
hPKU4_P3R17	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCAATACCTCGGCCCTTCTCA	34356
hPKU4_P3R18	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCACAATACCTCGGCCCTTCTCA	34357
hPKU4_P3R19	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCACAATACCTCGGCCCTTCTCA	34358
hPKU4_P3R20	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCCACAATACCTCGGCCCTTCTCA	34359
hPKU4_P3R21	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGCCACAATACCTCGGCCCTTCTCA	34360
hPKU4_P3R22	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGCCACAATACCTCGGCCCTTCTCA	34361
hPKU4_P3R23	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTGCCACAATACCTCGGCCCTTCTCA	34362
hPKU4_P3R24	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGCTGCCACAATACCTCGGCCCTTCTCA	34363
hPKU4_P3R25	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGCTGCCACAATACCTCGGCCCTTCTCA	34364
hPKU4_P3R26	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTGCTGCCACAATACCTCGGCCCTTCTCA	34365

hPKU4_P3R27	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTTGCTGCCACAATACCTCGGCCCTTCTCA	34366
hPKU4_P3R28	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTTTGCTGCCACAATACCTCGGCCCTTCTCA	34367
hPKU4_P3R29	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCACTTTGCTGCCACAATACCTCGGCCCTTCTCA	34368
hPKU4_P3R30	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAACTTTGCTGCCACAATACCTCGGCCCTTCTCA	34369
hPKU4_P3R31	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGAACTTTGCTGCCACAATACCTCGGCCCTTCTCA	34370
hPKU4_P3R32	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCA	34371
hPKU4_P3R33	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCA	34372
hPKU4_P3R34	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCA	34373
hPKU4_P3R35	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCA	34374
hPKU4_P3R36	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCA	34375
hPKU4_P3R37	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCA	34376
hPKU4_P3R38	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCA	34377
hPKU4_P3R39	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCA	34378
hPKU4_P3R40	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCA	34379
hPKU4_P3R41	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCA	34380
hPKU4_P3R42	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCA	34381
hPKU4_P3R43	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCA	34382

hPKU4_P3R44	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCA	34383
hPKU4_P3R45	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCA	34384
hPKU4_P3R46	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCA	34385
hPKU4_P3R47	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCA	34386
hPKU4_P3R48	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCA	34387
hPKU4_P3R49	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCA	34388
hPKU4_P3R50	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCA	34389
hPKU4_P3R51	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCA	34390
hPKU4_P3R52	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCA	34391
hPKU4_P3R53	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCA	34392
hPKU4_P3R54	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCA	34393
hPKU4_P3R55	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCA	34394
hPKU4_P3R56	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCA	34395
hPKU4_P3R57	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCACTCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCA	34396
hPKU4_P3R58	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCACTCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCA	34397
hPKU4_P3R59	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTCACTCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCA	34398
hPKU4_P3R9	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCGGCCCTTCTCA	34399

hPKU4_P4R10	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTCGGCCCTTCTCAG	34400
hPKU4_P4R11	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTCGGCCCTTCTCAG	34401
hPKU4_P4R12	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCCTCGGCCCTTCTCAG	34402
hPKU4_P4R13	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCACCTCGGCCCTTCTCAG	34403
hPKU4_P4R14	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTACCTCGGCCCTTCTCAG	34404
hPKU4_P4R15	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCATACCTCGGCCCTTCTCAG	34405
hPKU4_P4R16	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAATACCTCGGCCCTTCTCAG	34406
hPKU4_P4R17	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCAATACCTCGGCCCTTCTCAG	34407
hPKU4_P4R18	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCACAATACCTCGGCCCTTCTCAG	34408
hPKU4_P4R19	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCACAATACCTCGGCCCTTCTCAG	34409
hPKU4_P4R20	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCCACAATACCTCGGCCCTTCTCAG	34410
hPKU4_P4R21	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGCCACAATACCTCGGCCCTTCTCAG	34411
hPKU4_P4R22	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGCCACAATACCTCGGCCCTTCTCAG	34412
hPKU4_P4R23	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTGCCACAATACCTCGGCCCTTCTCAG	34413
hPKU4_P4R24	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGCTGCCACAATACCTCGGCCCTTCTCAG	34414
hPKU4_P4R25	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGCTGCCACAATACCTCGGCCCTTCTCAG	34415
hPKU4_P4R26	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTGCTGCCACAATACCTCGGCCCTTCTCAG	34416

hPKU4_P4R27	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTTGCTGCCACAATACCTCGGCCCTTCTCAG	34417
hPKU4_P4R28	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTTTGCTGCCACAATACCTCGGCCCTTCTCAG	34418
hPKU4_P4R29	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCACTTTGCTGCCACAATACCTCGGCCCTTCTCAG	34419
hPKU4_P4R30	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAACTTTGCTGCCACAATACCTCGGCCCTTCTCAG	34420
hPKU4_P4R31	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAG	34421
hPKU4_P4R32	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAG	34422
hPKU4_P4R33	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAG	34423
hPKU4_P4R34	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAG	34424
hPKU4_P4R35	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAG	34425
hPKU4_P4R36	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAG	34426
hPKU4_P4R37	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAG	34427
hPKU4_P4R38	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAG	34428
hPKU4_P4R39	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAG	34429
hPKU4_P4R40	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAG	34430
hPKU4_P4R41	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAG	34431
hPKU4_P4R42	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAG	34432
hPKU4_P4R43	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAG	34433

hPKU4_P4R44	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAG	34434
hPKU4_P4R45	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAG	34435
hPKU4_P4R46	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAG	34436
hPKU4_P4R47	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAG	34437
hPKU4_P4R48	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAG	34438
hPKU4_P4R49	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAG	34439
hPKU4_P4R50	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAG	34440
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hPKU4_P4R52	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAG	34442
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hPKU4_P4R54	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAG	34444
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hPKU4_P4R58	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCACTCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAG	34448
hPKU4_P4R59	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTCACTCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAG	34449
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hPKU4_P6R35	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTT	34527
hPKU4_P6R36	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTT	34528
hPKU4_P6R37	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTT	34529
hPKU4_P6R38	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTT	34530
hPKU4_P6R39	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTT	34531
hPKU4_P6R40	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTT	34532
hPKU4_P6R41	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTT	34533
hPKU4_P6R42	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTT	34534
hPKU4_P6R43	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTT	34535

hPKU4_P6R44	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTT	34536
hPKU4_P6R45	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTT	34537
hPKU4_P6R46	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTT	34538
hPKU4_P6R47	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTT	34539
hPKU4_P6R48	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTT	34540
hPKU4_P6R49	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTT	34541
hPKU4_P6R50	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTT	34542
hPKU4_P6R51	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTT	34543
hPKU4_P6R52	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTT	34544
hPKU4_P6R53	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTT	34545
hPKU4_P6R54	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTT	34546
hPKU4_P6R55	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTT	34547
hPKU4_P6R56	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTT	34548
hPKU4_P6R57	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCACTCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTT	34549
hPKU4_P6R58	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCACTCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTT	34550
hPKU4_P6R59	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTCACTCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTT	34551
hPKU4_P6R9	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCGGCCCTTCTCAGTT	34552

hPKU4_P7R10	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTCGGCCCTTCTCAGTTC	34553
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hPKU4_P7R12	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCCTCGGCCCTTCTCAGTTC	34555
hPKU4_P7R13	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCACCTCGGCCCTTCTCAGTTC	34556
hPKU4_P7R14	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTACCTCGGCCCTTCTCAGTTC	34557
hPKU4_P7R15	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCATACCTCGGCCCTTCTCAGTTC	34558
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hPKU4_P7R21	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGCCACAATACCTCGGCCCTTCTCAGTTC	34564
hPKU4_P7R22	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGCCACAATACCTCGGCCCTTCTCAGTTC	34565
hPKU4_P7R23	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTGCCACAATACCTCGGCCCTTCTCAGTTC	34566
hPKU4_P7R24	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGCTGCCACAATACCTCGGCCCTTCTCAGTTC	34567
hPKU4_P7R25	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGCTGCCACAATACCTCGGCCCTTCTCAGTTC	34568
hPKU4_P7R26	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTGCTGCCACAATACCTCGGCCCTTCTCAGTTC	34569

hPKU4_P7R27	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTC	34570
hPKU4_P7R28	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTC	34571
hPKU4_P7R29	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTC	34572
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hPKU4_P7R32	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTC	34575
hPKU4_P7R33	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTC	34576
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hPKU4_P7R37	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTC	34580
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hPKU4_P7R39	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTC	34582
hPKU4_P7R40	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTC	34583
hPKU4_P7R41	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTC	34584
hPKU4_P7R42	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTC	34585
hPKU4_P7R43	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTC	34586

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hPKU4_P7R46	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTC	34589
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hPKU4_P7R48	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTC	34591
hPKU4_P7R49	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTC	34592
hPKU4_P7R50	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTC	34593
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hPKU4_P7R52	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTC	34595
hPKU4_P7R53	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTC	34596
hPKU4_P7R54	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTC	34597
hPKU4_P7R55	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTC	34598
hPKU4_P7R56	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTC	34599
hPKU4_P7R57	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCACTCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTC	34600
hPKU4_P7R58	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCACTCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTC	34601
hPKU4_P7R59	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTCACTCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTC	34602
hPKU4_P7R9	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCGGCCCTTCTCAGTTC	34603

hPKU4_P8R10	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTCGGCCCTTCTCAGTTCG	34604
hPKU4_P8R11	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTCGGCCCTTCTCAGTTCG	34605
hPKU4_P8R12	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCCTCGGCCCTTCTCAGTTCG	34606
hPKU4_P8R13	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCACCTCGGCCCTTCTCAGTTCG	34607
hPKU4_P8R14	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTACCTCGGCCCTTCTCAGTTCG	34608
hPKU4_P8R15	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCATACCTCGGCCCTTCTCAGTTCG	34609
hPKU4_P8R16	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAATACCTCGGCCCTTCTCAGTTCG	34610
hPKU4_P8R17	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCAATACCTCGGCCCTTCTCAGTTCG	34611
hPKU4_P8R18	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCACAATACCTCGGCCCTTCTCAGTTCG	34612
hPKU4_P8R19	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCACAATACCTCGGCCCTTCTCAGTTCG	34613
hPKU4_P8R20	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCCACAATACCTCGGCCCTTCTCAGTTCG	34614
hPKU4_P8R21	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGCCACAATACCTCGGCCCTTCTCAGTTCG	34615
hPKU4_P8R22	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGCCACAATACCTCGGCCCTTCTCAGTTCG	34616
hPKU4_P8R23	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTGCCACAATACCTCGGCCCTTCTCAGTTCG	34617
hPKU4_P8R24	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGCTGCCACAATACCTCGGCCCTTCTCAGTTCG	34618
hPKU4_P8R25	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGCTGCCACAATACCTCGGCCCTTCTCAGTTCG	34619
hPKU4_P8R26	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCG	34620

hPKU4_P8R27	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCG	34621
hPKU4_P8R28	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCG	34622
hPKU4_P8R29	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCG	34623
hPKU4_P8R30	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCG	34624
hPKU4_P8R31	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCG	34625
hPKU4_P8R32	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCG	34626
hPKU4_P8R33	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCG	34627
hPKU4_P8R34	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCG	34628
hPKU4_P8R35	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCG	34629
hPKU4_P8R36	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCG	34630
hPKU4_P8R37	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCG	34631
hPKU4_P8R38	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCG	34632
hPKU4_P8R39	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCG	34633
hPKU4_P8R40	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCG	34634
hPKU4_P8R41	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCG	34635
hPKU4_P8R42	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCG	34636
hPKU4_P8R43	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCG	34637

hPKU4_P8R44	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCG	34638
hPKU4_P8R45	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCG	34639
hPKU4_P8R46	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCG	34640
hPKU4_P8R47	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCG	34641
hPKU4_P8R48	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCG	34642
hPKU4_P8R49	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCG	34643
hPKU4_P8R50	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCG	34644
hPKU4_P8R51	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCG	34645
hPKU4_P8R52	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCG	34646
hPKU4_P8R53	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCG	34647
hPKU4_P8R54	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCG	34648
hPKU4_P8R55	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCG	34649
hPKU4_P8R56	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCG	34650
hPKU4_P8R57	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCACTCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCG	34651
hPKU4_P8R58	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCACTCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCG	34652
hPKU4_P8R59	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTCACTCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCG	34653

hPKU4_P8R9	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCGGCCCTTCTCAGTTCG	34654
hPKU4_P9R10	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTCGGCCCTTCTCAGTTCGC	34655
hPKU4_P9R11	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTCGGCCCTTCTCAGTTCGC	34656
hPKU4_P9R12	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCCTCGGCCCTTCTCAGTTCGC	34657
hPKU4_P9R13	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCACCTCGGCCCTTCTCAGTTCGC	34658
hPKU4_P9R14	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTACCTCGGCCCTTCTCAGTTCGC	34659
hPKU4_P9R15	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCATACCTCGGCCCTTCTCAGTTCGC	34660
hPKU4_P9R16	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAATACCTCGGCCCTTCTCAGTTCGC	34661
hPKU4_P9R17	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCAATACCTCGGCCCTTCTCAGTTCGC	34662
hPKU4_P9R18	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCACAATACCTCGGCCCTTCTCAGTTCGC	34663
hPKU4_P9R19	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCACAATACCTCGGCCCTTCTCAGTTCGC	34664
hPKU4_P9R20	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCCACAATACCTCGGCCCTTCTCAGTTCGC	34665
hPKU4_P9R21	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGCCACAATACCTCGGCCCTTCTCAGTTCGC	34666
hPKU4_P9R22	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGC	34667
hPKU4_P9R23	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTGCCACAATACCTCGGCCCTTCTCAGTTCGC	34668
hPKU4_P9R24	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGCTGCCACAATACCTCGGCCCTTCTCAGTTCGC	34669
hPKU4_P9R25	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGC	34670

hPKU4_P9R26	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGC	34671
hPKU4_P9R27	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGC	34672
hPKU4_P9R28	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGC	34673
hPKU4_P9R29	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGC	34674
hPKU4_P9R30	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGC	34675
hPKU4_P9R31	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGC	34676
hPKU4_P9R32	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGC	34677
hPKU4_P9R33	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGC	34678
hPKU4_P9R34	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGC	34679
hPKU4_P9R35	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGC	34680
hPKU4_P9R36	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGC	34681
hPKU4_P9R37	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGC	34682
hPKU4_P9R38	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGC	34683
hPKU4_P9R39	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGC	34684
hPKU4_P9R40	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGC	34685
hPKU4_P9R41	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGC	34686
hPKU4_P9R42	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGC	34687

hPKU4_P9R43	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGC	34688
hPKU4_P9R44	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGC	34689
hPKU4_P9R45	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGC	34690
hPKU4_P9R46	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGC	34691
hPKU4_P9R47	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGC	34692
hPKU4_P9R48	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGC	34693
hPKU4_P9R49	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGC	34694
hPKU4_P9R50	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGC	34695
hPKU4_P9R51	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGC	34696
hPKU4_P9R52	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGC	34697
hPKU4_P9R53	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGC	34698
hPKU4_P9R54	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGC	34699
hPKU4_P9R55	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGC	34700
hPKU4_P9R56	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGC	34701
hPKU4_P9R57	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCACTCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGC	34702
hPKU4_P9R58	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCACTCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGC	34703

hPKU4_P9R59	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTCACTCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGC	34704
hPKU4_P9R9	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCGGCCCTTCTCAGTTCGC	34705

Table 5E. Exemplary template RNA sequences

Table 5E provides design of exemplary DNA components of gene modifying systems for correcting the pathogenic R408W mutation in PAH to the wild-type form. This table details the sequence of a complete template RNA for use in exemplary gene modifying systems comprising a gene modifying polypeptide. Templates in this table employ the hPKU5 spacer TAGCGAACTGAGAAGGGCCA (SEQ ID NO: 16011).

Name	tgRNA sequence	SEQ ID NO
hPKU5_P0R10	TAGCGAACTGAGAAGGGCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAATACCTCGG	34706
hPKU5_P0R11	TAGCGAACTGAGAAGGGCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCAATACCTCGG	34707
hPKU5_P0R12	TAGCGAACTGAGAAGGGCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCACAATACCTCGG	34708
hPKU5_P0R13	TAGCGAACTGAGAAGGGCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCACAATACCTCGG	34709
hPKU5_P0R14	TAGCGAACTGAGAAGGGCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCCACAATACCTCGG	34710
hPKU5_P0R15	TAGCGAACTGAGAAGGGCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGCCACAATACCTCGG	34711

hPKU5_P0R16	TAGCGAACTGAGAAGGGCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGCCACAATACCTCGG	34712
hPKU5_P0R17	TAGCGAACTGAGAAGGGCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTGCCACAATACCTCGG	34713
hPKU5_P0R18	TAGCGAACTGAGAAGGGCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGCTGCCACAATACCTCGG	34714
hPKU5_P0R19	TAGCGAACTGAGAAGGGCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGCTGCCACAATACCTCGG	34715
hPKU5_P0R20	TAGCGAACTGAGAAGGGCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTGCTGCCACAATACCTCGG	34716
hPKU5_P0R21	TAGCGAACTGAGAAGGGCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTTGCTGCCACAATACCTCGG	34717
hPKU5_P0R22	TAGCGAACTGAGAAGGGCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTTTGCTGCCACAATACCTCGG	34718
hPKU5_P0R23	TAGCGAACTGAGAAGGGCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCACTTTGCTGCCACAATACCTCGG	34719
hPKU5_P0R24	TAGCGAACTGAGAAGGGCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAACTTTGCTGCCACAATACCTCGG	34720
hPKU5_P0R25	TAGCGAACTGAGAAGGGCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGAACTTTGCTGCCACAATACCTCGG	34721
hPKU5_P0R26	TAGCGAACTGAGAAGGGCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGGAACTTTGCTGCCACAATACCTCGG	34722

hPKU5_P0R27	TAGCGAACTGAGAAGGGCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAGGAACTTTGCTGCCACAATACCTCGG	34723
hPKU5_P0R28	TAGCGAACTGAGAAGGGCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTAGGAACTTTGCTGCCACAATACCTCGG	34724
hPKU5_P0R29	TAGCGAACTGAGAAGGGCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTAGGAACTTTGCTGCCACAATACCTCGG	34725
hPKU5_P0R3	TAGCGAACTGAGAAGGGCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCGG	34726
hPKU5_P0R30	TAGCGAACTGAGAAGGGCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTTAGGAACTTTGCTGCCACAATACCTCGG	34727
hPKU5_P0R31	TAGCGAACTGAGAAGGGCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTCTTAGGAACTTTGCTGCCACAATACCTCGG	34728
hPKU5_P0R32	TAGCGAACTGAGAAGGGCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGTCTTAGGAACTTTGCTGCCACAATACCTCGG	34729
hPKU5_P0R33	TAGCGAACTGAGAAGGGCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGGTCTTAGGAACTTTGCTGCCACAATACCTCGG	34730
hPKU5_P0R34	TAGCGAACTGAGAAGGGCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGGTCTTAGGAACTTTGCTGCCACAATACCTCGG	34731
hPKU5_P0R35	TAGCGAACTGAGAAGGGCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGG	34732
hPKU5_P0R36	TAGCGAACTGAGAAGGGCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGG	34733

hPKU5_P0R37	TAGCGAACTGAGAAGGGCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGG	34734
hPKU5_P0R38	TAGCGAACTGAGAAGGGCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGG	34735
hPKU5_P0R39	TAGCGAACTGAGAAGGGCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGG	34736
hPKU5_P0R4	TAGCGAACTGAGAAGGGCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTCGG	34737
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hPKU5_P0R44	TAGCGAACTGAGAAGGGCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGG	34742
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hPKU5_P11R47	TAGCGAACTGAGAAGGGCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGT	34847
hPKU5_P11R48	TAGCGAACTGAGAAGGGCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGT	34848
hPKU5_P11R49	TAGCGAACTGAGAAGGGCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGT	34849
hPKU5_P11R5	TAGCGAACTGAGAAGGGCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTCGGCCCTTCTCAGT	34850
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hPKU5_P11R53	TAGCGAACTGAGAAGGGCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTCACTCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGT	34854
hPKU5_P11R6	TAGCGAACTGAGAAGGGCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCCTCGGCCCTTCTCAGT	34855
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hPKU5_P13R4	TAGCGAACTGAGAAGGGCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTCGGCCCTTCTCAGTTC	34941
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hPKU5_P13R42	TAGCGAACTGAGAAGGGCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTC	34944

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hPKU5_P13R49	TAGCGAACTGAGAAGGGCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTC	34951
hPKU5_P13R5	TAGCGAACTGAGAAGGGCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTCGGCCCTTCTCAGTTC	34952
hPKU5_P13R50	TAGCGAACTGAGAAGGGCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTC	34953
hPKU5_P13R51	TAGCGAACTGAGAAGGGCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCACTCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTC	34954
hPKU5_P13R52	TAGCGAACTGAGAAGGGCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCACTCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTC	34955

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hPKU5_P13R6	TAGCGAACTGAGAAGGGCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCCTCGGCCCTTCTCAGTTC	34957
hPKU5_P13R7	TAGCGAACTGAGAAGGGCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCACCTCGGCCCTTCTCAGTTC	34958
hPKU5_P13R8	TAGCGAACTGAGAAGGGCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTACCTCGGCCCTTCTCAGTTC	34959
hPKU5_P13R9	TAGCGAACTGAGAAGGGCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCATACCTCGGCCCTTCTCAGTTC	34960
hPKU5_P14R10	TAGCGAACTGAGAAGGGCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAATACCTCGGCCCTTCTCAGTTCG	34961
hPKU5_P14R11	TAGCGAACTGAGAAGGGCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCAATACCTCGGCCCTTCTCAGTTCG	34962
hPKU5_P14R12	TAGCGAACTGAGAAGGGCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCACAATACCTCGGCCCTTCTCAGTTCG	34963
hPKU5_P14R13	TAGCGAACTGAGAAGGGCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCACAATACCTCGGCCCTTCTCAGTTCG	34964
hPKU5_P14R14	TAGCGAACTGAGAAGGGCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCCACAATACCTCGGCCCTTCTCAGTTCG	34965
hPKU5_P14R15	TAGCGAACTGAGAAGGGCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGCCACAATACCTCGGCCCTTCTCAGTTCG	34966

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hPKU5_P14R17	TAGCGAACTGAGAAGGGCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTGCCACAATACCTCGGCCCTTCTCAGTTCG	34968
hPKU5_P14R18	TAGCGAACTGAGAAGGGCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGCTGCCACAATACCTCGGCCCTTCTCAGTTCG	34969
hPKU5_P14R19	TAGCGAACTGAGAAGGGCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGCTGCCACAATACCTCGGCCCTTCTCAGTTCG	34970
hPKU5_P14R20	TAGCGAACTGAGAAGGGCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCG	34971
hPKU5_P14R21	TAGCGAACTGAGAAGGGCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCG	34972
hPKU5_P14R22	TAGCGAACTGAGAAGGGCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCG	34973
hPKU5_P14R23	TAGCGAACTGAGAAGGGCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCG	34974
hPKU5_P14R24	TAGCGAACTGAGAAGGGCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCG	34975
hPKU5_P14R25	TAGCGAACTGAGAAGGGCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCG	34976
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hPKU5_P14R27	TAGCGAACTGAGAAGGGCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCG	34978
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hPKU5_P14R29	TAGCGAACTGAGAAGGGCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCG	34980
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hPKU5_P14R30	TAGCGAACTGAGAAGGGCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCG	34982
hPKU5_P14R31	TAGCGAACTGAGAAGGGCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCG	34983
hPKU5_P14R32	TAGCGAACTGAGAAGGGCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCG	34984
hPKU5_P14R33	TAGCGAACTGAGAAGGGCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCG	34985
hPKU5_P14R34	TAGCGAACTGAGAAGGGCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCG	34986
hPKU5_P14R35	TAGCGAACTGAGAAGGGCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCG	34987
hPKU5_P14R36	TAGCGAACTGAGAAGGGCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCG	34988

hPKU5_P14R37	TAGCGAACTGAGAAGGGCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCG	34989
hPKU5_P14R38	TAGCGAACTGAGAAGGGCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCG	34990
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hPKU5_P14R4	TAGCGAACTGAGAAGGGCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTCGGCCCTTCTCAGTTCG	34992
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hPKU5_P14R42	TAGCGAACTGAGAAGGGCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCG	34995
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hPKU5_P14R44	TAGCGAACTGAGAAGGGCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCG	34997
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hPKU5_P14R49	TAGCGAACTGAGAAGGGCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCG	35002
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hPKU5_P15R35	TAGCGAACTGAGAAGGGCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGC	35038
hPKU5_P15R36	TAGCGAACTGAGAAGGGCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGC	35039
hPKU5_P15R37	TAGCGAACTGAGAAGGGCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGC	35040
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hPKU5_P15R39	TAGCGAACTGAGAAGGGCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGC	35042
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hPKU5_P15R43	TAGCGAACTGAGAAGGGCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGC	35047
hPKU5_P15R44	TAGCGAACTGAGAAGGGCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGC	35048
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hPKU5_P15R46	TAGCGAACTGAGAAGGGCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGC	35050
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hPKU5_P15R48	TAGCGAACTGAGAAGGGCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGC	35052
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hPKU5_P15R5	TAGCGAACTGAGAAGGGCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTCGGCCCTTCTCAGTTCGC	35054

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hPKU5_P15R51	TAGCGAACTGAGAAGGGCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCACTCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGC	35056
hPKU5_P15R52	TAGCGAACTGAGAAGGGCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCACTCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGC	35057
hPKU5_P15R53	TAGCGAACTGAGAAGGGCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTCACTCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGC	35058
hPKU5_P15R6	TAGCGAACTGAGAAGGGCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCCTCGGCCCTTCTCAGTTCGC	35059
hPKU5_P15R7	TAGCGAACTGAGAAGGGCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCACCTCGGCCCTTCTCAGTTCGC	35060
hPKU5_P15R8	TAGCGAACTGAGAAGGGCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTACCTCGGCCCTTCTCAGTTCGC	35061
hPKU5_P15R9	TAGCGAACTGAGAAGGGCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCATACCTCGGCCCTTCTCAGTTCGC	35062
hPKU5_P16R10	TAGCGAACTGAGAAGGGCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAATACCTCGGCCCTTCTCAGTTCGCT	35063
hPKU5_P16R11	TAGCGAACTGAGAAGGGCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCAATACCTCGGCCCTTCTCAGTTCGCT	35064
hPKU5_P16R12	TAGCGAACTGAGAAGGGCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCACAATACCTCGGCCCTTCTCAGTTCGCT	35065

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hPKU5_P16R15	TAGCGAACTGAGAAGGGCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGCCACAATACCTCGGCCCTTCTCAGTTCGCT	35068
hPKU5_P16R16	TAGCGAACTGAGAAGGGCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCT	35069
hPKU5_P16R17	TAGCGAACTGAGAAGGGCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTGCCACAATACCTCGGCCCTTCTCAGTTCGCT	35070
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hPKU5_P16R20	TAGCGAACTGAGAAGGGCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCT	35073
hPKU5_P16R21	TAGCGAACTGAGAAGGGCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCT	35074
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hPKU5_P16R26	TAGCGAACTGAGAAGGGCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCT	35079
hPKU5_P16R27	TAGCGAACTGAGAAGGGCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCT	35080
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hPKU5_P16R3	TAGCGAACTGAGAAGGGCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCGGCCCTTCTCAGTTCGCT	35083
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hPKU5_P16R33	TAGCGAACTGAGAAGGGCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCT	35087

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hPKU5_P16R36	TAGCGAACTGAGAAGGGCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCT	35090
hPKU5_P16R37	TAGCGAACTGAGAAGGGCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCT	35091
hPKU5_P16R38	TAGCGAACTGAGAAGGGCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCT	35092
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hPKU5_P16R4	TAGCGAACTGAGAAGGGCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTCGGCCCTTCTCAGTTCGCT	35094
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hPKU5_P16R41	TAGCGAACTGAGAAGGGCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCT	35096
hPKU5_P16R42	TAGCGAACTGAGAAGGGCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCT	35097
hPKU5_P16R43	TAGCGAACTGAGAAGGGCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCT	35098

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hPKU5_P17R12	TAGCGAACTGAGAAGGGCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCACAATACCTCGGCCCTTCTCAGTTCGCTA	35116
hPKU5_P17R13	TAGCGAACTGAGAAGGGCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCACAATACCTCGGCCCTTCTCAGTTCGCTA	35117
hPKU5_P17R14	TAGCGAACTGAGAAGGGCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCCACAATACCTCGGCCCTTCTCAGTTCGCTA	35118
hPKU5_P17R15	TAGCGAACTGAGAAGGGCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGCCACAATACCTCGGCCCTTCTCAGTTCGCTA	35119
hPKU5_P17R16	TAGCGAACTGAGAAGGGCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTA	35120

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hPKU5_P17R3	TAGCGAACTGAGAAGGGCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCGGCCCTTCTCAGTTCGCTA	35134
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hPKU5_P17R32	TAGCGAACTGAGAAGGGCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTA	35137
hPKU5_P17R33	TAGCGAACTGAGAAGGGCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTA	35138
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hPKU5_P17R36	TAGCGAACTGAGAAGGGCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTA	35141
hPKU5_P17R37	TAGCGAACTGAGAAGGGCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTA	35142

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hPKU5_P17R43	TAGCGAACTGAGAAGGGCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTA	35149
hPKU5_P17R44	TAGCGAACTGAGAAGGGCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTA	35150
hPKU5_P17R45	TAGCGAACTGAGAAGGGCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTA	35151
hPKU5_P17R46	TAGCGAACTGAGAAGGGCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTA	35152
hPKU5_P17R47	TAGCGAACTGAGAAGGGCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTA	35153

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hPKU5_P17R5	TAGCGAACTGAGAAGGGCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTCGGCCCTTCTCAGTTCGCTA	35156
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hPKU5_P17R52	TAGCGAACTGAGAAGGGCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCACTCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTA	35159
hPKU5_P17R53	TAGCGAACTGAGAAGGGCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTCACTCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCAGTTCGCTA	35160
hPKU5_P17R6	TAGCGAACTGAGAAGGGCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCCTCGGCCCTTCTCAGTTCGCTA	35161
hPKU5_P17R7	TAGCGAACTGAGAAGGGCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCACCTCGGCCCTTCTCAGTTCGCTA	35162
hPKU5_P17R8	TAGCGAACTGAGAAGGGCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTACCTCGGCCCTTCTCAGTTCGCTA	35163
hPKU5_P17R9	TAGCGAACTGAGAAGGGCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCATACCTCGGCCCTTCTCAGTTCGCTA	35164

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hPKU5_P1R20	TAGCGAACTGAGAAGGGCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTGCTGCCACAATACCTCGGC	35175

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hPKU5_P1R3	TAGCGAACTGAGAAGGGCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCGGC	35185
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hPKU5_P3R13	TAGCGAACTGAGAAGGGCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCACAATACCTCGGCCC	35270
hPKU5_P3R14	TAGCGAACTGAGAAGGGCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCCACAATACCTCGGCCC	35271
hPKU5_P3R15	TAGCGAACTGAGAAGGGCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGCCACAATACCTCGGCCC	35272
hPKU5_P3R16	TAGCGAACTGAGAAGGGCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGCCACAATACCTCGGCCC	35273
hPKU5_P3R17	TAGCGAACTGAGAAGGGCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTGCCACAATACCTCGGCCC	35274
hPKU5_P3R18	TAGCGAACTGAGAAGGGCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGCTGCCACAATACCTCGGCCC	35275
hPKU5_P3R19	TAGCGAACTGAGAAGGGCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGCTGCCACAATACCTCGGCCC	35276
hPKU5_P3R20	TAGCGAACTGAGAAGGGCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTGCTGCCACAATACCTCGGCCC	35277

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hPKU5_P3R22	TAGCGAACTGAGAAGGGCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTTTGCTGCCACAATACCTCGGCCC	35279
hPKU5_P3R23	TAGCGAACTGAGAAGGGCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCACTTTGCTGCCACAATACCTCGGCCC	35280
hPKU5_P3R24	TAGCGAACTGAGAAGGGCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAACTTTGCTGCCACAATACCTCGGCCC	35281
hPKU5_P3R25	TAGCGAACTGAGAAGGGCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGAACTTTGCTGCCACAATACCTCGGCCC	35282
hPKU5_P3R26	TAGCGAACTGAGAAGGGCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGGAACTTTGCTGCCACAATACCTCGGCCC	35283
hPKU5_P3R27	TAGCGAACTGAGAAGGGCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAGGAACTTTGCTGCCACAATACCTCGGCCC	35284
hPKU5_P3R28	TAGCGAACTGAGAAGGGCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTAGGAACTTTGCTGCCACAATACCTCGGCCC	35285
hPKU5_P3R29	TAGCGAACTGAGAAGGGCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTAGGAACTTTGCTGCCACAATACCTCGGCCC	35286
hPKU5_P3R3	TAGCGAACTGAGAAGGGCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCGGCCC	35287
hPKU5_P3R30	TAGCGAACTGAGAAGGGCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTTAGGAACTTTGCTGCCACAATACCTCGGCCC	35288

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hPKU5_P3R32	TAGCGAACTGAGAAGGGCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCC	35290
hPKU5_P3R33	TAGCGAACTGAGAAGGGCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCC	35291
hPKU5_P3R34	TAGCGAACTGAGAAGGGCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCC	35292
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hPKU5_P3R38	TAGCGAACTGAGAAGGGCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCC	35296
hPKU5_P3R39	TAGCGAACTGAGAAGGGCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCC	35297
hPKU5_P3R4	TAGCGAACTGAGAAGGGCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTCGGCCC	35298
hPKU5_P3R40	TAGCGAACTGAGAAGGGCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCC	35299

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hPKU5_P3R47	TAGCGAACTGAGAAGGGCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCC	35306
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hPKU5_P3R5	TAGCGAACTGAGAAGGGCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTCGGCCC	35309
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hPKU5_P3R6	TAGCGAACTGAGAAGGGCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCCTCGGCCC	35314
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hPKU5_P4R12	TAGCGAACTGAGAAGGGCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCACAATACCTCGGCCCT	35320
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hPKU5_P4R42	TAGCGAACTGAGAAGGGCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCT	35352
hPKU5_P4R43	TAGCGAACTGAGAAGGGCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCT	35353
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hPKU5_P4R48	TAGCGAACTGAGAAGGGCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCT	35358
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hPKU5_P4R51	TAGCGAACTGAGAAGGGCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCACTCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCT	35362
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hPKU5_P4R53	TAGCGAACTGAGAAGGGCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTCACTCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCT	35364
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hPKU5_P4R8	TAGCGAACTGAGAAGGGCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTACCTCGGCCCT	35367
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hPKU5_P5R13	TAGCGAACTGAGAAGGGCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCACAATACCTCGGCCCTT	35372
hPKU5_P5R14	TAGCGAACTGAGAAGGGCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCCACAATACCTCGGCCCTT	35373
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hPKU5_P5R16	TAGCGAACTGAGAAGGGCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGCCACAATACCTCGGCCCTT	35375
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hPKU5_P5R26	TAGCGAACTGAGAAGGGCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGGAACTTTGCTGCCACAATACCTCGGCCCTT	35385
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hPKU5_P5R3	TAGCGAACTGAGAAGGGCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCGGCCCTT	35389
hPKU5_P5R30	TAGCGAACTGAGAAGGGCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTT	35390

hPKU5_P5R31	TAGCGAACTGAGAAGGGCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTT	35391
hPKU5_P5R32	TAGCGAACTGAGAAGGGCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTT	35392
hPKU5_P5R33	TAGCGAACTGAGAAGGGCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTT	35393
hPKU5_P5R34	TAGCGAACTGAGAAGGGCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTT	35394
hPKU5_P5R35	TAGCGAACTGAGAAGGGCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTT	35395
hPKU5_P5R36	TAGCGAACTGAGAAGGGCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTT	35396
hPKU5_P5R37	TAGCGAACTGAGAAGGGCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTT	35397
hPKU5_P5R38	TAGCGAACTGAGAAGGGCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTT	35398
hPKU5_P5R39	TAGCGAACTGAGAAGGGCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTT	35399
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hPKU5_P5R43	TAGCGAACTGAGAAGGGCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTT	35404
hPKU5_P5R44	TAGCGAACTGAGAAGGGCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTT	35405
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hPKU5_P5R46	TAGCGAACTGAGAAGGGCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTT	35407
hPKU5_P5R47	TAGCGAACTGAGAAGGGCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTT	35408
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hPKU5_P5R7	TAGCGAACTGAGAAGGGCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCACCTCGGCCCTT	35417
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hPKU5_P6R5	TAGCGAACTGAGAAGGGCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTCGGCCCTTC	35462
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hPKU5_P7R25	TAGCGAACTGAGAAGGGCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGAACTTTGCTGCCACAATACCTCGGCCCTTCT	35486
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hPKU5_P7R34	TAGCGAACTGAGAAGGGCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCT	35496
hPKU5_P7R35	TAGCGAACTGAGAAGGGCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCT	35497
hPKU5_P7R36	TAGCGAACTGAGAAGGGCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCT	35498
hPKU5_P7R37	TAGCGAACTGAGAAGGGCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCT	35499
hPKU5_P7R38	TAGCGAACTGAGAAGGGCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCT	35500
hPKU5_P7R39	TAGCGAACTGAGAAGGGCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCT	35501
hPKU5_P7R4	TAGCGAACTGAGAAGGGCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTCGGCCCTTCT	35502
hPKU5_P7R40	TAGCGAACTGAGAAGGGCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCT	35503

hPKU5_P7R41	TAGCGAACTGAGAAGGGCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCT	35504
hPKU5_P7R42	TAGCGAACTGAGAAGGGCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCT	35505
hPKU5_P7R43	TAGCGAACTGAGAAGGGCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCT	35506
hPKU5_P7R44	TAGCGAACTGAGAAGGGCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCT	35507
hPKU5_P7R45	TAGCGAACTGAGAAGGGCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCT	35508
hPKU5_P7R46	TAGCGAACTGAGAAGGGCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCT	35509
hPKU5_P7R47	TAGCGAACTGAGAAGGGCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCT	35510
hPKU5_P7R48	TAGCGAACTGAGAAGGGCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCT	35511
hPKU5_P7R49	TAGCGAACTGAGAAGGGCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCT	35512
hPKU5_P7R5	TAGCGAACTGAGAAGGGCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTCGGCCCTTCT	35513
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hPKU5_P7R52	TAGCGAACTGAGAAGGGCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCACTCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCT	35516
hPKU5_P7R53	TAGCGAACTGAGAAGGGCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTCACTCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCT	35517
hPKU5_P7R6	TAGCGAACTGAGAAGGGCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCCTCGGCCCTTCT	35518
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hPKU5_P9R4	TAGCGAACTGAGAAGGGCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTCGGCCCTTCTCA	35604
hPKU5_P9R40	TAGCGAACTGAGAAGGGCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCA	35605

hPKU5_P9R41	TAGCGAACTGAGAAGGGCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCA	35606
hPKU5_P9R42	TAGCGAACTGAGAAGGGCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCA	35607
hPKU5_P9R43	TAGCGAACTGAGAAGGGCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCA	35608
hPKU5_P9R44	TAGCGAACTGAGAAGGGCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCA	35609
hPKU5_P9R45	TAGCGAACTGAGAAGGGCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCA	35610
hPKU5_P9R46	TAGCGAACTGAGAAGGGCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCA	35611
hPKU5_P9R47	TAGCGAACTGAGAAGGGCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCA	35612
hPKU5_P9R48	TAGCGAACTGAGAAGGGCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCA	35613
hPKU5_P9R49	TAGCGAACTGAGAAGGGCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCA	35614
hPKU5_P9R5	TAGCGAACTGAGAAGGGCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTCGGCCCTTCTCA	35615
hPKU5_P9R50	TAGCGAACTGAGAAGGGCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCA	35616

hPKU5_P9R51	TAGCGAACTGAGAAGGGCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCACTCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCA	35617
hPKU5_P9R52	TAGCGAACTGAGAAGGGCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCACTCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCA	35618
hPKU5_P9R53	TAGCGAACTGAGAAGGGCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTCACTCAAGCCTGTGGTTTTGGTCTTAGGAACTTTGCTGCCACAATACCTCGGCCCTTCTCA	35619
hPKU5_P9R6	TAGCGAACTGAGAAGGGCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCCTCGGCCCTTCTCA	35620
hPKU5_P9R7	TAGCGAACTGAGAAGGGCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCACCTCGGCCCTTCTCA	35621
hPKU5_P9R8	TAGCGAACTGAGAAGGGCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTACCTCGGCCCTTCTCA	35622
hPKU5_P9R9	TAGCGAACTGAGAAGGGCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCATACCTCGGCCCTTCTCA	35623

Table 5F. Exemplary template RNA sequences

Table 5F provides design of exemplary DNA components of gene modifying systems for correcting the pathogenic R408W mutation in PAH to the wild-type form. This table details the sequence of a complete template RNA for use in exemplary gene modifying systems comprising a gene modifying polypeptide. Templates in this table employ the hPKU6 spacer ACTTTGCTGCCACAATACCT (SEQ ID NO: 16032).

Name	tgRNA sequence	SEQ ID NO
hPKU6_P0R10	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAGGGCCGAGG	35624
hPKU6_P0R11	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAAGGGCCGAGG	35625
hPKU6_P0R12	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGAAGGGCCGAGG	35626

hPKU6_P0 R13	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCA CCGAGTCGGTGCAGAAGGGCCGAGG	35627
hPKU6_P0 R14	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCA CCGAGTCGGTGCGAGAAGGGCCGAGG	35628
hPKU6_P0 R15	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCA CCGAGTCGGTGCTGAGAAGGGCCGAGG	35629
hPKU6_P0 R16	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCA CCGAGTCGGTGCCTGAGAAGGGCCGAGG	35630
hPKU6_P0 R17	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCA CCGAGTCGGTGCACTGAGAAGGGCCGAGG	35631
hPKU6_P0 R18	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCA CCGAGTCGGTGCAACTGAGAAGGGCCGAGG	35632
hPKU6_P0 R19	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCA CCGAGTCGGTGCGAACTGAGAAGGGCCGAGG	35633
hPKU6_P0 R20	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCA CCGAGTCGGTGCCGAACTGAGAAGGGCCGAGG	35634
hPKU6_P0 R21	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCA CCGAGTCGGTGCGCGAACTGAGAAGGGCCGAGG	35635
hPKU6_P0 R22	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCA CCGAGTCGGTGCAGCGAACTGAGAAGGGCCGAGG	35636
hPKU6_P0 R23	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCA CCGAGTCGGTGCTAGCGAACTGAGAAGGGCCGAGG	35637
hPKU6_P0 R24	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCA CCGAGTCGGTGCGTAGCGAACTGAGAAGGGCCGAGG	35638
hPKU6_P0 R25	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCA CCGAGTCGGTGCCGTAGCGAACTGAGAAGGGCCGAGG	35639
hPKU6_P0 R26	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCA CCGAGTCGGTGCTCGTAGCGAACTGAGAAGGGCCGAGG	35640
hPKU6_P0 R27	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCA CCGAGTCGGTGCGTCGTAGCGAACTGAGAAGGGCCGAGG	35641
hPKU6_P0 R28	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCA CCGAGTCGGTGCGGTCGTAGCGAACTGAGAAGGGCCGAGG	35642
hPKU6_P0 R29	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCA CCGAGTCGGTGCGGGTCGTAGCGAACTGAGAAGGGCCGAGG	35643

hPKU6_P0R30	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGGGTCGTAGCGAACTGAGAAGGGCCGAGG	35644
hPKU6_P0R31	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCATGGGTCGTAGCGAACTGAGAAGGGCCGAGG	35645
hPKU6_P0R32	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTATGGGTCGTAGCGAACTGAGAAGGGCCGAGG	35646
hPKU6_P0R33	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGTATGGGTCGTAGCGAACTGAGAAGGGCCGAGG	35647
hPKU6_P0R34	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGTATGGGTCGTAGCGAACTGAGAAGGGCCGAGG	35648
hPKU6_P0R35	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGTGTATGGGTCGTAGCGAACTGAGAAGGGCCGAGG	35649
hPKU6_P0R36	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGGTGTATGGGTCGTAGCGAACTGAGAAGGGCCGAGG	35650
hPKU6_P0R37	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGGGTGTATGGGTCGTAGCGAACTGAGAAGGGCCGAGG	35651
hPKU6_P0R38	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGGGTGTATGGGTCGTAGCGAACTGAGAAGGGCCGAGG	35652
hPKU6_P0R39	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTGGGTGTATGGGTCGTAGCGAACTGAGAAGGGCCGAGG	35653
hPKU6_P0R4	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGAGG	35654
hPKU6_P0R40	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTTGGGTGTATGGGTCGTAGCGAACTGAGAAGGGCCGAGG	35655
hPKU6_P0R41	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTTTGGGTGTATGGGTCGTAGCGAACTGAGAAGGGCCGAGG	35656
hPKU6_P0R42	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCCTTTGGGTGTATGGGTCGTAGCGAACTGAGAAGGGCCGAGG	35657
hPKU6_P0R43	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTCCTTTGGGTGTATGGGTCGTAGCGAACTGAGAAGGGCCGAGG	35658
hPKU6_P0R44	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCATCCTTTGGGTGTATGGGTCGTAGCGAACTGAGAAGGGCCGAGG	35659
hPKU6_P0R45	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAATCCTTTGGGTGTATGGGTCGTAGCGAACTGAGAAGGGCCGAGG	35660

hPKU6_P0R46	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCAATCCTTTGGGTGTATGGGTCGTAGCGAACTGAGAAGGGCCGAGG	35661
hPKU6_P0R47	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTCAATCCTTTGGGTGTATGGGTCGTAGCGAACTGAGAAGGGCCGAGG	35662
hPKU6_P0R48	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTCAATCCTTTGGGTGTATGGGTCGTAGCGAACTGAGAAGGGCCGAGG	35663
hPKU6_P0R49	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCCTCAATCCTTTGGGTGTATGGGTCGTAGCGAACTGAGAAGGGCCGAGG	35664
hPKU6_P0R5	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCGAGG	35665
hPKU6_P0R50	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCACCTCAATCCTTTGGGTGTATGGGTCGTAGCGAACTGAGAAGGGCCGAGG	35666
hPKU6_P0R51	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGACCTCAATCCTTTGGGTGTATGGGTCGTAGCGAACTGAGAAGGGCCGAGG	35667
hPKU6_P0R52	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAGACCTCAATCCTTTGGGTGTATGGGTCGTAGCGAACTGAGAAGGGCCGAGG	35668
hPKU6_P0R53	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAAGACCTCAATCCTTTGGGTGTATGGGTCGTAGCGAACTGAGAAGGGCCGAGG	35669
hPKU6_P0R54	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCAAGACCTCAATCCTTTGGGTGTATGGGTCGTAGCGAACTGAGAAGGGCCGAGG	35670
hPKU6_P0R6	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCCGAGG	35671
hPKU6_P0R7	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGCCGAGG	35672
hPKU6_P0R8	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGGCCGAGG	35673
hPKU6_P0R9	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGGGCCGAGG	35674
hPKU6_P10R10	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAGGGCCGAGGTATTGTGGCA	35675
hPKU6_P10R11	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAAGGGCCGAGGTATTGTGGCA	35676
hPKU6_P10R12	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGAAGGGCCGAGGTATTGTGGCA	35677

hPKU6_P10R13	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAGAAGGGCCGAGGTATTGTGGCA	35678
hPKU6_P10R14	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGAGAAGGGCCGAGGTATTGTGGCA	35679
hPKU6_P10R15	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGAGAAGGGCCGAGGTATTGTGGCA	35680
hPKU6_P10R16	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTGAGAAGGGCCGAGGTATTGTGGCA	35681
hPKU6_P10R17	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCACTGAGAAGGGCCGAGGTATTGTGGCA	35682
hPKU6_P10R18	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAACTGAGAAGGGCCGAGGTATTGTGGCA	35683
hPKU6_P10R19	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGAACTGAGAAGGGCCGAGGTATTGTGGCA	35684
hPKU6_P10R20	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCGAACTGAGAAGGGCCGAGGTATTGTGGCA	35685
hPKU6_P10R21	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGCGAACTGAGAAGGGCCGAGGTATTGTGGCA	35686
hPKU6_P10R22	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAGCGAACTGAGAAGGGCCGAGGTATTGTGGCA	35687
hPKU6_P10R23	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTAGCGAACTGAGAAGGGCCGAGGTATTGTGGCA	35688
hPKU6_P10R24	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGTAGCGAACTGAGAAGGGCCGAGGTATTGTGGCA	35689
hPKU6_P10R25	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCGTAGCGAACTGAGAAGGGCCGAGGTATTGTGGCA	35690
hPKU6_P10R26	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTCGTAGCGAACTGAGAAGGGCCGAGGTATTGTGGCA	35691
hPKU6_P10R27	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGTCGTAGCGAACTGAGAAGGGCCGAGGTATTGTGGCA	35692
hPKU6_P10R28	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGGTCGTAGCGAACTGAGAAGGGCCGAGGTATTGTGGCA	35693
hPKU6_P10R29	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGGGTCGTAGCGAACTGAGAAGGGCCGAGGTATTGTGGCA	35694

hPKU6_P10R30	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGGGTCGTAGCGAACTGAGAAGGGCCGAGGTATTGTGGCA	35695
hPKU6_P10R31	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCATGGGTCGTAGCGAACTGAGAAGGGCCGAGGTATTGTGGCA	35696
hPKU6_P10R32	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTATGGGTCGTAGCGAACTGAGAAGGGCCGAGGTATTGTGGCA	35697
hPKU6_P10R33	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGTATGGGTCGTAGCGAACTGAGAAGGGCCGAGGTATTGTGGCA	35698
hPKU6_P10R34	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGTATGGGTCGTAGCGAACTGAGAAGGGCCGAGGTATTGTGGCA	35699
hPKU6_P10R35	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGTGTATGGGTCGTAGCGAACTGAGAAGGGCCGAGGTATTGTGGCA	35700
hPKU6_P10R36	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGGTGTATGGGTCGTAGCGAACTGAGAAGGGCCGAGGTATTGTGGCA	35701
hPKU6_P10R37	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGGGTGTATGGGTCGTAGCGAACTGAGAAGGGCCGAGGTATTGTGGCA	35702
hPKU6_P10R38	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGGGTGTATGGGTCGTAGCGAACTGAGAAGGGCCGAGGTATTGTGGCA	35703
hPKU6_P10R39	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTGGGTGTATGGGTCGTAGCGAACTGAGAAGGGCCGAGGTATTGTGGCA	35704
hPKU6_P10R4	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGAGGTATTGTGGCA	35705
hPKU6_P10R40	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTTGGGTGTATGGGTCGTAGCGAACTGAGAAGGGCCGAGGTATTGTGGCA	35706
hPKU6_P10R41	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTTTGGGTGTATGGGTCGTAGCGAACTGAGAAGGGCCGAGGTATTGTGGCA	35707
hPKU6_P10R42	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCCTTTGGGTGTATGGGTCGTAGCGAACTGAGAAGGGCCGAGGTATTGTGGCA	35708
hPKU6_P10R43	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTCCTTTGGGTGTATGGGTCGTAGCGAACTGAGAAGGGCCGAGGTATTGTGGCA	35709
hPKU6_P10R44	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCATCCTTTGGGTGTATGGGTCGTAGCGAACTGAGAAGGGCCGAGGTATTGTGGCA	35710
hPKU6_P10R45	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAATCCTTTGGGTGTATGGGTCGTAGCGAACTGAGAAGGGCCGAGGTATTGTGGCA	35711

hPKU6_P10R46	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCAATCCTTTGGGTGTATGGGTCGTAGCGAACTGAGAAGGGCCGAGGTATTGTGGCA	35712
hPKU6_P10R47	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTCAATCCTTTGGGTGTATGGGTCGTAGCGAACTGAGAAGGGCCGAGGTATTGTGGCA	35713
hPKU6_P10R48	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTCAATCCTTTGGGTGTATGGGTCGTAGCGAACTGAGAAGGGCCGAGGTATTGTGGCA	35714
hPKU6_P10R49	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCCTCAATCCTTTGGGTGTATGGGTCGTAGCGAACTGAGAAGGGCCGAGGTATTGTGGCA	35715
hPKU6_P10R5	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCGAGGTATTGTGGCA	35716
hPKU6_P10R50	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCACCTCAATCCTTTGGGTGTATGGGTCGTAGCGAACTGAGAAGGGCCGAGGTATTGTGGCA	35717
hPKU6_P10R51	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGACCTCAATCCTTTGGGTGTATGGGTCGTAGCGAACTGAGAAGGGCCGAGGTATTGTGGCA	35718
hPKU6_P10R52	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAGACCTCAATCCTTTGGGTGTATGGGTCGTAGCGAACTGAGAAGGGCCGAGGTATTGTGGCA	35719
hPKU6_P10R53	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAAGACCTCAATCCTTTGGGTGTATGGGTCGTAGCGAACTGAGAAGGGCCGAGGTATTGTGGCA	35720
hPKU6_P10R54	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCAAGACCTCAATCCTTTGGGTGTATGGGTCGTAGCGAACTGAGAAGGGCCGAGGTATTGTGGCA	35721
hPKU6_P10R6	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCCGAGGTATTGTGGCA	35722
hPKU6_P10R7	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGCCGAGGTATTGTGGCA	35723
hPKU6_P10R8	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGGCCGAGGTATTGTGGCA	35724
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hPKU6_P11R10	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAGGGCCGAGGTATTGTGGCAG	35726
hPKU6_P11R11	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAAGGGCCGAGGTATTGTGGCAG	35727
hPKU6_P11R12	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGAAGGGCCGAGGTATTGTGGCAG	35728

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hPKU6_P11R15	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGAGAAGGGCCGAGGTATTGTGGCAG	35731
hPKU6_P11R16	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTGAGAAGGGCCGAGGTATTGTGGCAG	35732
hPKU6_P11R17	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCACTGAGAAGGGCCGAGGTATTGTGGCAG	35733
hPKU6_P11R18	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAACTGAGAAGGGCCGAGGTATTGTGGCAG	35734
hPKU6_P11R19	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGAACTGAGAAGGGCCGAGGTATTGTGGCAG	35735
hPKU6_P11R20	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCGAACTGAGAAGGGCCGAGGTATTGTGGCAG	35736
hPKU6_P11R21	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGCGAACTGAGAAGGGCCGAGGTATTGTGGCAG	35737
hPKU6_P11R22	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAGCGAACTGAGAAGGGCCGAGGTATTGTGGCAG	35738
hPKU6_P11R23	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTAGCGAACTGAGAAGGGCCGAGGTATTGTGGCAG	35739
hPKU6_P11R24	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGTAGCGAACTGAGAAGGGCCGAGGTATTGTGGCAG	35740
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hPKU6_P11R26	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTCGTAGCGAACTGAGAAGGGCCGAGGTATTGTGGCAG	35742
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hPKU6_P11R28	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGGTCGTAGCGAACTGAGAAGGGCCGAGGTATTGTGGCAG	35744
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hPKU6_P11R30	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGGGTCGTAGCGAACTGAGAAGGGCCGAGGTATTGTGGCAG	35746
hPKU6_P11R31	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCATGGGTCGTAGCGAACTGAGAAGGGCCGAGGTATTGTGGCAG	35747
hPKU6_P11R32	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTATGGGTCGTAGCGAACTGAGAAGGGCCGAGGTATTGTGGCAG	35748
hPKU6_P11R33	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGTATGGGTCGTAGCGAACTGAGAAGGGCCGAGGTATTGTGGCAG	35749
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hPKU6_P11R44	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCATCCTTTGGGTGTATGGGTCGTAGCGAACTGAGAAGGGCCGAGGTATTGTGGCAG	35761
hPKU6_P11R45	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAATCCTTTGGGTGTATGGGTCGTAGCGAACTGAGAAGGGCCGAGGTATTGTGGCAG	35762

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hPKU6_P11R48	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTCAATCCTTTGGGTGTATGGGTCGTAGCGAACTGAGAAGGGCCGAGGTATTGTGGCAG	35765
hPKU6_P11R49	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCCTCAATCCTTTGGGTGTATGGGTCGTAGCGAACTGAGAAGGGCCGAGGTATTGTGGCAG	35766
hPKU6_P11R5	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCGAGGTATTGTGGCAG	35767
hPKU6_P11R50	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCACCTCAATCCTTTGGGTGTATGGGTCGTAGCGAACTGAGAAGGGCCGAGGTATTGTGGCAG	35768
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hPKU6_P12R15	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGAGAAGGGCCGAGGTATTGTGGCAGC	35782
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hPKU6_P12R20	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCGAACTGAGAAGGGCCGAGGTATTGTGGCAGC	35787
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hPKU6_P12R33	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGTATGGGTCGTAGCGAACTGAGAAGGGCCGAGGTATTGTGGCAGC	35800
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hPKU6_P12R4	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGAGGTATTGTGGCAGC	35807
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hPKU6_P12R42	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCCTTTGGGTGTATGGGTCGTAGCGAACTGAGAAGGGCCGAGGTATTGTGGCAGC	35810
hPKU6_P12R43	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTCCTTTGGGTGTATGGGTCGTAGCGAACTGAGAAGGGCCGAGGTATTGTGGCAGC	35811
hPKU6_P12R44	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCATCCTTTGGGTGTATGGGTCGTAGCGAACTGAGAAGGGCCGAGGTATTGTGGCAGC	35812
hPKU6_P12R45	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAATCCTTTGGGTGTATGGGTCGTAGCGAACTGAGAAGGGCCGAGGTATTGTGGCAGC	35813

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hPKU6_P12R47	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTCAATCCTTTGGGTGTATGGGTCGTAGCGAACTGAGAAGGGCCGAGGTATTGTGGCAGC	35815
hPKU6_P12R48	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTCAATCCTTTGGGTGTATGGGTCGTAGCGAACTGAGAAGGGCCGAGGTATTGTGGCAGC	35816
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hPKU6_P12R5	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCGAGGTATTGTGGCAGC	35818
hPKU6_P12R50	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCACCTCAATCCTTTGGGTGTATGGGTCGTAGCGAACTGAGAAGGGCCGAGGTATTGTGGCAGC	35819
hPKU6_P12R51	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGACCTCAATCCTTTGGGTGTATGGGTCGTAGCGAACTGAGAAGGGCCGAGGTATTGTGGCAGC	35820
hPKU6_P12R52	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAGACCTCAATCCTTTGGGTGTATGGGTCGTAGCGAACTGAGAAGGGCCGAGGTATTGTGGCAGC	35821
hPKU6_P12R53	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAAGACCTCAATCCTTTGGGTGTATGGGTCGTAGCGAACTGAGAAGGGCCGAGGTATTGTGGCAGC	35822
hPKU6_P12R54	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCAAGACCTCAATCCTTTGGGTGTATGGGTCGTAGCGAACTGAGAAGGGCCGAGGTATTGTGGCAGC	35823
hPKU6_P12R6	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCCGAGGTATTGTGGCAGC	35824
hPKU6_P12R7	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGCCGAGGTATTGTGGCAGC	35825
hPKU6_P12R8	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGGCCGAGGTATTGTGGCAGC	35826
hPKU6_P12R9	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGGGCCGAGGTATTGTGGCAGC	35827
hPKU6_P13R10	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAGGGCCGAGGTATTGTGGCAGCA	35828
hPKU6_P13R11	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAAGGGCCGAGGTATTGTGGCAGCA	35829
hPKU6_P13R12	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGAAGGGCCGAGGTATTGTGGCAGCA	35830

hPKU6_P13R13	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAGAAGGGCCGAGGTATTGTGGCAGCA	35831
hPKU6_P13R14	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGAGAAGGGCCGAGGTATTGTGGCAGCA	35832
hPKU6_P13R15	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGAGAAGGGCCGAGGTATTGTGGCAGCA	35833
hPKU6_P13R16	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTGAGAAGGGCCGAGGTATTGTGGCAGCA	35834
hPKU6_P13R17	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCACTGAGAAGGGCCGAGGTATTGTGGCAGCA	35835
hPKU6_P13R18	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAACTGAGAAGGGCCGAGGTATTGTGGCAGCA	35836
hPKU6_P13R19	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGAACTGAGAAGGGCCGAGGTATTGTGGCAGCA	35837
hPKU6_P13R20	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCGAACTGAGAAGGGCCGAGGTATTGTGGCAGCA	35838
hPKU6_P13R21	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGCGAACTGAGAAGGGCCGAGGTATTGTGGCAGCA	35839
hPKU6_P13R22	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAGCGAACTGAGAAGGGCCGAGGTATTGTGGCAGCA	35840
hPKU6_P13R23	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTAGCGAACTGAGAAGGGCCGAGGTATTGTGGCAGCA	35841
hPKU6_P13R24	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGTAGCGAACTGAGAAGGGCCGAGGTATTGTGGCAGCA	35842
hPKU6_P13R25	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCGTAGCGAACTGAGAAGGGCCGAGGTATTGTGGCAGCA	35843
hPKU6_P13R26	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTCGTAGCGAACTGAGAAGGGCCGAGGTATTGTGGCAGCA	35844
hPKU6_P13R27	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGTCGTAGCGAACTGAGAAGGGCCGAGGTATTGTGGCAGCA	35845
hPKU6_P13R28	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGGTCGTAGCGAACTGAGAAGGGCCGAGGTATTGTGGCAGCA	35846
hPKU6_P13R29	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGGGTCGTAGCGAACTGAGAAGGGCCGAGGTATTGTGGCAGCA	35847

hPKU6_P13R30	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGGGTCGTAGCGAACTGAGAAGGGCCGAGGTATTGTGGCAGCA	35848
hPKU6_P13R31	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCATGGGTCGTAGCGAACTGAGAAGGGCCGAGGTATTGTGGCAGCA	35849
hPKU6_P13R32	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTATGGGTCGTAGCGAACTGAGAAGGGCCGAGGTATTGTGGCAGCA	35850
hPKU6_P13R33	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGTATGGGTCGTAGCGAACTGAGAAGGGCCGAGGTATTGTGGCAGCA	35851
hPKU6_P13R34	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGTATGGGTCGTAGCGAACTGAGAAGGGCCGAGGTATTGTGGCAGCA	35852
hPKU6_P13R35	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGTGTATGGGTCGTAGCGAACTGAGAAGGGCCGAGGTATTGTGGCAGCA	35853
hPKU6_P13R36	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGGTGTATGGGTCGTAGCGAACTGAGAAGGGCCGAGGTATTGTGGCAGCA	35854
hPKU6_P13R37	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGGGTGTATGGGTCGTAGCGAACTGAGAAGGGCCGAGGTATTGTGGCAGCA	35855
hPKU6_P13R38	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGGGTGTATGGGTCGTAGCGAACTGAGAAGGGCCGAGGTATTGTGGCAGCA	35856
hPKU6_P13R39	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTGGGTGTATGGGTCGTAGCGAACTGAGAAGGGCCGAGGTATTGTGGCAGCA	35857
hPKU6_P13R4	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGAGGTATTGTGGCAGCA	35858
hPKU6_P13R40	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTTGGGTGTATGGGTCGTAGCGAACTGAGAAGGGCCGAGGTATTGTGGCAGCA	35859
hPKU6_P13R41	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTTTGGGTGTATGGGTCGTAGCGAACTGAGAAGGGCCGAGGTATTGTGGCAGCA	35860
hPKU6_P13R42	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCCTTTGGGTGTATGGGTCGTAGCGAACTGAGAAGGGCCGAGGTATTGTGGCAGCA	35861
hPKU6_P13R43	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTCCTTTGGGTGTATGGGTCGTAGCGAACTGAGAAGGGCCGAGGTATTGTGGCAGCA	35862
hPKU6_P13R44	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCATCCTTTGGGTGTATGGGTCGTAGCGAACTGAGAAGGGCCGAGGTATTGTGGCAGCA	35863
hPKU6_P13R45	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAATCCTTTGGGTGTATGGGTCGTAGCGAACTGAGAAGGGCCGAGGTATTGTGGCAGCA	35864

hPKU6_P13R46	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCAATCCTTTGGGTGTATGGGTCGTAGCGAACTGAGAAGGGCCGAGGTATTGTGGCAGCA	35865
hPKU6_P13R47	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTCAATCCTTTGGGTGTATGGGTCGTAGCGAACTGAGAAGGGCCGAGGTATTGTGGCAGCA	35866
hPKU6_P13R48	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTCAATCCTTTGGGTGTATGGGTCGTAGCGAACTGAGAAGGGCCGAGGTATTGTGGCAGCA	35867
hPKU6_P13R49	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCCTCAATCCTTTGGGTGTATGGGTCGTAGCGAACTGAGAAGGGCCGAGGTATTGTGGCAGCA	35868
hPKU6_P13R5	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCGAGGTATTGTGGCAGCA	35869
hPKU6_P13R50	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCACCTCAATCCTTTGGGTGTATGGGTCGTAGCGAACTGAGAAGGGCCGAGGTATTGTGGCAGCA	35870
hPKU6_P13R51	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGACCTCAATCCTTTGGGTGTATGGGTCGTAGCGAACTGAGAAGGGCCGAGGTATTGTGGCAGCA	35871
hPKU6_P13R52	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAGACCTCAATCCTTTGGGTGTATGGGTCGTAGCGAACTGAGAAGGGCCGAGGTATTGTGGCAGCA	35872
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hPKU6_P13R6	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCCGAGGTATTGTGGCAGCA	35875
hPKU6_P13R7	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGCCGAGGTATTGTGGCAGCA	35876
hPKU6_P13R8	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGGCCGAGGTATTGTGGCAGCA	35877
hPKU6_P13R9	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGGGCCGAGGTATTGTGGCAGCA	35878
hPKU6_P14R10	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAGGGCCGAGGTATTGTGGCAGCAA	35879
hPKU6_P14R11	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAAGGGCCGAGGTATTGTGGCAGCAA	35880
hPKU6_P14R12	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGAAGGGCCGAGGTATTGTGGCAGCAA	35881

hPKU6_P14R13	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAGAAGGGCCGAGGTATTGTGGCAGCAA	35882
hPKU6_P14R14	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGAGAAGGGCCGAGGTATTGTGGCAGCAA	35883
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hPKU6_P14R16	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTGAGAAGGGCCGAGGTATTGTGGCAGCAA	35885
hPKU6_P14R17	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCACTGAGAAGGGCCGAGGTATTGTGGCAGCAA	35886
hPKU6_P14R18	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAACTGAGAAGGGCCGAGGTATTGTGGCAGCAA	35887
hPKU6_P14R19	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGAACTGAGAAGGGCCGAGGTATTGTGGCAGCAA	35888
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hPKU6_P14R21	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGCGAACTGAGAAGGGCCGAGGTATTGTGGCAGCAA	35890
hPKU6_P14R22	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAGCGAACTGAGAAGGGCCGAGGTATTGTGGCAGCAA	35891
hPKU6_P14R23	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTAGCGAACTGAGAAGGGCCGAGGTATTGTGGCAGCAA	35892
hPKU6_P14R24	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGTAGCGAACTGAGAAGGGCCGAGGTATTGTGGCAGCAA	35893
hPKU6_P14R25	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCGTAGCGAACTGAGAAGGGCCGAGGTATTGTGGCAGCAA	35894
hPKU6_P14R26	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTCGTAGCGAACTGAGAAGGGCCGAGGTATTGTGGCAGCAA	35895
hPKU6_P14R27	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGTCGTAGCGAACTGAGAAGGGCCGAGGTATTGTGGCAGCAA	35896
hPKU6_P14R28	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGGTCGTAGCGAACTGAGAAGGGCCGAGGTATTGTGGCAGCAA	35897
hPKU6_P14R29	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGGGTCGTAGCGAACTGAGAAGGGCCGAGGTATTGTGGCAGCAA	35898

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hPKU6_P14R31	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCATGGGTCGTAGCGAACTGAGAAGGGCCGAGGTATTGTGGCAGCAA	35900
hPKU6_P14R32	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTATGGGTCGTAGCGAACTGAGAAGGGCCGAGGTATTGTGGCAGCAA	35901
hPKU6_P14R33	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGTATGGGTCGTAGCGAACTGAGAAGGGCCGAGGTATTGTGGCAGCAA	35902
hPKU6_P14R34	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGTATGGGTCGTAGCGAACTGAGAAGGGCCGAGGTATTGTGGCAGCAA	35903
hPKU6_P14R35	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGTGTATGGGTCGTAGCGAACTGAGAAGGGCCGAGGTATTGTGGCAGCAA	35904
hPKU6_P14R36	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGGTGTATGGGTCGTAGCGAACTGAGAAGGGCCGAGGTATTGTGGCAGCAA	35905
hPKU6_P14R37	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGGGTGTATGGGTCGTAGCGAACTGAGAAGGGCCGAGGTATTGTGGCAGCAA	35906
hPKU6_P14R38	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGGGTGTATGGGTCGTAGCGAACTGAGAAGGGCCGAGGTATTGTGGCAGCAA	35907
hPKU6_P14R39	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTGGGTGTATGGGTCGTAGCGAACTGAGAAGGGCCGAGGTATTGTGGCAGCAA	35908
hPKU6_P14R4	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGAGGTATTGTGGCAGCAA	35909
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hPKU6_P14R41	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTTTGGGTGTATGGGTCGTAGCGAACTGAGAAGGGCCGAGGTATTGTGGCAGCAA	35911
hPKU6_P14R42	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCCTTTGGGTGTATGGGTCGTAGCGAACTGAGAAGGGCCGAGGTATTGTGGCAGCAA	35912
hPKU6_P14R43	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTCCTTTGGGTGTATGGGTCGTAGCGAACTGAGAAGGGCCGAGGTATTGTGGCAGCAA	35913
hPKU6_P14R44	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCATCCTTTGGGTGTATGGGTCGTAGCGAACTGAGAAGGGCCGAGGTATTGTGGCAGCAA	35914
hPKU6_P14R45	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAATCCTTTGGGTGTATGGGTCGTAGCGAACTGAGAAGGGCCGAGGTATTGTGGCAGCAA	35915

hPKU6_P14R46	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCAATCCTTTGGGTGTATGGGTCGTAGCGAACTGAGAAGGGCCGAGGTATTGTGGCAGCAA	35916
hPKU6_P14R47	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTCAATCCTTTGGGTGTATGGGTCGTAGCGAACTGAGAAGGGCCGAGGTATTGTGGCAGCAA	35917
hPKU6_P14R48	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTCAATCCTTTGGGTGTATGGGTCGTAGCGAACTGAGAAGGGCCGAGGTATTGTGGCAGCAA	35918
hPKU6_P14R49	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCCTCAATCCTTTGGGTGTATGGGTCGTAGCGAACTGAGAAGGGCCGAGGTATTGTGGCAGCAA	35919
hPKU6_P14R5	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCGAGGTATTGTGGCAGCAA	35920
hPKU6_P14R50	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCACCTCAATCCTTTGGGTGTATGGGTCGTAGCGAACTGAGAAGGGCCGAGGTATTGTGGCAGCAA	35921
hPKU6_P14R51	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGACCTCAATCCTTTGGGTGTATGGGTCGTAGCGAACTGAGAAGGGCCGAGGTATTGTGGCAGCAA	35922
hPKU6_P14R52	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAGACCTCAATCCTTTGGGTGTATGGGTCGTAGCGAACTGAGAAGGGCCGAGGTATTGTGGCAGCAA	35923
hPKU6_P14R53	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAAGACCTCAATCCTTTGGGTGTATGGGTCGTAGCGAACTGAGAAGGGCCGAGGTATTGTGGCAGCAA	35924
hPKU6_P14R54	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCAAGACCTCAATCCTTTGGGTGTATGGGTCGTAGCGAACTGAGAAGGGCCGAGGTATTGTGGCAGCAA	35925
hPKU6_P14R6	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCCGAGGTATTGTGGCAGCAA	35926
hPKU6_P14R7	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGCCGAGGTATTGTGGCAGCAA	35927
hPKU6_P14R8	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGGCCGAGGTATTGTGGCAGCAA	35928
hPKU6_P14R9	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGGGCCGAGGTATTGTGGCAGCAA	35929
hPKU6_P15R10	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAGGGCCGAGGTATTGTGGCAGCAAA	35930
hPKU6_P15R11	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAAGGGCCGAGGTATTGTGGCAGCAAA	35931
hPKU6_P15R12	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGAAGGGCCGAGGTATTGTGGCAGCAAA	35932

hPKU6_P15R13	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAGAAGGGCCGAGGTATTGTGGCAGCAAA	35933
hPKU6_P15R14	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGAGAAGGGCCGAGGTATTGTGGCAGCAAA	35934
hPKU6_P15R15	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGAGAAGGGCCGAGGTATTGTGGCAGCAAA	35935
hPKU6_P15R16	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTGAGAAGGGCCGAGGTATTGTGGCAGCAAA	35936
hPKU6_P15R17	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCACTGAGAAGGGCCGAGGTATTGTGGCAGCAAA	35937
hPKU6_P15R18	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAACTGAGAAGGGCCGAGGTATTGTGGCAGCAAA	35938
hPKU6_P15R19	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGAACTGAGAAGGGCCGAGGTATTGTGGCAGCAAA	35939
hPKU6_P15R20	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCGAACTGAGAAGGGCCGAGGTATTGTGGCAGCAAA	35940
hPKU6_P15R21	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGCGAACTGAGAAGGGCCGAGGTATTGTGGCAGCAAA	35941
hPKU6_P15R22	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAGCGAACTGAGAAGGGCCGAGGTATTGTGGCAGCAAA	35942
hPKU6_P15R23	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTAGCGAACTGAGAAGGGCCGAGGTATTGTGGCAGCAAA	35943
hPKU6_P15R24	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGTAGCGAACTGAGAAGGGCCGAGGTATTGTGGCAGCAAA	35944
hPKU6_P15R25	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCGTAGCGAACTGAGAAGGGCCGAGGTATTGTGGCAGCAAA	35945
hPKU6_P15R26	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTCGTAGCGAACTGAGAAGGGCCGAGGTATTGTGGCAGCAAA	35946
hPKU6_P15R27	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGTCGTAGCGAACTGAGAAGGGCCGAGGTATTGTGGCAGCAAA	35947
hPKU6_P15R28	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGGTCGTAGCGAACTGAGAAGGGCCGAGGTATTGTGGCAGCAAA	35948
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hPKU6_P15R30	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGGGTCGTAGCGAACTGAGAAGGGCCGAGGTATTGTGGCAGCAAA	35950
hPKU6_P15R31	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCATGGGTCGTAGCGAACTGAGAAGGGCCGAGGTATTGTGGCAGCAAA	35951
hPKU6_P15R32	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTATGGGTCGTAGCGAACTGAGAAGGGCCGAGGTATTGTGGCAGCAAA	35952
hPKU6_P15R33	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGTATGGGTCGTAGCGAACTGAGAAGGGCCGAGGTATTGTGGCAGCAAA	35953
hPKU6_P15R34	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGTATGGGTCGTAGCGAACTGAGAAGGGCCGAGGTATTGTGGCAGCAAA	35954
hPKU6_P15R35	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGTGTATGGGTCGTAGCGAACTGAGAAGGGCCGAGGTATTGTGGCAGCAAA	35955
hPKU6_P15R36	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGGTGTATGGGTCGTAGCGAACTGAGAAGGGCCGAGGTATTGTGGCAGCAAA	35956
hPKU6_P15R37	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGGGTGTATGGGTCGTAGCGAACTGAGAAGGGCCGAGGTATTGTGGCAGCAAA	35957
hPKU6_P15R38	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGGGTGTATGGGTCGTAGCGAACTGAGAAGGGCCGAGGTATTGTGGCAGCAAA	35958
hPKU6_P15R39	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTGGGTGTATGGGTCGTAGCGAACTGAGAAGGGCCGAGGTATTGTGGCAGCAAA	35959
hPKU6_P15R4	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGAGGTATTGTGGCAGCAAA	35960
hPKU6_P15R40	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTTGGGTGTATGGGTCGTAGCGAACTGAGAAGGGCCGAGGTATTGTGGCAGCAAA	35961
hPKU6_P15R41	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTTTGGGTGTATGGGTCGTAGCGAACTGAGAAGGGCCGAGGTATTGTGGCAGCAAA	35962
hPKU6_P15R42	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCCTTTGGGTGTATGGGTCGTAGCGAACTGAGAAGGGCCGAGGTATTGTGGCAGCAAA	35963
hPKU6_P15R43	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTCCTTTGGGTGTATGGGTCGTAGCGAACTGAGAAGGGCCGAGGTATTGTGGCAGCAAA	35964
hPKU6_P15R44	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCATCCTTTGGGTGTATGGGTCGTAGCGAACTGAGAAGGGCCGAGGTATTGTGGCAGCAAA	35965
hPKU6_P15R45	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAATCCTTTGGGTGTATGGGTCGTAGCGAACTGAGAAGGGCCGAGGTATTGTGGCAGCAAA	35966

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hPKU6_P15R48	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTCAATCCTTTGGGTGTATGGGTCGTAGCGAACTGAGAAGGGCCGAGGTATTGTGGCAGCAAA	35969
hPKU6_P15R49	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCCTCAATCCTTTGGGTGTATGGGTCGTAGCGAACTGAGAAGGGCCGAGGTATTGTGGCAGCAAA	35970
hPKU6_P15R5	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCGAGGTATTGTGGCAGCAAA	35971
hPKU6_P15R50	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCACCTCAATCCTTTGGGTGTATGGGTCGTAGCGAACTGAGAAGGGCCGAGGTATTGTGGCAGCAAA	35972
hPKU6_P15R51	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGACCTCAATCCTTTGGGTGTATGGGTCGTAGCGAACTGAGAAGGGCCGAGGTATTGTGGCAGCAAA	35973
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hPKU6_P16R11	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAAGGGCCGAGGTATTGTGGCAGCAAAG	35982
hPKU6_P16R12	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGAAGGGCCGAGGTATTGTGGCAGCAAAG	35983

hPKU6_P16R13	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAGAAGGGCCGAGGTATTGTGGCAGCAAAG	35984
hPKU6_P16R14	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGAGAAGGGCCGAGGTATTGTGGCAGCAAAG	35985
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hPKU6_P16R16	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTGAGAAGGGCCGAGGTATTGTGGCAGCAAAG	35987
hPKU6_P16R17	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCACTGAGAAGGGCCGAGGTATTGTGGCAGCAAAG	35988
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hPKU6_P16R19	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGAACTGAGAAGGGCCGAGGTATTGTGGCAGCAAAG	35990
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hPKU6_P16R22	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAGCGAACTGAGAAGGGCCGAGGTATTGTGGCAGCAAAG	35993
hPKU6_P16R23	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTAGCGAACTGAGAAGGGCCGAGGTATTGTGGCAGCAAAG	35994
hPKU6_P16R24	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGTAGCGAACTGAGAAGGGCCGAGGTATTGTGGCAGCAAAG	35995
hPKU6_P16R25	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCGTAGCGAACTGAGAAGGGCCGAGGTATTGTGGCAGCAAAG	35996
hPKU6_P16R26	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTCGTAGCGAACTGAGAAGGGCCGAGGTATTGTGGCAGCAAAG	35997
hPKU6_P16R27	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGTCGTAGCGAACTGAGAAGGGCCGAGGTATTGTGGCAGCAAAG	35998
hPKU6_P16R28	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGGTCGTAGCGAACTGAGAAGGGCCGAGGTATTGTGGCAGCAAAG	35999
hPKU6_P16R29	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGGGTCGTAGCGAACTGAGAAGGGCCGAGGTATTGTGGCAGCAAAG	36000

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hPKU6_P16R31	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCATGGGTCGTAGCGAACTGAGAAGGGCCGAGGTATTGTGGCAGCAAAG	36002
hPKU6_P16R32	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTATGGGTCGTAGCGAACTGAGAAGGGCCGAGGTATTGTGGCAGCAAAG	36003
hPKU6_P16R33	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGTATGGGTCGTAGCGAACTGAGAAGGGCCGAGGTATTGTGGCAGCAAAG	36004
hPKU6_P16R34	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGTATGGGTCGTAGCGAACTGAGAAGGGCCGAGGTATTGTGGCAGCAAAG	36005
hPKU6_P16R35	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGTGTATGGGTCGTAGCGAACTGAGAAGGGCCGAGGTATTGTGGCAGCAAAG	36006
hPKU6_P16R36	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGGTGTATGGGTCGTAGCGAACTGAGAAGGGCCGAGGTATTGTGGCAGCAAAG	36007
hPKU6_P16R37	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGGGTGTATGGGTCGTAGCGAACTGAGAAGGGCCGAGGTATTGTGGCAGCAAAG	36008
hPKU6_P16R38	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGGGTGTATGGGTCGTAGCGAACTGAGAAGGGCCGAGGTATTGTGGCAGCAAAG	36009
hPKU6_P16R39	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTGGGTGTATGGGTCGTAGCGAACTGAGAAGGGCCGAGGTATTGTGGCAGCAAAG	36010
hPKU6_P16R4	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGAGGTATTGTGGCAGCAAAG	36011
hPKU6_P16R40	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTTGGGTGTATGGGTCGTAGCGAACTGAGAAGGGCCGAGGTATTGTGGCAGCAAAG	36012
hPKU6_P16R41	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTTTGGGTGTATGGGTCGTAGCGAACTGAGAAGGGCCGAGGTATTGTGGCAGCAAAG	36013
hPKU6_P16R42	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCCTTTGGGTGTATGGGTCGTAGCGAACTGAGAAGGGCCGAGGTATTGTGGCAGCAAAG	36014
hPKU6_P16R43	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTCCTTTGGGTGTATGGGTCGTAGCGAACTGAGAAGGGCCGAGGTATTGTGGCAGCAAAG	36015
hPKU6_P16R44	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCATCCTTTGGGTGTATGGGTCGTAGCGAACTGAGAAGGGCCGAGGTATTGTGGCAGCAAAG	36016
hPKU6_P16R45	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAATCCTTTGGGTGTATGGGTCGTAGCGAACTGAGAAGGGCCGAGGTATTGTGGCAGCAAAG	36017

hPKU6_P16R46	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCAATCCTTTGGGTGTATGGGTCGTAGCGAACTGAGAAGGGCCGAGGTATTGTGGCAGCAAAG	36018
hPKU6_P16R47	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTCAATCCTTTGGGTGTATGGGTCGTAGCGAACTGAGAAGGGCCGAGGTATTGTGGCAGCAAAG	36019
hPKU6_P16R48	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTCAATCCTTTGGGTGTATGGGTCGTAGCGAACTGAGAAGGGCCGAGGTATTGTGGCAGCAAAG	36020
hPKU6_P16R49	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCCTCAATCCTTTGGGTGTATGGGTCGTAGCGAACTGAGAAGGGCCGAGGTATTGTGGCAGCAAAG	36021
hPKU6_P16R5	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCGAGGTATTGTGGCAGCAAAG	36022
hPKU6_P16R50	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCACCTCAATCCTTTGGGTGTATGGGTCGTAGCGAACTGAGAAGGGCCGAGGTATTGTGGCAGCAAAG	36023
hPKU6_P16R51	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGACCTCAATCCTTTGGGTGTATGGGTCGTAGCGAACTGAGAAGGGCCGAGGTATTGTGGCAGCAAAG	36024
hPKU6_P16R52	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAGACCTCAATCCTTTGGGTGTATGGGTCGTAGCGAACTGAGAAGGGCCGAGGTATTGTGGCAGCAAAG	36025
hPKU6_P16R53	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAAGACCTCAATCCTTTGGGTGTATGGGTCGTAGCGAACTGAGAAGGGCCGAGGTATTGTGGCAGCAAAG	36026
hPKU6_P16R54	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCAAGACCTCAATCCTTTGGGTGTATGGGTCGTAGCGAACTGAGAAGGGCCGAGGTATTGTGGCAGCAAAG	36027
hPKU6_P16R6	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCCGAGGTATTGTGGCAGCAAAG	36028
hPKU6_P16R7	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGCCGAGGTATTGTGGCAGCAAAG	36029
hPKU6_P16R8	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGGCCGAGGTATTGTGGCAGCAAAG	36030
hPKU6_P16R9	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGGGCCGAGGTATTGTGGCAGCAAAG	36031
hPKU6_P17R10	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAGGGCCGAGGTATTGTGGCAGCAAAGT	36032
hPKU6_P17R11	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAAGGGCCGAGGTATTGTGGCAGCAAAGT	36033
hPKU6_P17R12	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGAAGGGCCGAGGTATTGTGGCAGCAAAGT	36034

hPKU6_P17R13	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAGAAGGGCCGAGGTATTGTGGCAGCAAAGT	36035
hPKU6_P17R14	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGAGAAGGGCCGAGGTATTGTGGCAGCAAAGT	36036
hPKU6_P17R15	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGAGAAGGGCCGAGGTATTGTGGCAGCAAAGT	36037
hPKU6_P17R16	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTGAGAAGGGCCGAGGTATTGTGGCAGCAAAGT	36038
hPKU6_P17R17	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCACTGAGAAGGGCCGAGGTATTGTGGCAGCAAAGT	36039
hPKU6_P17R18	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAACTGAGAAGGGCCGAGGTATTGTGGCAGCAAAGT	36040
hPKU6_P17R19	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGAACTGAGAAGGGCCGAGGTATTGTGGCAGCAAAGT	36041
hPKU6_P17R20	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCGAACTGAGAAGGGCCGAGGTATTGTGGCAGCAAAGT	36042
hPKU6_P17R21	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGCGAACTGAGAAGGGCCGAGGTATTGTGGCAGCAAAGT	36043
hPKU6_P17R22	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAGCGAACTGAGAAGGGCCGAGGTATTGTGGCAGCAAAGT	36044
hPKU6_P17R23	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTAGCGAACTGAGAAGGGCCGAGGTATTGTGGCAGCAAAGT	36045
hPKU6_P17R24	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGTAGCGAACTGAGAAGGGCCGAGGTATTGTGGCAGCAAAGT	36046
hPKU6_P17R25	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCGTAGCGAACTGAGAAGGGCCGAGGTATTGTGGCAGCAAAGT	36047
hPKU6_P17R26	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTCGTAGCGAACTGAGAAGGGCCGAGGTATTGTGGCAGCAAAGT	36048
hPKU6_P17R27	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGTCGTAGCGAACTGAGAAGGGCCGAGGTATTGTGGCAGCAAAGT	36049
hPKU6_P17R28	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGGTCGTAGCGAACTGAGAAGGGCCGAGGTATTGTGGCAGCAAAGT	36050
hPKU6_P17R29	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGGGTCGTAGCGAACTGAGAAGGGCCGAGGTATTGTGGCAGCAAAGT	36051

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hPKU6_P17R31	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCATGGGTCGTAGCGAACTGAGAAGGGCCGAGGTATTGTGGCAGCAAAGT	36053
hPKU6_P17R32	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTATGGGTCGTAGCGAACTGAGAAGGGCCGAGGTATTGTGGCAGCAAAGT	36054
hPKU6_P17R33	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGTATGGGTCGTAGCGAACTGAGAAGGGCCGAGGTATTGTGGCAGCAAAGT	36055
hPKU6_P17R34	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGTATGGGTCGTAGCGAACTGAGAAGGGCCGAGGTATTGTGGCAGCAAAGT	36056
hPKU6_P17R35	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGTGTATGGGTCGTAGCGAACTGAGAAGGGCCGAGGTATTGTGGCAGCAAAGT	36057
hPKU6_P17R36	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGGTGTATGGGTCGTAGCGAACTGAGAAGGGCCGAGGTATTGTGGCAGCAAAGT	36058
hPKU6_P17R37	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGGGTGTATGGGTCGTAGCGAACTGAGAAGGGCCGAGGTATTGTGGCAGCAAAGT	36059
hPKU6_P17R38	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGGGTGTATGGGTCGTAGCGAACTGAGAAGGGCCGAGGTATTGTGGCAGCAAAGT	36060
hPKU6_P17R39	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTGGGTGTATGGGTCGTAGCGAACTGAGAAGGGCCGAGGTATTGTGGCAGCAAAGT	36061
hPKU6_P17R4	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGAGGTATTGTGGCAGCAAAGT	36062
hPKU6_P17R40	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTTGGGTGTATGGGTCGTAGCGAACTGAGAAGGGCCGAGGTATTGTGGCAGCAAAGT	36063
hPKU6_P17R41	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTTTGGGTGTATGGGTCGTAGCGAACTGAGAAGGGCCGAGGTATTGTGGCAGCAAAGT	36064
hPKU6_P17R42	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCCTTTGGGTGTATGGGTCGTAGCGAACTGAGAAGGGCCGAGGTATTGTGGCAGCAAAGT	36065
hPKU6_P17R43	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTCCTTTGGGTGTATGGGTCGTAGCGAACTGAGAAGGGCCGAGGTATTGTGGCAGCAAAGT	36066
hPKU6_P17R44	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCATCCTTTGGGTGTATGGGTCGTAGCGAACTGAGAAGGGCCGAGGTATTGTGGCAGCAAAGT	36067
hPKU6_P17R45	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAATCCTTTGGGTGTATGGGTCGTAGCGAACTGAGAAGGGCCGAGGTATTGTGGCAGCAAAGT	36068

hPKU6_P17R46	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCAATCCTTTGGGTGTATGGGTCGTAGCGAACTGAGAAGGGCCGAGGTATTGTGGCAGCAAAGT	36069
hPKU6_P17R47	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTCAATCCTTTGGGTGTATGGGTCGTAGCGAACTGAGAAGGGCCGAGGTATTGTGGCAGCAAAGT	36070
hPKU6_P17R48	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTCAATCCTTTGGGTGTATGGGTCGTAGCGAACTGAGAAGGGCCGAGGTATTGTGGCAGCAAAGT	36071
hPKU6_P17R49	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCCTCAATCCTTTGGGTGTATGGGTCGTAGCGAACTGAGAAGGGCCGAGGTATTGTGGCAGCAAAGT	36072
hPKU6_P17R5	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCGAGGTATTGTGGCAGCAAAGT	36073
hPKU6_P17R50	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCACCTCAATCCTTTGGGTGTATGGGTCGTAGCGAACTGAGAAGGGCCGAGGTATTGTGGCAGCAAAGT	36074
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hPKU6_P17R52	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAGACCTCAATCCTTTGGGTGTATGGGTCGTAGCGAACTGAGAAGGGCCGAGGTATTGTGGCAGCAAAGT	36076
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hPKU6_P1R14	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGAGAAGGGCCGAGGT	36087
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hPKU6_P1R25	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCGTAGCGAACTGAGAAGGGCCGAGGT	36098
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hPKU6_P1R31	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCATGGGTCGTAGCGAACTGAGAAGGGCCGAGGT	36104
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hPKU6_P1R34	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGTATGGGTCGTAGCGAACTGAGAAGGGCCGAGGT	36107
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hPKU6_P1R36	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGGTGTATGGGTCGTAGCGAACTGAGAAGGGCCGAGGT	36109
hPKU6_P1R37	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGGGTGTATGGGTCGTAGCGAACTGAGAAGGGCCGAGGT	36110
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hPKU6_P1R40	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTTGGGTGTATGGGTCGTAGCGAACTGAGAAGGGCCGAGGT	36114
hPKU6_P1R41	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTTTGGGTGTATGGGTCGTAGCGAACTGAGAAGGGCCGAGGT	36115
hPKU6_P1R42	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCCTTTGGGTGTATGGGTCGTAGCGAACTGAGAAGGGCCGAGGT	36116
hPKU6_P1R43	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTCCTTTGGGTGTATGGGTCGTAGCGAACTGAGAAGGGCCGAGGT	36117
hPKU6_P1R44	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCATCCTTTGGGTGTATGGGTCGTAGCGAACTGAGAAGGGCCGAGGT	36118

hPKU6_P1R45	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAATCCTTTGGGTGTATGGGTCGTAGCGAACTGAGAAGGGCCGAGGT	36119
hPKU6_P1R46	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCAATCCTTTGGGTGTATGGGTCGTAGCGAACTGAGAAGGGCCGAGGT	36120
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hPKU6_P1R48	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTCAATCCTTTGGGTGTATGGGTCGTAGCGAACTGAGAAGGGCCGAGGT	36122
hPKU6_P1R49	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCCTCAATCCTTTGGGTGTATGGGTCGTAGCGAACTGAGAAGGGCCGAGGT	36123
hPKU6_P1R5	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCGAGGT	36124
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hPKU6_P2R11	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAAGGGCCGAGGTA	36135

hPKU6_P2R12	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGAAGGGCCGAGGTA	36136
hPKU6_P2R13	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAGAAGGGCCGAGGTA	36137
hPKU6_P2R14	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGAGAAGGGCCGAGGTA	36138
hPKU6_P2R15	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGAGAAGGGCCGAGGTA	36139
hPKU6_P2R16	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTGAGAAGGGCCGAGGTA	36140
hPKU6_P2R17	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCACTGAGAAGGGCCGAGGTA	36141
hPKU6_P2R18	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAACTGAGAAGGGCCGAGGTA	36142
hPKU6_P2R19	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGAACTGAGAAGGGCCGAGGTA	36143
hPKU6_P2R20	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCGAACTGAGAAGGGCCGAGGTA	36144
hPKU6_P2R21	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGCGAACTGAGAAGGGCCGAGGTA	36145
hPKU6_P2R22	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAGCGAACTGAGAAGGGCCGAGGTA	36146
hPKU6_P2R23	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTAGCGAACTGAGAAGGGCCGAGGTA	36147
hPKU6_P2R24	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGTAGCGAACTGAGAAGGGCCGAGGTA	36148
hPKU6_P2R25	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCGTAGCGAACTGAGAAGGGCCGAGGTA	36149
hPKU6_P2R26	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTCGTAGCGAACTGAGAAGGGCCGAGGTA	36150
hPKU6_P2R27	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGTCGTAGCGAACTGAGAAGGGCCGAGGTA	36151
hPKU6_P2R28	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGGTCGTAGCGAACTGAGAAGGGCCGAGGTA	36152

hPKU6_P2R29	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGGGTCGTAGCGAACTGAGAAGGGCCGAGGTA	36153
hPKU6_P2R30	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGGGTCGTAGCGAACTGAGAAGGGCCGAGGTA	36154
hPKU6_P2R31	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCATGGGTCGTAGCGAACTGAGAAGGGCCGAGGTA	36155
hPKU6_P2R32	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTATGGGTCGTAGCGAACTGAGAAGGGCCGAGGTA	36156
hPKU6_P2R33	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGTATGGGTCGTAGCGAACTGAGAAGGGCCGAGGTA	36157
hPKU6_P2R34	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGTATGGGTCGTAGCGAACTGAGAAGGGCCGAGGTA	36158
hPKU6_P2R35	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGTGTATGGGTCGTAGCGAACTGAGAAGGGCCGAGGTA	36159
hPKU6_P2R36	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGGTGTATGGGTCGTAGCGAACTGAGAAGGGCCGAGGTA	36160
hPKU6_P2R37	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGGGTGTATGGGTCGTAGCGAACTGAGAAGGGCCGAGGTA	36161
hPKU6_P2R38	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGGGTGTATGGGTCGTAGCGAACTGAGAAGGGCCGAGGTA	36162
hPKU6_P2R39	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTGGGTGTATGGGTCGTAGCGAACTGAGAAGGGCCGAGGTA	36163
hPKU6_P2R4	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGAGGTA	36164
hPKU6_P2R40	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTTGGGTGTATGGGTCGTAGCGAACTGAGAAGGGCCGAGGTA	36165
hPKU6_P2R41	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTTTGGGTGTATGGGTCGTAGCGAACTGAGAAGGGCCGAGGTA	36166
hPKU6_P2R42	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCCTTTGGGTGTATGGGTCGTAGCGAACTGAGAAGGGCCGAGGTA	36167
hPKU6_P2R43	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTCCTTTGGGTGTATGGGTCGTAGCGAACTGAGAAGGGCCGAGGTA	36168
hPKU6_P2R44	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCATCCTTTGGGTGTATGGGTCGTAGCGAACTGAGAAGGGCCGAGGTA	36169

hPKU6_P2R45	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAATCCTTTGGGTGTATGGGTCGTAGCGAACTGAGAAGGGCCGAGGTA	36170
hPKU6_P2R46	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCAATCCTTTGGGTGTATGGGTCGTAGCGAACTGAGAAGGGCCGAGGTA	36171
hPKU6_P2R47	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTCAATCCTTTGGGTGTATGGGTCGTAGCGAACTGAGAAGGGCCGAGGTA	36172
hPKU6_P2R48	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTCAATCCTTTGGGTGTATGGGTCGTAGCGAACTGAGAAGGGCCGAGGTA	36173
hPKU6_P2R49	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCCTCAATCCTTTGGGTGTATGGGTCGTAGCGAACTGAGAAGGGCCGAGGTA	36174
hPKU6_P2R5	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCGAGGTA	36175
hPKU6_P2R50	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCACCTCAATCCTTTGGGTGTATGGGTCGTAGCGAACTGAGAAGGGCCGAGGTA	36176
hPKU6_P2R51	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGACCTCAATCCTTTGGGTGTATGGGTCGTAGCGAACTGAGAAGGGCCGAGGTA	36177
hPKU6_P2R52	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAGACCTCAATCCTTTGGGTGTATGGGTCGTAGCGAACTGAGAAGGGCCGAGGTA	36178
hPKU6_P2R53	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAAGACCTCAATCCTTTGGGTGTATGGGTCGTAGCGAACTGAGAAGGGCCGAGGTA	36179
hPKU6_P2R54	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCAAGACCTCAATCCTTTGGGTGTATGGGTCGTAGCGAACTGAGAAGGGCCGAGGTA	36180
hPKU6_P2R6	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCCGAGGTA	36181
hPKU6_P2R7	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGCCGAGGTA	36182
hPKU6_P2R8	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGGCCGAGGTA	36183
hPKU6_P2R9	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGGGCCGAGGTA	36184
hPKU6_P3R10	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAGGGCCGAGGTAT	36185
hPKU6_P3R11	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAAGGGCCGAGGTAT	36186

hPKU6_P3R12	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGAAGGGCCGAGGTAT	36187
hPKU6_P3R13	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAGAAGGGCCGAGGTAT	36188
hPKU6_P3R14	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGAGAAGGGCCGAGGTAT	36189
hPKU6_P3R15	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGAGAAGGGCCGAGGTAT	36190
hPKU6_P3R16	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTGAGAAGGGCCGAGGTAT	36191
hPKU6_P3R17	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCACTGAGAAGGGCCGAGGTAT	36192
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hPKU6_P3R19	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGAACTGAGAAGGGCCGAGGTAT	36194
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hPKU6_P3R22	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAGCGAACTGAGAAGGGCCGAGGTAT	36197
hPKU6_P3R23	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTAGCGAACTGAGAAGGGCCGAGGTAT	36198
hPKU6_P3R24	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGTAGCGAACTGAGAAGGGCCGAGGTAT	36199
hPKU6_P3R25	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCGTAGCGAACTGAGAAGGGCCGAGGTAT	36200
hPKU6_P3R26	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTCGTAGCGAACTGAGAAGGGCCGAGGTAT	36201
hPKU6_P3R27	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGTCGTAGCGAACTGAGAAGGGCCGAGGTAT	36202
hPKU6_P3R28	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGGTCGTAGCGAACTGAGAAGGGCCGAGGTAT	36203

hPKU6_P3R29	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGGGTCGTAGCGAACTGAGAAGGGCCGAGGTAT	36204
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hPKU6_P3R31	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCATGGGTCGTAGCGAACTGAGAAGGGCCGAGGTAT	36206
hPKU6_P3R32	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTATGGGTCGTAGCGAACTGAGAAGGGCCGAGGTAT	36207
hPKU6_P3R33	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGTATGGGTCGTAGCGAACTGAGAAGGGCCGAGGTAT	36208
hPKU6_P3R34	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGTATGGGTCGTAGCGAACTGAGAAGGGCCGAGGTAT	36209
hPKU6_P3R35	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGTGTATGGGTCGTAGCGAACTGAGAAGGGCCGAGGTAT	36210
hPKU6_P3R36	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGGTGTATGGGTCGTAGCGAACTGAGAAGGGCCGAGGTAT	36211
hPKU6_P3R37	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGGGTGTATGGGTCGTAGCGAACTGAGAAGGGCCGAGGTAT	36212
hPKU6_P3R38	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGGGTGTATGGGTCGTAGCGAACTGAGAAGGGCCGAGGTAT	36213
hPKU6_P3R39	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTGGGTGTATGGGTCGTAGCGAACTGAGAAGGGCCGAGGTAT	36214
hPKU6_P3R4	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGAGGTAT	36215
hPKU6_P3R40	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTTGGGTGTATGGGTCGTAGCGAACTGAGAAGGGCCGAGGTAT	36216
hPKU6_P3R41	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTTTGGGTGTATGGGTCGTAGCGAACTGAGAAGGGCCGAGGTAT	36217
hPKU6_P3R42	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCCTTTGGGTGTATGGGTCGTAGCGAACTGAGAAGGGCCGAGGTAT	36218
hPKU6_P3R43	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTCCTTTGGGTGTATGGGTCGTAGCGAACTGAGAAGGGCCGAGGTAT	36219
hPKU6_P3R44	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCATCCTTTGGGTGTATGGGTCGTAGCGAACTGAGAAGGGCCGAGGTAT	36220

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hPKU6_P3R47	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTCAATCCTTTGGGTGTATGGGTCGTAGCGAACTGAGAAGGGCCGAGGTAT	36223
hPKU6_P3R48	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTCAATCCTTTGGGTGTATGGGTCGTAGCGAACTGAGAAGGGCCGAGGTAT	36224
hPKU6_P3R49	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCCTCAATCCTTTGGGTGTATGGGTCGTAGCGAACTGAGAAGGGCCGAGGTAT	36225
hPKU6_P3R5	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCGAGGTAT	36226
hPKU6_P3R50	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCACCTCAATCCTTTGGGTGTATGGGTCGTAGCGAACTGAGAAGGGCCGAGGTAT	36227
hPKU6_P3R51	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGACCTCAATCCTTTGGGTGTATGGGTCGTAGCGAACTGAGAAGGGCCGAGGTAT	36228
hPKU6_P3R52	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAGACCTCAATCCTTTGGGTGTATGGGTCGTAGCGAACTGAGAAGGGCCGAGGTAT	36229
hPKU6_P3R53	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAAGACCTCAATCCTTTGGGTGTATGGGTCGTAGCGAACTGAGAAGGGCCGAGGTAT	36230
hPKU6_P3R54	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCAAGACCTCAATCCTTTGGGTGTATGGGTCGTAGCGAACTGAGAAGGGCCGAGGTAT	36231
hPKU6_P3R6	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCCGAGGTAT	36232
hPKU6_P3R7	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGCCGAGGTAT	36233
hPKU6_P3R8	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGGCCGAGGTAT	36234
hPKU6_P3R9	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGGGCCGAGGTAT	36235
hPKU6_P4R10	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAGGGCCGAGGTATT	36236
hPKU6_P4R11	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAAGGGCCGAGGTATT	36237

hPKU6_P4R12	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGAAGGGCCGAGGTATT	36238
hPKU6_P4R13	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAGAAGGGCCGAGGTATT	36239
hPKU6_P4R14	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGAGAAGGGCCGAGGTATT	36240
hPKU6_P4R15	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGAGAAGGGCCGAGGTATT	36241
hPKU6_P4R16	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTGAGAAGGGCCGAGGTATT	36242
hPKU6_P4R17	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCACTGAGAAGGGCCGAGGTATT	36243
hPKU6_P4R18	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAACTGAGAAGGGCCGAGGTATT	36244
hPKU6_P4R19	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGAACTGAGAAGGGCCGAGGTATT	36245
hPKU6_P4R20	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCGAACTGAGAAGGGCCGAGGTATT	36246
hPKU6_P4R21	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGCGAACTGAGAAGGGCCGAGGTATT	36247
hPKU6_P4R22	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAGCGAACTGAGAAGGGCCGAGGTATT	36248
hPKU6_P4R23	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTAGCGAACTGAGAAGGGCCGAGGTATT	36249
hPKU6_P4R24	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGTAGCGAACTGAGAAGGGCCGAGGTATT	36250
hPKU6_P4R25	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCGTAGCGAACTGAGAAGGGCCGAGGTATT	36251
hPKU6_P4R26	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTCGTAGCGAACTGAGAAGGGCCGAGGTATT	36252
hPKU6_P4R27	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGTCGTAGCGAACTGAGAAGGGCCGAGGTATT	36253
hPKU6_P4R28	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGGTCGTAGCGAACTGAGAAGGGCCGAGGTATT	36254

hPKU6_P4R29	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGGGTCGTAGCGAACTGAGAAGGGCCGAGGTATT	36255
hPKU6_P4R30	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGGGTCGTAGCGAACTGAGAAGGGCCGAGGTATT	36256
hPKU6_P4R31	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCATGGGTCGTAGCGAACTGAGAAGGGCCGAGGTATT	36257
hPKU6_P4R32	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTATGGGTCGTAGCGAACTGAGAAGGGCCGAGGTATT	36258
hPKU6_P4R33	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGTATGGGTCGTAGCGAACTGAGAAGGGCCGAGGTATT	36259
hPKU6_P4R34	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGTATGGGTCGTAGCGAACTGAGAAGGGCCGAGGTATT	36260
hPKU6_P4R35	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGTGTATGGGTCGTAGCGAACTGAGAAGGGCCGAGGTATT	36261
hPKU6_P4R36	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGGTGTATGGGTCGTAGCGAACTGAGAAGGGCCGAGGTATT	36262
hPKU6_P4R37	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGGGTGTATGGGTCGTAGCGAACTGAGAAGGGCCGAGGTATT	36263
hPKU6_P4R38	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGGGTGTATGGGTCGTAGCGAACTGAGAAGGGCCGAGGTATT	36264
hPKU6_P4R39	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTGGGTGTATGGGTCGTAGCGAACTGAGAAGGGCCGAGGTATT	36265
hPKU6_P4R4	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGAGGTATT	36266
hPKU6_P4R40	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTTGGGTGTATGGGTCGTAGCGAACTGAGAAGGGCCGAGGTATT	36267
hPKU6_P4R41	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTTTGGGTGTATGGGTCGTAGCGAACTGAGAAGGGCCGAGGTATT	36268
hPKU6_P4R42	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCCTTTGGGTGTATGGGTCGTAGCGAACTGAGAAGGGCCGAGGTATT	36269
hPKU6_P4R43	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTCCTTTGGGTGTATGGGTCGTAGCGAACTGAGAAGGGCCGAGGTATT	36270
hPKU6_P4R44	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCATCCTTTGGGTGTATGGGTCGTAGCGAACTGAGAAGGGCCGAGGTATT	36271

hPKU6_P4R45	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAATCCTTTGGGTGTATGGGTCGTAGCGAACTGAGAAGGGCCGAGGTATT	36272
hPKU6_P4R46	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCAATCCTTTGGGTGTATGGGTCGTAGCGAACTGAGAAGGGCCGAGGTATT	36273
hPKU6_P4R47	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTCAATCCTTTGGGTGTATGGGTCGTAGCGAACTGAGAAGGGCCGAGGTATT	36274
hPKU6_P4R48	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTCAATCCTTTGGGTGTATGGGTCGTAGCGAACTGAGAAGGGCCGAGGTATT	36275
hPKU6_P4R49	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCCTCAATCCTTTGGGTGTATGGGTCGTAGCGAACTGAGAAGGGCCGAGGTATT	36276
hPKU6_P4R5	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCGAGGTATT	36277
hPKU6_P4R50	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCACCTCAATCCTTTGGGTGTATGGGTCGTAGCGAACTGAGAAGGGCCGAGGTATT	36278
hPKU6_P4R51	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGACCTCAATCCTTTGGGTGTATGGGTCGTAGCGAACTGAGAAGGGCCGAGGTATT	36279
hPKU6_P4R52	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAGACCTCAATCCTTTGGGTGTATGGGTCGTAGCGAACTGAGAAGGGCCGAGGTATT	36280
hPKU6_P4R53	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAAGACCTCAATCCTTTGGGTGTATGGGTCGTAGCGAACTGAGAAGGGCCGAGGTATT	36281
hPKU6_P4R54	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCAAGACCTCAATCCTTTGGGTGTATGGGTCGTAGCGAACTGAGAAGGGCCGAGGTATT	36282
hPKU6_P4R6	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCCGAGGTATT	36283
hPKU6_P4R7	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGCCGAGGTATT	36284
hPKU6_P4R8	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGGCCGAGGTATT	36285
hPKU6_P4R9	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGGGCCGAGGTATT	36286
hPKU6_P5R10	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAGGGCCGAGGTATTG	36287
hPKU6_P5R11	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAAGGGCCGAGGTATTG	36288

hPKU6_P5R12	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGAAGGGCCGAGGTATTG	36289
hPKU6_P5R13	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAGAAGGGCCGAGGTATTG	36290
hPKU6_P5R14	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGAGAAGGGCCGAGGTATTG	36291
hPKU6_P5R15	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGAGAAGGGCCGAGGTATTG	36292
hPKU6_P5R16	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTGAGAAGGGCCGAGGTATTG	36293
hPKU6_P5R17	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCACTGAGAAGGGCCGAGGTATTG	36294
hPKU6_P5R18	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAACTGAGAAGGGCCGAGGTATTG	36295
hPKU6_P5R19	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGAACTGAGAAGGGCCGAGGTATTG	36296
hPKU6_P5R20	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCGAACTGAGAAGGGCCGAGGTATTG	36297
hPKU6_P5R21	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGCGAACTGAGAAGGGCCGAGGTATTG	36298
hPKU6_P5R22	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAGCGAACTGAGAAGGGCCGAGGTATTG	36299
hPKU6_P5R23	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTAGCGAACTGAGAAGGGCCGAGGTATTG	36300
hPKU6_P5R24	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGTAGCGAACTGAGAAGGGCCGAGGTATTG	36301
hPKU6_P5R25	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCGTAGCGAACTGAGAAGGGCCGAGGTATTG	36302
hPKU6_P5R26	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTCGTAGCGAACTGAGAAGGGCCGAGGTATTG	36303
hPKU6_P5R27	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGTCGTAGCGAACTGAGAAGGGCCGAGGTATTG	36304
hPKU6_P5R28	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGGTCGTAGCGAACTGAGAAGGGCCGAGGTATTG	36305

hPKU6_P5R29	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGGGTCGTAGCGAACTGAGAAGGGCCGAGGTATTG	36306
hPKU6_P5R30	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGGGTCGTAGCGAACTGAGAAGGGCCGAGGTATTG	36307
hPKU6_P5R31	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCATGGGTCGTAGCGAACTGAGAAGGGCCGAGGTATTG	36308
hPKU6_P5R32	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTATGGGTCGTAGCGAACTGAGAAGGGCCGAGGTATTG	36309
hPKU6_P5R33	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGTATGGGTCGTAGCGAACTGAGAAGGGCCGAGGTATTG	36310
hPKU6_P5R34	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGTATGGGTCGTAGCGAACTGAGAAGGGCCGAGGTATTG	36311
hPKU6_P5R35	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGTGTATGGGTCGTAGCGAACTGAGAAGGGCCGAGGTATTG	36312
hPKU6_P5R36	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGGTGTATGGGTCGTAGCGAACTGAGAAGGGCCGAGGTATTG	36313
hPKU6_P5R37	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGGGTGTATGGGTCGTAGCGAACTGAGAAGGGCCGAGGTATTG	36314
hPKU6_P5R38	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGGGTGTATGGGTCGTAGCGAACTGAGAAGGGCCGAGGTATTG	36315
hPKU6_P5R39	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTGGGTGTATGGGTCGTAGCGAACTGAGAAGGGCCGAGGTATTG	36316
hPKU6_P5R4	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGAGGTATTG	36317
hPKU6_P5R40	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTTGGGTGTATGGGTCGTAGCGAACTGAGAAGGGCCGAGGTATTG	36318
hPKU6_P5R41	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTTTGGGTGTATGGGTCGTAGCGAACTGAGAAGGGCCGAGGTATTG	36319
hPKU6_P5R42	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCCTTTGGGTGTATGGGTCGTAGCGAACTGAGAAGGGCCGAGGTATTG	36320
hPKU6_P5R43	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTCCTTTGGGTGTATGGGTCGTAGCGAACTGAGAAGGGCCGAGGTATTG	36321
hPKU6_P5R44	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCATCCTTTGGGTGTATGGGTCGTAGCGAACTGAGAAGGGCCGAGGTATTG	36322

hPKU6_P5R45	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAATCCTTTGGGTGTATGGGTCGTAGCGAACTGAGAAGGGCCGAGGTATTG	36323
hPKU6_P5R46	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCAATCCTTTGGGTGTATGGGTCGTAGCGAACTGAGAAGGGCCGAGGTATTG	36324
hPKU6_P5R47	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTCAATCCTTTGGGTGTATGGGTCGTAGCGAACTGAGAAGGGCCGAGGTATTG	36325
hPKU6_P5R48	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTCAATCCTTTGGGTGTATGGGTCGTAGCGAACTGAGAAGGGCCGAGGTATTG	36326
hPKU6_P5R49	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCCTCAATCCTTTGGGTGTATGGGTCGTAGCGAACTGAGAAGGGCCGAGGTATTG	36327
hPKU6_P5R5	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCGAGGTATTG	36328
hPKU6_P5R50	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCACCTCAATCCTTTGGGTGTATGGGTCGTAGCGAACTGAGAAGGGCCGAGGTATTG	36329
hPKU6_P5R51	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGACCTCAATCCTTTGGGTGTATGGGTCGTAGCGAACTGAGAAGGGCCGAGGTATTG	36330
hPKU6_P5R52	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAGACCTCAATCCTTTGGGTGTATGGGTCGTAGCGAACTGAGAAGGGCCGAGGTATTG	36331
hPKU6_P5R53	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAAGACCTCAATCCTTTGGGTGTATGGGTCGTAGCGAACTGAGAAGGGCCGAGGTATTG	36332
hPKU6_P5R54	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCAAGACCTCAATCCTTTGGGTGTATGGGTCGTAGCGAACTGAGAAGGGCCGAGGTATTG	36333
hPKU6_P5R6	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCCGAGGTATTG	36334
hPKU6_P5R7	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGCCGAGGTATTG	36335
hPKU6_P5R8	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGGCCGAGGTATTG	36336
hPKU6_P5R9	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGGGCCGAGGTATTG	36337
hPKU6_P6R10	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAGGGCCGAGGTATTGT	36338
hPKU6_P6R11	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAAGGGCCGAGGTATTGT	36339

hPKU6_P6R12	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGAAGGGCCGAGGTATTGT	36340
hPKU6_P6R13	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAGAAGGGCCGAGGTATTGT	36341
hPKU6_P6R14	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGAGAAGGGCCGAGGTATTGT	36342
hPKU6_P6R15	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGAGAAGGGCCGAGGTATTGT	36343
hPKU6_P6R16	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTGAGAAGGGCCGAGGTATTGT	36344
hPKU6_P6R17	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCACTGAGAAGGGCCGAGGTATTGT	36345
hPKU6_P6R18	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAACTGAGAAGGGCCGAGGTATTGT	36346
hPKU6_P6R19	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGAACTGAGAAGGGCCGAGGTATTGT	36347
hPKU6_P6R20	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCGAACTGAGAAGGGCCGAGGTATTGT	36348
hPKU6_P6R21	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGCGAACTGAGAAGGGCCGAGGTATTGT	36349
hPKU6_P6R22	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAGCGAACTGAGAAGGGCCGAGGTATTGT	36350
hPKU6_P6R23	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTAGCGAACTGAGAAGGGCCGAGGTATTGT	36351
hPKU6_P6R24	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGTAGCGAACTGAGAAGGGCCGAGGTATTGT	36352
hPKU6_P6R25	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCGTAGCGAACTGAGAAGGGCCGAGGTATTGT	36353
hPKU6_P6R26	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTCGTAGCGAACTGAGAAGGGCCGAGGTATTGT	36354
hPKU6_P6R27	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGTCGTAGCGAACTGAGAAGGGCCGAGGTATTGT	36355
hPKU6_P6R28	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGGTCGTAGCGAACTGAGAAGGGCCGAGGTATTGT	36356

hPKU6_P6R29	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGGGTCGTAGCGAACTGAGAAGGGCCGAGGTATTGT	36357
hPKU6_P6R30	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGGGTCGTAGCGAACTGAGAAGGGCCGAGGTATTGT	36358
hPKU6_P6R31	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCATGGGTCGTAGCGAACTGAGAAGGGCCGAGGTATTGT	36359
hPKU6_P6R32	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTATGGGTCGTAGCGAACTGAGAAGGGCCGAGGTATTGT	36360
hPKU6_P6R33	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGTATGGGTCGTAGCGAACTGAGAAGGGCCGAGGTATTGT	36361
hPKU6_P6R34	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGTATGGGTCGTAGCGAACTGAGAAGGGCCGAGGTATTGT	36362
hPKU6_P6R35	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGTGTATGGGTCGTAGCGAACTGAGAAGGGCCGAGGTATTGT	36363
hPKU6_P6R36	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGGTGTATGGGTCGTAGCGAACTGAGAAGGGCCGAGGTATTGT	36364
hPKU6_P6R37	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGGGTGTATGGGTCGTAGCGAACTGAGAAGGGCCGAGGTATTGT	36365
hPKU6_P6R38	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGGGTGTATGGGTCGTAGCGAACTGAGAAGGGCCGAGGTATTGT	36366
hPKU6_P6R39	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTGGGTGTATGGGTCGTAGCGAACTGAGAAGGGCCGAGGTATTGT	36367
hPKU6_P6R4	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGAGGTATTGT	36368
hPKU6_P6R40	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTTGGGTGTATGGGTCGTAGCGAACTGAGAAGGGCCGAGGTATTGT	36369
hPKU6_P6R41	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTTTGGGTGTATGGGTCGTAGCGAACTGAGAAGGGCCGAGGTATTGT	36370
hPKU6_P6R42	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCCTTTGGGTGTATGGGTCGTAGCGAACTGAGAAGGGCCGAGGTATTGT	36371
hPKU6_P6R43	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTCCTTTGGGTGTATGGGTCGTAGCGAACTGAGAAGGGCCGAGGTATTGT	36372
hPKU6_P6R44	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCATCCTTTGGGTGTATGGGTCGTAGCGAACTGAGAAGGGCCGAGGTATTGT	36373

hPKU6_P6R45	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAATCCTTTGGGTGTATGGGTCGTAGCGAACTGAGAAGGGCCGAGGTATTGT	36374
hPKU6_P6R46	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCAATCCTTTGGGTGTATGGGTCGTAGCGAACTGAGAAGGGCCGAGGTATTGT	36375
hPKU6_P6R47	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTCAATCCTTTGGGTGTATGGGTCGTAGCGAACTGAGAAGGGCCGAGGTATTGT	36376
hPKU6_P6R48	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTCAATCCTTTGGGTGTATGGGTCGTAGCGAACTGAGAAGGGCCGAGGTATTGT	36377
hPKU6_P6R49	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCCTCAATCCTTTGGGTGTATGGGTCGTAGCGAACTGAGAAGGGCCGAGGTATTGT	36378
hPKU6_P6R5	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCGAGGTATTGT	36379
hPKU6_P6R50	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCACCTCAATCCTTTGGGTGTATGGGTCGTAGCGAACTGAGAAGGGCCGAGGTATTGT	36380
hPKU6_P6R51	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGACCTCAATCCTTTGGGTGTATGGGTCGTAGCGAACTGAGAAGGGCCGAGGTATTGT	36381
hPKU6_P6R52	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAGACCTCAATCCTTTGGGTGTATGGGTCGTAGCGAACTGAGAAGGGCCGAGGTATTGT	36382
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hPKU6_P6R54	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCAAGACCTCAATCCTTTGGGTGTATGGGTCGTAGCGAACTGAGAAGGGCCGAGGTATTGT	36384
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hPKU6_P6R9	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGGGCCGAGGTATTGT	36388
hPKU6_P7R10	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAGGGCCGAGGTATTGTG	36389
hPKU6_P7R11	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAAGGGCCGAGGTATTGTG	36390

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hPKU6_P7R19	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGAACTGAGAAGGGCCGAGGTATTGTG	36398
hPKU6_P7R20	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCGAACTGAGAAGGGCCGAGGTATTGTG	36399
hPKU6_P7R21	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGCGAACTGAGAAGGGCCGAGGTATTGTG	36400
hPKU6_P7R22	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAGCGAACTGAGAAGGGCCGAGGTATTGTG	36401
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hPKU6_P7R24	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGTAGCGAACTGAGAAGGGCCGAGGTATTGTG	36403
hPKU6_P7R25	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCGTAGCGAACTGAGAAGGGCCGAGGTATTGTG	36404
hPKU6_P7R26	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTCGTAGCGAACTGAGAAGGGCCGAGGTATTGTG	36405
hPKU6_P7R27	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGTCGTAGCGAACTGAGAAGGGCCGAGGTATTGTG	36406
hPKU6_P7R28	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGGTCGTAGCGAACTGAGAAGGGCCGAGGTATTGTG	36407

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hPKU6_P7R31	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCATGGGTCGTAGCGAACTGAGAAGGGCCGAGGTATTGTG	36410
hPKU6_P7R32	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTATGGGTCGTAGCGAACTGAGAAGGGCCGAGGTATTGTG	36411
hPKU6_P7R33	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGTATGGGTCGTAGCGAACTGAGAAGGGCCGAGGTATTGTG	36412
hPKU6_P7R34	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGTATGGGTCGTAGCGAACTGAGAAGGGCCGAGGTATTGTG	36413
hPKU6_P7R35	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGTGTATGGGTCGTAGCGAACTGAGAAGGGCCGAGGTATTGTG	36414
hPKU6_P7R36	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGGTGTATGGGTCGTAGCGAACTGAGAAGGGCCGAGGTATTGTG	36415
hPKU6_P7R37	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGGGTGTATGGGTCGTAGCGAACTGAGAAGGGCCGAGGTATTGTG	36416
hPKU6_P7R38	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGGGTGTATGGGTCGTAGCGAACTGAGAAGGGCCGAGGTATTGTG	36417
hPKU6_P7R39	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTGGGTGTATGGGTCGTAGCGAACTGAGAAGGGCCGAGGTATTGTG	36418
hPKU6_P7R4	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGAGGTATTGTG	36419
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hPKU6_P7R42	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCCTTTGGGTGTATGGGTCGTAGCGAACTGAGAAGGGCCGAGGTATTGTG	36422
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hPKU6_P7R44	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCATCCTTTGGGTGTATGGGTCGTAGCGAACTGAGAAGGGCCGAGGTATTGTG	36424

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hPKU6_P7R48	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTCAATCCTTTGGGTGTATGGGTCGTAGCGAACTGAGAAGGGCCGAGGTATTGTG	36428
hPKU6_P7R49	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCCTCAATCCTTTGGGTGTATGGGTCGTAGCGAACTGAGAAGGGCCGAGGTATTGTG	36429
hPKU6_P7R5	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCGAGGTATTGTG	36430
hPKU6_P7R50	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCACCTCAATCCTTTGGGTGTATGGGTCGTAGCGAACTGAGAAGGGCCGAGGTATTGTG	36431
hPKU6_P7R51	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGACCTCAATCCTTTGGGTGTATGGGTCGTAGCGAACTGAGAAGGGCCGAGGTATTGTG	36432
hPKU6_P7R52	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAGACCTCAATCCTTTGGGTGTATGGGTCGTAGCGAACTGAGAAGGGCCGAGGTATTGTG	36433
hPKU6_P7R53	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAAGACCTCAATCCTTTGGGTGTATGGGTCGTAGCGAACTGAGAAGGGCCGAGGTATTGTG	36434
hPKU6_P7R54	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCAAGACCTCAATCCTTTGGGTGTATGGGTCGTAGCGAACTGAGAAGGGCCGAGGTATTGTG	36435
hPKU6_P7R6	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCCGAGGTATTGTG	36436
hPKU6_P7R7	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGCCGAGGTATTGTG	36437
hPKU6_P7R8	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGGCCGAGGTATTGTG	36438
hPKU6_P7R9	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGGGCCGAGGTATTGTG	36439
hPKU6_P8R10	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAGGGCCGAGGTATTGTGG	36440
hPKU6_P8R11	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAAGGGCCGAGGTATTGTGG	36441

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hPKU6_P8R14	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGAGAAGGGCCGAGGTATTGTGG	36444
hPKU6_P8R15	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGAGAAGGGCCGAGGTATTGTGG	36445
hPKU6_P8R16	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTGAGAAGGGCCGAGGTATTGTGG	36446
hPKU6_P8R17	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCACTGAGAAGGGCCGAGGTATTGTGG	36447
hPKU6_P8R18	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAACTGAGAAGGGCCGAGGTATTGTGG	36448
hPKU6_P8R19	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGAACTGAGAAGGGCCGAGGTATTGTGG	36449
hPKU6_P8R20	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCGAACTGAGAAGGGCCGAGGTATTGTGG	36450
hPKU6_P8R21	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGCGAACTGAGAAGGGCCGAGGTATTGTGG	36451
hPKU6_P8R22	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAGCGAACTGAGAAGGGCCGAGGTATTGTGG	36452
hPKU6_P8R23	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTAGCGAACTGAGAAGGGCCGAGGTATTGTGG	36453
hPKU6_P8R24	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGTAGCGAACTGAGAAGGGCCGAGGTATTGTGG	36454
hPKU6_P8R25	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCGTAGCGAACTGAGAAGGGCCGAGGTATTGTGG	36455
hPKU6_P8R26	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTCGTAGCGAACTGAGAAGGGCCGAGGTATTGTGG	36456
hPKU6_P8R27	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGTCGTAGCGAACTGAGAAGGGCCGAGGTATTGTGG	36457
hPKU6_P8R28	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGGTCGTAGCGAACTGAGAAGGGCCGAGGTATTGTGG	36458

hPKU6_P8R29	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGGGTCGTAGCGAACTGAGAAGGGCCGAGGTATTGTGG	36459
hPKU6_P8R30	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGGGTCGTAGCGAACTGAGAAGGGCCGAGGTATTGTGG	36460
hPKU6_P8R31	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCATGGGTCGTAGCGAACTGAGAAGGGCCGAGGTATTGTGG	36461
hPKU6_P8R32	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTATGGGTCGTAGCGAACTGAGAAGGGCCGAGGTATTGTGG	36462
hPKU6_P8R33	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGTATGGGTCGTAGCGAACTGAGAAGGGCCGAGGTATTGTGG	36463
hPKU6_P8R34	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGTATGGGTCGTAGCGAACTGAGAAGGGCCGAGGTATTGTGG	36464
hPKU6_P8R35	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGTGTATGGGTCGTAGCGAACTGAGAAGGGCCGAGGTATTGTGG	36465
hPKU6_P8R36	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGGTGTATGGGTCGTAGCGAACTGAGAAGGGCCGAGGTATTGTGG	36466
hPKU6_P8R37	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGGGTGTATGGGTCGTAGCGAACTGAGAAGGGCCGAGGTATTGTGG	36467
hPKU6_P8R38	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGGGTGTATGGGTCGTAGCGAACTGAGAAGGGCCGAGGTATTGTGG	36468
hPKU6_P8R39	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTGGGTGTATGGGTCGTAGCGAACTGAGAAGGGCCGAGGTATTGTGG	36469
hPKU6_P8R4	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGAGGTATTGTGG	36470
hPKU6_P8R40	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTTGGGTGTATGGGTCGTAGCGAACTGAGAAGGGCCGAGGTATTGTGG	36471
hPKU6_P8R41	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTTTGGGTGTATGGGTCGTAGCGAACTGAGAAGGGCCGAGGTATTGTGG	36472
hPKU6_P8R42	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCCTTTGGGTGTATGGGTCGTAGCGAACTGAGAAGGGCCGAGGTATTGTGG	36473
hPKU6_P8R43	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTCCTTTGGGTGTATGGGTCGTAGCGAACTGAGAAGGGCCGAGGTATTGTGG	36474
hPKU6_P8R44	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCATCCTTTGGGTGTATGGGTCGTAGCGAACTGAGAAGGGCCGAGGTATTGTGG	36475

hPKU6_P8R45	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAATCCTTTGGGTGTATGGGTCGTAGCGAACTGAGAAGGGCCGAGGTATTGTGG	36476
hPKU6_P8R46	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCAATCCTTTGGGTGTATGGGTCGTAGCGAACTGAGAAGGGCCGAGGTATTGTGG	36477
hPKU6_P8R47	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTCAATCCTTTGGGTGTATGGGTCGTAGCGAACTGAGAAGGGCCGAGGTATTGTGG	36478
hPKU6_P8R48	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTCAATCCTTTGGGTGTATGGGTCGTAGCGAACTGAGAAGGGCCGAGGTATTGTGG	36479
hPKU6_P8R49	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCCTCAATCCTTTGGGTGTATGGGTCGTAGCGAACTGAGAAGGGCCGAGGTATTGTGG	36480
hPKU6_P8R5	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCGAGGTATTGTGG	36481
hPKU6_P8R50	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCACCTCAATCCTTTGGGTGTATGGGTCGTAGCGAACTGAGAAGGGCCGAGGTATTGTGG	36482
hPKU6_P8R51	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGACCTCAATCCTTTGGGTGTATGGGTCGTAGCGAACTGAGAAGGGCCGAGGTATTGTGG	36483
hPKU6_P8R52	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAGACCTCAATCCTTTGGGTGTATGGGTCGTAGCGAACTGAGAAGGGCCGAGGTATTGTGG	36484
hPKU6_P8R53	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAAGACCTCAATCCTTTGGGTGTATGGGTCGTAGCGAACTGAGAAGGGCCGAGGTATTGTGG	36485
hPKU6_P8R54	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCAAGACCTCAATCCTTTGGGTGTATGGGTCGTAGCGAACTGAGAAGGGCCGAGGTATTGTGG	36486
hPKU6_P8R6	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCCGAGGTATTGTGG	36487
hPKU6_P8R7	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGCCGAGGTATTGTGG	36488
hPKU6_P8R8	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGGCCGAGGTATTGTGG	36489
hPKU6_P8R9	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGGGCCGAGGTATTGTGG	36490
hPKU6_P9R10	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAGGGCCGAGGTATTGTGGC	36491
hPKU6_P9R11	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAAGGGCCGAGGTATTGTGGC	36492

hPKU6_P9R12	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGAAGGGCCGAGGTATTGTGGC	36493
hPKU6_P9R13	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAGAAGGGCCGAGGTATTGTGGC	36494
hPKU6_P9R14	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGAGAAGGGCCGAGGTATTGTGGC	36495
hPKU6_P9R15	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGAGAAGGGCCGAGGTATTGTGGC	36496
hPKU6_P9R16	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTGAGAAGGGCCGAGGTATTGTGGC	36497
hPKU6_P9R17	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCACTGAGAAGGGCCGAGGTATTGTGGC	36498
hPKU6_P9R18	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAACTGAGAAGGGCCGAGGTATTGTGGC	36499
hPKU6_P9R19	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGAACTGAGAAGGGCCGAGGTATTGTGGC	36500
hPKU6_P9R20	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCGAACTGAGAAGGGCCGAGGTATTGTGGC	36501
hPKU6_P9R21	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGCGAACTGAGAAGGGCCGAGGTATTGTGGC	36502
hPKU6_P9R22	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAGCGAACTGAGAAGGGCCGAGGTATTGTGGC	36503
hPKU6_P9R23	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTAGCGAACTGAGAAGGGCCGAGGTATTGTGGC	36504
hPKU6_P9R24	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGTAGCGAACTGAGAAGGGCCGAGGTATTGTGGC	36505
hPKU6_P9R25	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCGTAGCGAACTGAGAAGGGCCGAGGTATTGTGGC	36506
hPKU6_P9R26	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTCGTAGCGAACTGAGAAGGGCCGAGGTATTGTGGC	36507
hPKU6_P9R27	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGTCGTAGCGAACTGAGAAGGGCCGAGGTATTGTGGC	36508
hPKU6_P9R28	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGGTCGTAGCGAACTGAGAAGGGCCGAGGTATTGTGGC	36509

hPKU6_P9R29	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGGGTCGTAGCGAACTGAGAAGGGCCGAGGTATTGTGGC	36510
hPKU6_P9R30	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGGGTCGTAGCGAACTGAGAAGGGCCGAGGTATTGTGGC	36511
hPKU6_P9R31	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCATGGGTCGTAGCGAACTGAGAAGGGCCGAGGTATTGTGGC	36512
hPKU6_P9R32	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTATGGGTCGTAGCGAACTGAGAAGGGCCGAGGTATTGTGGC	36513
hPKU6_P9R33	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGTATGGGTCGTAGCGAACTGAGAAGGGCCGAGGTATTGTGGC	36514
hPKU6_P9R34	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGTATGGGTCGTAGCGAACTGAGAAGGGCCGAGGTATTGTGGC	36515
hPKU6_P9R35	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGTGTATGGGTCGTAGCGAACTGAGAAGGGCCGAGGTATTGTGGC	36516
hPKU6_P9R36	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGGTGTATGGGTCGTAGCGAACTGAGAAGGGCCGAGGTATTGTGGC	36517
hPKU6_P9R37	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGGGTGTATGGGTCGTAGCGAACTGAGAAGGGCCGAGGTATTGTGGC	36518
hPKU6_P9R38	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTGGGTGTATGGGTCGTAGCGAACTGAGAAGGGCCGAGGTATTGTGGC	36519
hPKU6_P9R39	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTGGGTGTATGGGTCGTAGCGAACTGAGAAGGGCCGAGGTATTGTGGC	36520
hPKU6_P9R4	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGAGGTATTGTGGC	36521
hPKU6_P9R40	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTTGGGTGTATGGGTCGTAGCGAACTGAGAAGGGCCGAGGTATTGTGGC	36522
hPKU6_P9R41	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTTTGGGTGTATGGGTCGTAGCGAACTGAGAAGGGCCGAGGTATTGTGGC	36523
hPKU6_P9R42	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCCTTTGGGTGTATGGGTCGTAGCGAACTGAGAAGGGCCGAGGTATTGTGGC	36524
hPKU6_P9R43	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTCCTTTGGGTGTATGGGTCGTAGCGAACTGAGAAGGGCCGAGGTATTGTGGC	36525
hPKU6_P9R44	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCATCCTTTGGGTGTATGGGTCGTAGCGAACTGAGAAGGGCCGAGGTATTGTGGC	36526

hPKU6_P9R45	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAATCCTTTGGGTGTATGGGTCGTAGCGAACTGAGAAGGGCCGAGGTATTGTGGC	36527
hPKU6_P9R46	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCAATCCTTTGGGTGTATGGGTCGTAGCGAACTGAGAAGGGCCGAGGTATTGTGGC	36528
hPKU6_P9R47	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTCAATCCTTTGGGTGTATGGGTCGTAGCGAACTGAGAAGGGCCGAGGTATTGTGGC	36529
hPKU6_P9R48	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTCAATCCTTTGGGTGTATGGGTCGTAGCGAACTGAGAAGGGCCGAGGTATTGTGGC	36530
hPKU6_P9R49	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCCTCAATCCTTTGGGTGTATGGGTCGTAGCGAACTGAGAAGGGCCGAGGTATTGTGGC	36531
hPKU6_P9R5	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCGAGGTATTGTGGC	36532
hPKU6_P9R50	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCACCTCAATCCTTTGGGTGTATGGGTCGTAGCGAACTGAGAAGGGCCGAGGTATTGTGGC	36533
hPKU6_P9R51	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGACCTCAATCCTTTGGGTGTATGGGTCGTAGCGAACTGAGAAGGGCCGAGGTATTGTGGC	36534
hPKU6_P9R52	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAGACCTCAATCCTTTGGGTGTATGGGTCGTAGCGAACTGAGAAGGGCCGAGGTATTGTGGC	36535
hPKU6_P9R53	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAAGACCTCAATCCTTTGGGTGTATGGGTCGTAGCGAACTGAGAAGGGCCGAGGTATTGTGGC	36536
hPKU6_P9R54	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCAAGACCTCAATCCTTTGGGTGTATGGGTCGTAGCGAACTGAGAAGGGCCGAGGTATTGTGGC	36537
hPKU6_P9R6	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCCGAGGTATTGTGGC	36538
hPKU6_P9R7	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGCCGAGGTATTGTGGC	36539
hPKU6_P9R8	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGGCCGAGGTATTGTGGC	36540
hPKU6_P9R9	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCGGGCCGAGGTATTGTGGC	36541

In some embodiments, the systems and methods provided herein may comprise a template sequence listed in **Table 6A**. Table 6A provides exemplary template RNA sequences (column 4) and second-nick gRNA spacer sequences (column 3) designed to be paired with a gene modifying polypeptide to correct a R408W mutation in the PAH gene.

Table 6A. Exemplary second nick gRNA sequences

Table 6A provides spacer sequences for second-strand targeting gRNAs and relevant characteristics. Second-nick gRNAs in this table are designed to be used in combination with template RNAs comprising the particular spacers noted in Column 6. In some embodiments, a second-nick gRNA is selected with preference for a distance of less than or equal to 100 nt from the first nick (i.e., the nick specified by the template RNA). In some embodiments, a second-nick gRNA is selected with a preference for a PAM-in orientation with the template RNA of the gene modifying system, as described elsewhere in this application.

Name	Second-nick spacer	SEQ ID NO	Sequence	SEQ ID NO	Exemplary Compatible Spacer
hPKU_ngRNA_17-	TTACTTCTTTTTTAGGAACA	37082	TTACTTCTTTTTTAGGAACAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTTT	37124	hPKU6
hPKU_ngRNA_24-	TGGCATTTTACTTCTTTTTT	37083	TGGCATTTTACTTCTTTTTTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTTT	37125	hPKU6
hPKU_ngRNA_44-	AGTCTTAAGAGAGTTCTCAG	37084	AGTCTTAAGAGAGTTCTCAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTTT	37126	hPKU6
hPKU_ngRNA_68-	GAAGGGCACCATTTGGAGAA	37085	GAAGGGCACCATTTGGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTTT	37127	hPKU6
hPKU_ngRNA_75-	CTTGAGTGAAGGGCACCATT	37086	CTTGAGTGAAGGGCACCATTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGT	37128	hPKU6

			TATCAACTTGAAAAAGTGGCACCGAGTCGGT GCTTTT		
hPKU_ngRNA_57+	TAAGACTACCTTTCTCCAAA	37087	TAAGACTACCTTTCTCCAAAGTTTTAGAGCTA GAAATAGCAAGTTAAAATAAGGCTAGTCCGT TATCAACTTGAAAAAGTGGCACCGAGTCGGT GCTTTT	37129	hPKU1, hPKU2, hPKU3,hPKU4,hPKU5
hPKU_ngRNA_85-	AAACCACAGGCTTGAGTGAA	37088	AAACCACAGGCTTGAGTGAAGTTTTAGAGCT AGAAATAGCAAGTTAAAATAAGGCTAGTCCG TTATCAACTTGAAAAAGTGGCACCGAGTCGGT GCTTTT	37130	hPKU6
hPKU_ngRNA_86-	AAAACCACAGGCTTGAGTGA	37089	AAAACCACAGGCTTGAGTGAGTTTTAGAGCT AGAAATAGCAAGTTAAAATAAGGCTAGTCCG TTATCAACTTGAAAAAGTGGCACCGAGTCGGT GCTTTT	37131	hPKU6
hPKU_ngRNA_98-	GTTCCTAAGACCAAAACCAC	37090	GTTCCTAAGACCAAAACCACGTTTTAGAGCTA GAAATAGCAAGTTAAAATAAGGCTAGTCCGT TATCAACTTGAAAAAGTGGCACCGAGTCGGT GCTTTT	37132	hPKU6
hPKU_ngRNA_79+	GTGCCCTTCACTCAAGCCTG	37091	GTGCCCTTCACTCAAGCCTGGTTTTAGAGCTA GAAATAGCAAGTTAAAATAAGGCTAGTCCGT TATCAACTTGAAAAAGTGGCACCGAGTCGGT GCTTTT	37133	hPKU1, hPKU2, hPKU3,hPKU4,hPKU5
hPKU_ngRNA_85+	TTCACTCAAGCCTGTGGTTT	37092	TTCACTCAAGCCTGTGGTTTGTTTTAGAGCTA GAAATAGCAAGTTAAAATAAGGCTAGTCCGT TATCAACTTGAAAAAGTGGCACCGAGTCGGT GCTTTT	37134	hPKU1, hPKU2, hPKU3,hPKU4,hPKU5
hPKU_ngRNA_92+	AAGCCTGTGGTTTTGGTCTT	37093	AAGCCTGTGGTTTTGGTCTTGTTTTAGAGCTA GAAATAGCAAGTTAAAATAAGGCTAGTCCGT TATCAACTTGAAAAAGTGGCACCGAGTCGGT GCTTTT	37135	hPKU1, hPKU2, hPKU3,hPKU4,hPKU5
hPKU_ngRNA_170-	GTCCAAGACCTCAATCCTTT	37094	GTCCAAGACCTCAATCCTTTGTTTTAGAGCTA GAAATAGCAAGTTAAAATAAGGCTAGTCCGT TATCAACTTGAAAAAGTGGCACCGAGTCGGT GCTTTT	37136	hPKU6
hPKU_ngRNA_171-	TGTCCAAGACCTCAATCCTT	37095	TGTCCAAGACCTCAATCCTTGTTTTAGAGCTA GAAATAGCAAGTTAAAATAAGGCTAGTCCGT	37137	hPKU6

			TATCAACTTGAAAAAGTGGCACCGAGTCGGT GCTTTT		
hPKU_ngRNA_152+	GCTACGACCCATACACCCAA	37096	GCTACGACCCATACACCCAAGTTTTAGAGCTA GAAATAGCAAGTTAAAATAAGGCTAGTCCGT TATCAACTTGAAAAAGTGGCACCGAGTCGGT GCTTTT	37138	hPKU1, hPKU2, hPKU3,hPKU4,hPKU5
hPKU_ngRNA_159+	CCCATACACCCAAAGGATTG	37097	CCCATACACCCAAAGGATTGGTTTTAGAGCTA GAAATAGCAAGTTAAAATAAGGCTAGTCCGT TATCAACTTGAAAAAGTGGCACCGAGTCGGT GCTTTT	37139	hPKU1, hPKU2, hPKU3,hPKU4,hPKU5
hPKU_ngRNA_165+	CACCCAAAGGATTGAGGTCT	37098	CACCCAAAGGATTGAGGTCTGTTTTAGAGCTA GAAATAGCAAGTTAAAATAAGGCTAGTCCGT TATCAACTTGAAAAAGTGGCACCGAGTCGGT GCTTTT	37140	hPKU1, hPKU2, hPKU3,hPKU4,hPKU5
hPKU_ngRNA_197-	AGCCAAAATCTTAAGCTGCT	37099	AGCCAAAATCTTAAGCTGCTGTTTTAGAGCTA GAAATAGCAAGTTAAAATAAGGCTAGTCCGT TATCAACTTGAAAAAGTGGCACCGAGTCGGT GCTTTT	37141	hPKU6
hPKU_ngRNA_198-	CAGCCAAAATCTTAAGCTGC	37100	CAGCCAAAATCTTAAGCTGCGTTTTAGAGCTA GAAATAGCAAGTTAAAATAAGGCTAGTCCGT TATCAACTTGAAAAAGTGGCACCGAGTCGGT GCTTTT	37142	hPKU6
hPKU_ngRNA_192+	TACCCAGCAGCTTAAGATTT	37101	TACCCAGCAGCTTAAGATTTGTTTTAGAGCTA GAAATAGCAAGTTAAAATAAGGCTAGTCCGT TATCAACTTGAAAAAGTGGCACCGAGTCGGT GCTTTT	37143	hPKU1, hPKU2, hPKU3,hPKU4,hPKU5
hPKU_ngRNA_224-	TGTAAATTACTTACTGTTAA	37102	TGTAAATTACTTACTGTTAAGTTTTAGAGCTA GAAATAGCAAGTTAAAATAAGGCTAGTCCGT TATCAACTTGAAAAAGTGGCACCGAGTCGGT GCTTTT	37144	hPKU6
hPKU_ngRNA_247-	AGAAACCGAGTGGCCTCGTA	37103	AGAAACCGAGTGGCCTCGTAGTTTTAGAGCTA GAAATAGCAAGTTAAAATAAGGCTAGTCCGT TATCAACTTGAAAAAGTGGCACCGAGTCGGT GCTTTT	37145	hPKU6

hPKU_ngRNA_231+	TAAGTAATTTACACCTTACG	37104	TAAGTAATTTACACCTTACGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTTT	37146	hPKU1, hPKU2, hPKU3,hPKU4,hPKU5
hPKU_ngRNA_257-	TCGATTACTGAGAAACCGAG	37105	TCGATTACTGAGAAACCGAGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTTT	37147	hPKU6
hPKU_ngRNA_239+	TTACACCTTACGAGGCCACT	37106	TTACACCTTACGAGGCCACTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTTT	37148	hPKU1, hPKU2, hPKU3,hPKU4,hPKU5
hPKU_ngRNA_291-	TTTTTCCTATGGCGATGGTA	37107	TTTTTCCTATGGCGATGGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTTT	37149	hPKU6
hPKU_ngRNA_292-	ATTTTTCCTATGGCGATGGT	37108	ATTTTTCCTATGGCGATGGTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTTT	37150	hPKU6
hPKU_ngRNA_296-	TATTATTTTTCCTATGGCGA	37109	TATTATTTTTCCTATGGCGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTTT	37151	hPKU6
hPKU_ngRNA_302-	TAAATTTATTATTTTTCCTA	37110	TAAATTTATTATTTTTCCTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTTT	37152	hPKU6
hPKU_ngRNA_283+	TCTTTCCCTACCATCGCCAT	37111	TCTTTCCCTACCATCGCCATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTTT	37153	hPKU1, hPKU2, hPKU3,hPKU4,hPKU5
hPKU_ngRNA_318+	TTTATTGAAATATTTAATTA	37112	TTTATTGAAATATTTAATTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTTT	37154	hPKU1, hPKU2, hPKU3,hPKU4,hPKU5

hPKU_ngRNA3b_128-wt	TGAGAAGGGCCGAGGTATTG	37113	TGAGAAGGGCCGAGGTATTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTTT	37155	hPKU6
hPKU_ngRNA3b_136-mut	TAGCGAACTGAGAAGGGCCA	37114	TAGCGAACTGAGAAGGGCCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTTT	37156	hPKU6
hPKU_ngRNA3b_136-wt	TAGCGAACTGAGAAGGGCCG	37115	TAGCGAACTGAGAAGGGCCGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTTT	37157	hPKU6
hPKU_ngRNA3b_128-mut	TGAGAAGGGCCAAGGTATTG	37116	TGAGAAGGGCCAAGGTATTGGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTTT	37158	hPKU6
hPKU_ngRNA3b_136-mut	TAGCGAACTGAGAAGGGCCA	37117	TAGCGAACTGAGAAGGGCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTTT	37159	hPKU6
hPKU_ngRNA3b_136-wt	TAGCGAACTGAGAAGGGCCG	37118	TAGCGAACTGAGAAGGGCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTTT	37160	hPKU6
hPKU_ngRNA_116+	ACTTTGCTGCCACAATACCT	37119	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTTT	37161	hPKU1, hPKU2, hPKU3,hPKU4,hPKU5
hPKU_ngRNA_142-	GGGTCGTAGCGAACTGAGAA	37120	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTTT	37162	hPKU6
hPKU_ngRNA_143-	TGGGTCGTAGCGAACTGAGA	37121	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGT	37163	hPKU6

			TATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTTT		
hPKU_ngRNA_162-	CCTCAATCCTTTGGGTGTAT	37122	CCTCAATCCTTTGGGTGTATGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTTT	37164	hPKU6
hPKU_ngRNA_163-	ACCTCAATCCTTTGGGTGTA	37123	ACCTCAATCCTTTGGGTGTAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTTT	37165	hPKU6

The template RNA sequences shown in Tables 1-4, 5A-5F, and 6A may be customized depending on the cell being targeted. For example, in some embodiments it is desired to inactivate a PAM sequence upon editing (e.g., using a "PAM-kill" modification) to decrease the potential for further gene editing (e.g., by Cas retargeting) following the initial edit. Consequently, certain template RNAs described herein are designed to write a mutation (e.g., a substitution) into the PAM of the target site, such that upon editing, the PAM site will be mutated to a sequence no longer recognized by the gene modifying polypeptide. Thus, a mutation region within the heterologous object sequence of the template RNA may comprise a PAM-kill sequence. Without wishing to be bound by theory, in some embodiments, a PAM-kill sequence prevents re-engagement of the gene modifying polypeptide upon completion of a genetic modification, or decreases re-engagement relative to a template RNA lacking a PAM-kill sequence. In some embodiments, a PAM-kill sequence does not alter the amino acid sequence encoded by a gene, e.g., the PAM-kill sequence results in a silent mutation. In other embodiments, it is desired to leave the PAM sequence intact (no PAM-kill).

Similarly, in some embodiments, to decrease the potential for further gene editing (e.g., by Cas retargeting) following the initial edit, it may be desirable to alter the first three nucleotides of the RT template sequence via a "seed-kill" motif. Consequently, certain template RNAs described herein are designed to write a mutation (e.g., a substitution) into the portion of the target site corresponding to the first three nucleotides of the RT template sequence, such that upon editing, the target site will be mutated to a sequence with lower homology to the RT template sequence. Thus, a mutation region within the heterologous object sequence of the template RNA may comprise a seed-kill sequence. Without wishing to be bound by theory, in some embodiments, a seed-kill sequence prevents re-engagement of the gene modifying polypeptide upon completion of a genetic modification, or decreases re-engagement relative to an otherwise similar template RNA lacking a seed-kill sequence. In some embodiments, a seed-kill sequence does not alter the amino acid sequence encoded by a gene, e.g., the seed-kill sequence results in a silent mutation. In other embodiments, it is desired to leave the seed region intact, and a seed-kill sequence is not used.

In further embodiments, to optimize or improve gene editing efficiency, it may be desirable to evade the target cell's mismatch repair or nucleotide repair pathways or to bias the

target cell's repair pathways toward preservation of the edited strand. In some embodiments, multiple silent mutations (for example, silent substitutions) may be introduced within the RT template sequence to evade the target cell's mismatch repair or nucleotide repair pathways or to bias the target cell's repair pathways toward preservation of the edited strand.

Table 7A provides exemplary silent mutations for various positions within the PAH gene for use with a template to correct a R408W mutation.

Table 7A. Exemplary Silent Mutation Codons for the PAH Gene for Templates to Correct a R408W mutation

Amino Acid Position (Including the Initial Methionine)	WT Amino Acid	WT Codon	ALL CODONS					
401	N	AAC	AAT	AAC				
402	F	TTT	TTT	TTC				
403	A	GCT	GCT	GCC	GCA	GCG		
404	A	GCC	GCT	GCC	GCA	GCG		
405	T	ACA	ACT	ACC	ACA	ACG		
406	I	ATA	ATA	ATT	ATC			
407	P	CCT	CCT	CCC	CCA	CCG		
409	P	CCC	CCT	CCC	CCA	CCG		
410	F	TTC	TTT	TTC				
411	S	TCA	TCT	TCC	TCA	TCG	AGT	AGC
412	V	GTT	GTT	GTC	GTA	GTG		
413	R	CGC	CGT	CGC	CGA	CGG	AGA	AGG
414	Y	TAC	TAT	TAC				
415	D	GAC	GAT	GAC				
416	P	CCA	CCT	CCC	CCA	CCG		
417	Y	TAC	TAT	TAC				
418	T	ACC	ACT	ACC	ACA	ACG		
419	Q	CAA	CAA	CAG				
420	R	AGG	CGT	CGC	CGA	CGG	AGA	AGG
421	I	ATT	ATA	ATT	ATC			
422	E	GAG	GAA	GAG				
423	V	GTC	GTT	GTC	GTA	GTG		
424	L	TTG	TTA	TTG	CTT	CTC	CTA	CTG
425	D	GAC	GAT	GAC				
426	N	AAT	AAT	AAC				

427	T	ACC	ACT	ACC	ACA	ACG		
428	Q	CAG	CAA	CAG				
429	Q	CAG	CAA	CAG				
430	L	CTT	TTA	TTG	CTT	CTC	CTA	CTG
431	K	AAG	AAA	AAG				
432	I	ATT	ATA	ATT	ATC			
433	L	TTG	TTA	TTG	CTT	CTC	CTA	CTG
434	A	GCT	GCT	GCC	GCA	GCG		
435	D	GAT	GAT	GAC				
436	S	TCC	TCT	TCC	TCA	TCG	AGT	AGC
437	I	ATT	ATA	ATT	ATC			
438	N	AAC	AAT	AAC				

Table 7B provides exemplary silent mutations for various positions within the PAH gene for use with a template to correct a R261Q mutation.

Table 7B. Exemplary Silent Mutation Codons for the PAH Gene for Templates to Correct a R261Q mutation

Amino Acid Position (Including the Initial Methionine)	**WT Amino Acid**	**WT Codon**	**All Codons**					
237	C	TGC	TGT	TGC				
238	T	ACT	ACT	ACC	ACA	ACG		
239	G	GGT	GGT	GGC	GGA	GGG		
240	F	TTC	TTT	TTC				
241	R	CGC	CGT	CGC	CGA	CGG	AGA	AGG
242	L	CTC	TTA	TTG	CTT	CTC	CTA	CTG
243	R	CGA	CGT	CGC	CGA	CGG	AGA	AGG
244	P	CCT	CCT	CCC	CCA	CCG		
245	V	GTG	GTT	GTC	GTA	GTG		
246	A	GCT	GCT	GCC	GCA	GCG		
247	G	GGC	GGT	GGC	GGA	GGG		
248	L	CTG	TTA	TTG	CTT	CTC	CTA	CTG
249	L	CTT	TTA	TTG	CTT	CTC	CTA	CTG
250	S	TCC	TCT	TCC	TCA	TCG	AGT	AGC
251	S	TCT	TCT	TCC	TCA	TCG	AGT	AGC
252	R	CGG	CGT	CGC	CGA	CGG	AGA	AGG
253	D	GAT	GAT	GAC				

254	F	TTC	TTT	TTC				
255	L	TTG	TTA	TTG	CTT	CTC	CTA	CTG
256	G	GGT	GGT	GGC	GGA	GGG		
257	G	GGC	GGT	GGC	GGA	GGG		
258	L	CTG	TTA	TTG	CTT	CTC	CTA	CTG
259	A	GCC	GCT	GCC	GCA	GCG		
260	F	TTC	TTT	TTC				
262	V	GTC	GTT	GTC	GTA	GTG		
263	F	TTC	TTT	TTC				
264	H	CAC	CAT	CAC				
265	C	TGC	TGT	TGC				
266	T	ACA	ACT	ACC	ACA	ACG		
267	Q	CAG	CAA	CAG				
268	Y	TAC	TAT	TAC				
269	I	ATC	ATA	ATT	ATC			
270	R	AGA	CGT	CGC	CGA	CGG	AGA	AGG
271	H	CAT	CAT	CAC				
272	G	GGA	GGT	GGC	GGA	GGG		
273	S	TCC	TCT	TCC	TCA	TCG	AGT	AGC
274	K	AAG	AAA	AAG				
275	P	CCC	CCT	CCC	CCA	CCG		
276	M	ATG	ATG					
277	Y	TAT	TAT	TAC				
278	T	ACC	ACT	ACC	ACA	ACG		
279	P	CCC	CCT	CCC	CCA	CCG		
280	E	GAA	GAA	GAG				

Table 7C provides exemplary silent mutations for various positions within the PAH gene for use with a template to correct a R243Q mutation.

Table 7C. Exemplary Silent Mutation Codons for the PAH Gene for Templates to Correct a R243Q mutation

Amino Acid Position (Including the Initial Methionine)	**WT Amino Acid**	**WT Codon**	**ALL CODONS**					
237	C	TGC	TGT	TGC				
238	T	ACT	ACT	ACC	ACA	ACG		
239	G	GGT	GGT	GGC	GGA	GGG		

240	F	TTC	TTT	TTC				
241	R	CGC	CGT	CGC	CGA	CGG	AGA	AGG
242	L	CTC	TTA	TTG	CTT	CTC	CTA	CTG
244	P	CCT	CCT	CCC	CCA	CCG		
245	V	GTG	GTT	GTC	GTA	GTG		
246	A	GCT	GCT	GCC	GCA	GCG		
247	G	GGC	GGT	GGC	GGA	GGG		
248	L	CTG	TTA	TTG	CTT	CTC	CTA	CTG
249	L	CTT	TTA	TTG	CTT	CTC	CTA	CTG
250	S	TCC	TCT	TCC	TCA	TCG	AGT	AGC
251	S	TCT	TCT	TCC	TCA	TCG	AGT	AGC
252	R	CGG	CGT	CGC	CGA	CGG	AGA	AGG
253	D	GAT	GAT	GAC				
254	F	TTC	TTT	TTC				
255	L	TTG	TTA	TTG	CTT	CTC	CTA	CTG
256	G	GGT	GGT	GGC	GGA	GGG		
257	G	GGC	GGT	GGC	GGA	GGG		
258	L	CTG	TTA	TTG	CTT	CTC	CTA	CTG
259	A	GCC	GCT	GCC	GCA	GCG		
260	F	TTC	TTT	TTC				
261	R	CGA	CGT	CGC	CGA	CGG	AGA	AGG
262	V	GTC	GTT	GTC	GTA	GTG		
263	F	TTC	TTT	TTC				
264	H	CAC	CAT	CAC				
265	C	TGC	TGT	TGC				
266	T	ACA	ACT	ACC	ACA	ACG		
267	Q	CAG	CAA	CAG				
268	Y	TAC	TAT	TAC				
269	I	ATC	ATA	ATT	ATC			
270	R	AGA	CGT	CGC	CGA	CGG	AGA	AGG
271	H	CAT	CAT	CAC				
272	G	GGA	GGT	GGC	GGA	GGG		
273	S	TCC	TCT	TCC	TCA	TCG	AGT	AGC
274	K	AAG	AAA	AAG				
275	P	CCC	CCT	CCC	CCA	CCG		
276	M	ATG	ATG					
277	Y	TAT	TAT	TAC				
278	T	ACC	ACT	ACC	ACA	ACG		
279	P	CCC	CCT	CCC	CCA	CCG		
280	E	GAA	GAA	GAG				

In some embodiments, the template RNA comprises one or more silent mutations.

It should be understood that the silent mutations illustrated in Tables 7A-7C may be used individually or combined in any manner in a template RNA sequence described herein.
In some embodiments, the template RNA comprises a sequence having one or more silent substitutions as shown in Table E6 or E6A.

In some embodiments, the template RNA comprises a sequence listed in any one of Tables 8A-8D. Tables 8A-8D provide exemplary template RNA sequences comprising one or more silent substitutions (column 2) designed to be paired with a gene modifying polypeptide to correct a mutation in the PAH gene. The templates in Tables 5A-5F are meant to exemplify the total sequence of: (1) gRNA spacer (e.g., for targeting for first strand nick), (2) gRNA scaffold, (3) RT (heterologous object sequence) sequence, and (4) PBS sequence (e.g., for initiating TPRT at first strand nick).

Table 8A. Exemplary template RNA sequences

Table 8A provides design of exemplary components of gene modifying systems for correcting the pathogenic R408W mutation in PAH to the wild-type form. This table details the sequence of a complete template RNA comprising one or more silent substitutions described in Table 7A for use in a Cas-RT fusion gene modifying polypeptide. Templates in this table employ the hPKU3 spacer TGGGTCGTAGCGAACTGAGA (SEQ ID NO: 16102).

Name	tgRNA sequence	SEQ ID NO
hPKU3_R17_P10_sub0	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCaatacctCggcccttctcagttcgcta	36542
hPKU3_R17_P10_sub1	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCaataccgCggcccttctcagttcgcta	36543
hPKU3_R17_P10_sub2	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCaatccctCggcccttctcagttcgcta	36544
hPKU3_R17_P10_sub4	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCaatacctCgcccttctcagttcgcta	36545
hPKU3_R17_P10_sub7	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCaataccgCgcccttctcagttcgcta	36546
hPKU3_R17_P10_sub8	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCaataccgCgcccattctcagttcgcta	36547
hPKU3_R17_P8_sub0	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCaatacctCggcccttctcagttcgc	36548
hPKU3_R17_P8_sub1	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCaataccgCggcccttctcagttcgc	36549
hPKU3_R17_P8_sub2	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCaatccctCggcccttctcagttcgc	36550
hPKU3_R17_P8_sub4	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCaatacctCgcccttctcagttcgc	36551
hPKU3_R17_P8_sub7	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCaataccgCgcccttctcagttcgc	36552
hPKU3_R17_P8_sub8	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCaataccgCgcccattctcagttcgc	36553

hPKU3_R17_P9_sub0	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCaatacctCggcccttctcagttcgct	36554
hPKU3_R17_P9_sub1	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCaataccgCggcccttctcagttcgct	36555
hPKU3_R17_P9_sub2	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCaatccctCggcccttctcagttcgct	36556
hPKU3_R17_P9_sub4	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCaatacctCgccccttctcagttcgct	36557
hPKU3_R17_P9_sub7	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCaataccgCgcccttctcagttcgct	36558
hPKU3_R17_P9_sub8	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCaataccgCgcccattctcagttcgct	36559
hPKU3_R19_P10_sub0	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCacaatacctCggcccttctcagttcgcta	36560
hPKU3_R19_P10_sub1	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCacaataccgCggcccttctcagttcgcta	36561
hPKU3_R19_P10_sub2	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCacaatccctCggcccttctcagttcgcta	36562
hPKU3_R19_P10_sub4	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCacaatacctCgccccttctcagttcgcta	36563
hPKU3_R19_P10_sub7	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCacaataccgCgcccttctcagttcgcta	36564
hPKU3_R19_P10_sub8	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCacaataccgCgcccattctcagttcgcta	36565
hPKU3_R19_P8_sub0	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCacaatacctCggcccttctcagttcgc	36566
hPKU3_R19_P8_sub1	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCacaataccgCggcccttctcagttcgc	36567
hPKU3_R19_P8_sub2	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCacaatccctCggcccttctcagttcgc	36568
hPKU3_R19_P8_sub4	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCacaatacctCgccccttctcagttcgc	36569
hPKU3_R19_P8_sub7	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCacaataccgCgcccttctcagttcgc	36570

hPKU3_R19_P8_sub8	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCacaataccgCgcccattctcagttcgc	36571
hPKU3_R19_P9_sub0	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCacaatacctCggcccttctcagttcgct	36572
hPKU3_R19_P9_sub1	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCacaataccgCggcccttctcagttcgct	36573
hPKU3_R19_P9_sub2	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCacaatccctCggcccttctcagttcgct	36574
hPKU3_R19_P9_sub4	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCacaatacctCgccccttctcagttcgct	36575
hPKU3_R19_P9_sub7	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCacaataccgCgccccttctcagttcgct	36576
hPKU3_R19_P9_sub8	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCacaataccgCgcccattctcagttcgct	36577
hPKU3_R21_P10_sub0	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCccacaatacctCggcccttctcagttcgcta	36578
hPKU3_R21_P10_sub1	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCccacaataccgCggcccttctcagttcgcta	36579
hPKU3_R21_P10_sub2	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCccacaatccctCggcccttctcagttcgcta	36580
hPKU3_R21_P10_sub4	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCccacaatacctCgccccttctcagttcgcta	36581
hPKU3_R21_P10_sub7	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCccacaataccgCgccccttctcagttcgcta	36582
hPKU3_R21_P10_sub8	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCccacaataccgCgcccattctcagttcgcta	36583
hPKU3_R21_P8_sub0	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCccacaatacctCggcccttctcagttcgc	36584
hPKU3_R21_P8_sub1	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCccacaataccgCggcccttctcagttcgc	36585
hPKU3_R21_P8_sub2	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCccacaatccctCggcccttctcagttcgc	36586
hPKU3_R21_P8_sub4	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCccacaatacctCgccccttctcagttcgc	36587

hPKU3_R21_P8_sub7	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCccacaataccgCgccccttctcagttcgc	36588
hPKU3_R21_P8_sub8	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCccacaataccgCgcccattctcagttcgc	36589
hPKU3_R21_P9_sub0	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCccacaatacctCggcccttctcagttcgct	36590
hPKU3_R21_P9_sub1	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCccacaataccgCggcccttctcagttcgct	36591
hPKU3_R21_P9_sub2	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCccacaatccctCggcccttctcagttcgct	36592
hPKU3_R21_P9_sub4	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCccacaatacctCgccccttctcagttcgct	36593
hPKU3_R21_P9_sub7	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCccacaataccgCgccccttctcagttcgct	36594
hPKU3_R21_P9_sub8	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCccacaataccgCgcccattctcagttcgct	36595
hPKU3_R23_P10_sub0	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCtgccacaatacctCggcccttctcagttcgcta	36596
hPKU3_R23_P10_sub1	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCtgccacaataccgCggcccttctcagttcgcta	36597
hPKU3_R23_P10_sub2	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCtgccacaatccctCggcccttctcagttcgcta	36598
hPKU3_R23_P10_sub4	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCtgccacaatacctCgccccttctcagttcgcta	36599
hPKU3_R23_P10_sub7	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCtgccacaataccgCgccccttctcagttcgcta	36600
hPKU3_R23_P10_sub8	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCtgccacaataccgCgcccattctcagttcgcta	36601
hPKU3_R23_P8_sub0	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCtgccacaatacctCggcccttctcagttcgc	36602
hPKU3_R23_P8_sub1	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCtgccacaataccgCggcccttctcagttcgc	36603
hPKU3_R23_P8_sub2	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCtgccacaatccctCggcccttctcagttcgc	36604

hPKU3_R23_P8_sub4	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCtgccacaataccttCgccccttctcagttcgc	36605
hPKU3_R23_P8_sub7	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCtgccacaataccgCgccccttctcagttcgc	36606
hPKU3_R23_P8_sub8	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCtgccacaataccgCgcccattctcagttcgc	36607
hPKU3_R23_P9_sub0	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCtgccacaataccttCggcccttctcagttcgct	36608
hPKU3_R23_P9_sub1	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCtgccacaataccgCggcccttctcagttcgct	36609
hPKU3_R23_P9_sub2	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCtgccacaatccctCggcccttctcagttcgct	36610
hPKU3_R23_P9_sub4	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCtgccacaataccttCgccccttctcagttcgct	36611
hPKU3_R23_P9_sub7	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCtgccacaataccgCgccccttctcagttcgct	36612
hPKU3_R23_P9_sub8	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCtgccacaataccgCgcccattctcagttcgct	36613
hPKU3_R25_P10_sub0	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCgctgccacaataccttCggcccttctcagttcgcta	36614
hPKU3_R25_P10_sub1	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCgctgccacaataccgCggcccttctcagttcgcta	36615
hPKU3_R25_P10_sub2	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCgctgccacaatccctCggcccttctcagttcgcta	36616
hPKU3_R25_P10_sub4	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCgctgccacaataccttCgccccttctcagttcgcta	36617
hPKU3_R25_P10_sub7	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCgctgccacaataccgCgccccttctcagttcgcta	36618
hPKU3_R25_P10_sub8	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCgctgccacaataccgCgcccattctcagttcgcta	36619
hPKU3_R25_P8_sub0	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCgctgccacaataccttCggcccttctcagttcgc	36620
hPKU3_R25_P8_sub1	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCgctgccacaataccgCggcccttctcagttcgc	36621

hPKU3_R25_P8_sub2	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCgctgccacaatccctCggcccttctcagttcgc	36622
hPKU3_R25_P8_sub4	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCgctgccacaatacctCgccccttctcagttcgc	36623
hPKU3_R25_P8_sub7	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCgctgccacaataccgCgccccttctcagttcgc	36624
hPKU3_R25_P8_sub8	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCgctgccacaataccgCgcccattctcagttcgc	36625
hPKU3_R25_P9_sub0	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCgctgccacaatacctCggcccttctcagttcgct	36626
hPKU3_R25_P9_sub1	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCgctgccacaataccgCggcccttctcagttcgct	36627
hPKU3_R25_P9_sub2	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCgctgccacaatccctCggcccttctcagttcgct	36628
hPKU3_R25_P9_sub4	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCgctgccacaatacctCgccccttctcagttcgct	36629
hPKU3_R25_P9_sub7	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCgctgccacaataccgCgccccttctcagttcgct	36630
hPKU3_R25_P9_sub8	TGGGTCGTAGCGAACTGAGAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCgctgccacaataccgCgcccattctcagttcgct	36631

Table 8B. Exemplary template RNA sequences

Table 8B provides design of exemplary DNA components of gene modifying systems for correcting the pathogenic R408W mutation in PAH to the wild-type form. This table details the sequence of a complete template RNA comprising one or more silent substitutions described in Table 7A for use in a Cas-RT fusion gene modifying polypeptide. Templates in this table employ the hPKU4 spacer GGGTCGTAGCGAACTGAGAA (SEQ ID NO:16084).

Name	tgRNA sequence	SEQ ID NO
hPKU4_R16_P10_sub0	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCaatacctCggcccttctcagttcgct	36632
hPKU4_R16_P10_sub1	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCaataccgCggcccttctcagttcgct	36633

hPKU4_R16_P10_sub4	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCaatacctCgccccttctcagttcgct	36634
hPKU4_R16_P10_sub5	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCaatacctCgcccattctcagttcgct	36635
hPKU4_R16_P10_sub7	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCaataccgCgccccttctcagttcgct	36636
hPKU4_R16_P10_sub8	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCaataccgCgcccattctcagttcgct	36637
hPKU4_R16_P8_sub0	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCaatacctCggcccttctcagttcg	36638
hPKU4_R16_P8_sub1	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCaataccgCggcccttctcagttcg	36639
hPKU4_R16_P8_sub4	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCaatacctCgccccttctcagttcg	36640
hPKU4_R16_P8_sub5	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCaatacctCgcccattctcagttcg	36641
hPKU4_R16_P8_sub7	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCaataccgCgccccttctcagttcg	36642
hPKU4_R16_P8_sub8	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCaataccgCgcccattctcagttcg	36643
hPKU4_R16_P9_sub0	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCaatacctCggcccttctcagttcgc	36644
hPKU4_R16_P9_sub1	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCaataccgCggcccttctcagttcgc	36645
hPKU4_R16_P9_sub4	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCaatacctCgccccttctcagttcgc	36646
hPKU4_R16_P9_sub5	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCaatacctCgcccattctcagttcgc	36647
hPKU4_R16_P9_sub7	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCaataccgCgccccttctcagttcgc	36648
hPKU4_R16_P9_sub8	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCaataccgCgcccattctcagttcgc	36649
hPKU4_R18_P10_sub0	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCacaatacctCggcccttctcagttcgct	36650

hPKU4_R18_P10_sub1	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCacaataccgCggcccttctcagttcgct	36651
hPKU4_R18_P10_sub4	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCacaatacctCgccccttctcagttcgct	36652
hPKU4_R18_P10_sub5	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCacaatacctCgcccattctcagttcgct	36653
hPKU4_R18_P10_sub7	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCacaataccgCgccccttctcagttcgct	36654
hPKU4_R18_P10_sub8	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCacaataccgCgcccattctcagttcgct	36655
hPKU4_R18_P8_sub0	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCacaatacctCggcccttctcagttcg	36656
hPKU4_R18_P8_sub1	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCacaataccgCggcccttctcagttcg	36657
hPKU4_R18_P8_sub4	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCacaatacctCgccccttctcagttcg	36658
hPKU4_R18_P8_sub5	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCacaatacctCgcccattctcagttcg	36659
hPKU4_R18_P8_sub7	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCacaataccgCgccccttctcagttcg	36660
hPKU4_R18_P8_sub8	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCacaataccgCgcccattctcagttcg	36661
hPKU4_R18_P9_sub0	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCacaatacctCggcccttctcagttcgc	36662
hPKU4_R18_P9_sub1	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCacaataccgCggcccttctcagttcgc	36663
hPKU4_R18_P9_sub4	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCacaatacctCgccccttctcagttcgc	36664
hPKU4_R18_P9_sub5	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCacaatacctCgcccattctcagttcgc	36665
hPKU4_R18_P9_sub7	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCacaataccgCgccccttctcagttcgc	36666
hPKU4_R18_P9_sub8	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCacaataccgCgcccattctcagttcgc	36667

hPKU4_R20_P10_sub0	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCccacaatacctCggcccttctcagttcgct	36668
hPKU4_R20_P10_sub1	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCccacaataccgCggcccttctcagttcgct	36669
hPKU4_R20_P10_sub4	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCccacaatacctCgcccttctcagttcgct	36670
hPKU4_R20_P10_sub5	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCccacaatacctCgcccattctcagttcgct	36671
hPKU4_R20_P10_sub7	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCccacaataccgCgcccttctcagttcgct	36672
hPKU4_R20_P10_sub8	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCccacaataccgCgcccattctcagttcgct	36673
hPKU4_R20_P8_sub0	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCccacaatacctCggcccttctcagttcg	36674
hPKU4_R20_P8_sub1	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCccacaataccgCggcccttctcagttcg	36675
hPKU4_R20_P8_sub4	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCccacaatacctCgcccttctcagttcg	36676
hPKU4_R20_P8_sub5	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCccacaatacctCgcccattctcagttcg	36677
hPKU4_R20_P8_sub7	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCccacaataccgCgcccttctcagttcg	36678
hPKU4_R20_P8_sub8	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCccacaataccgCgcccattctcagttcg	36679
hPKU4_R20_P9_sub0	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCccacaatacctCggcccttctcagttcgc	36680
hPKU4_R20_P9_sub1	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCccacaataccgCggcccttctcagttcgc	36681
hPKU4_R20_P9_sub4	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCccacaatacctCgcccttctcagttcgc	36682
hPKU4_R20_P9_sub5	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCccacaatacctCgcccattctcagttcgc	36683
hPKU4_R20_P9_sub7	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCccacaataccgCgcccttctcagttcgc	36684

hPKU4_R20_P9_sub8	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCccacaataccgCgcccattctcagttcgc	36685
hPKU4_R22_P10_sub0	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCtgccacaatacctCggccttctcagttcgct	36686
hPKU4_R22_P10_sub1	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCtgccacaataccgCggccttctcagttcgct	36687
hPKU4_R22_P10_sub4	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCtgccacaatacctCgcccttctcagttcgct	36688
hPKU4_R22_P10_sub5	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCtgccacaatacctCgcccattctcagttcgct	36689
hPKU4_R22_P10_sub7	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCtgccacaataccgCgcccttctcagttcgct	36690
hPKU4_R22_P10_sub8	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCtgccacaataccgCgcccattctcagttcgct	36691
hPKU4_R22_P8_sub0	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCtgccacaatacctCggcccttctcagttcg	36692
hPKU4_R22_P8_sub1	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCtgccacaataccgCggcccttctcagttcg	36693
hPKU4_R22_P8_sub4	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCtgccacaatacctCgcccttctcagttcg	36694
hPKU4_R22_P8_sub5	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCtgccacaatacctCgcccattctcagttcg	36695
hPKU4_R22_P8_sub7	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCtgccacaataccgCgcccttctcagttcg	36696
hPKU4_R22_P8_sub8	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCtgccacaataccgCgcccattctcagttcg	36697
hPKU4_R22_P9_sub0	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCtgccacaatacctCggcccttctcagttcgc	36698
hPKU4_R22_P9_sub1	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCtgccacaataccgCggcccttctcagttcgc	36699
hPKU4_R22_P9_sub4	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCtgccacaatacctCgcccttctcagttcgc	36700
hPKU4_R22_P9_sub5	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCtgccacaatacctCgcccattctcagttcgc	36701

hPKU4_R22_P9_sub7	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCtgccacaataccgCgccccttctcagttcgc	36702
hPKU4_R22_P9_sub8	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCtgccacaataccgCgcccattctcagttcgc	36703
hPKU4_R24_P10_sub0	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCgctgccacaatacctCggcccttctcagttcgct	36704
hPKU4_R24_P10_sub1	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCgctgccacaataccgCggcccttctcagttcgct	36705
hPKU4_R24_P10_sub4	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCgctgccacaatacctCgccccttctcagttcgct	36706
hPKU4_R24_P10_sub5	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCgctgccacaatacctCgcccattctcagttcgct	36707
hPKU4_R24_P10_sub7	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCgctgccacaataccgCgcccttctcagttcgct	36708
hPKU4_R24_P10_sub8	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCgctgccacaataccgCgcccattctcagttcgct	36709
hPKU4_R24_P8_sub0	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCgctgccacaatacctCggcccttctcagttcg	36710
hPKU4_R24_P8_sub1	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCgctgccacaataccgCggcccttctcagttcg	36711
hPKU4_R24_P8_sub4	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCgctgccacaatacctCgccccttctcagttcg	36712
hPKU4_R24_P8_sub5	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCgctgccacaatacctCgcccattctcagttcg	36713
hPKU4_R24_P8_sub7	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCgctgccacaataccgCgcccttctcagttcg	36714
hPKU4_R24_P8_sub8	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCgctgccacaataccgCgcccattctcagttcg	36715
hPKU4_R24_P9_sub0	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCgctgccacaatacctCggcccttctcagttcgc	36716
hPKU4_R24_P9_sub1	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCgctgccacaataccgCggcccttctcagttcgc	36717
hPKU4_R24_P9_sub4	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCgctgccacaatacctCgccccttctcagttcgc	36718

hPKU4_R24_P9_sub5	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCgctgccacaatacctCgcccattctcagttcgc	36719
hPKU4_R24_P9_sub7	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCgctgccacaataccgCgccccttctcagttcgc	36720
hPKU4_R24_P9_sub8	GGGTCGTAGCGAACTGAGAAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCgctgccacaataccgCgcccattctcagttcgc	36721

Table 8C. Exemplary template RNA sequences

Table 8C provides design of exemplary DNA components of gene modifying systems for correcting the pathogenic R408W mutation in PAH to the wild-type form. This table details the sequence of a complete template RNA comprising one or more silent substitutions described in Table 7A for use in a Cas-RT fusion gene modifying polypeptide. Templates in this table employ the hPKU5 spacer TAGCGAACTGAGAAGGGCCA (SEQ ID NO: 16011).

Name	tgRNA sequence	SEQ ID NO
hPKU5_P10R10_sub5	tagcgaactgagaagggccAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCaataccgCgccccttctcag	36722
hPKU5_P10R12_sub5	tagcgaactgagaagggccAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCacaataccgCgccccttctcag	36723
hPKU5_P10R14_sub5	tagcgaactgagaagggccAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCccacaataccgCgccccttctcag	36724
hPKU5_P10R16_sub5	tagcgaactgagaagggccAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCtgccacaataccgCgccccttctcag	36725
hPKU5_P10R18_sub5	tagcgaactgagaagggccAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCgctgccacaataccgCgccccttctcag	36726
hPKU5_P10R20_sub5	tagcgaactgagaagggccAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCttgctgccacaataccgCgccccttctcag	36727
hPKU5_P10R22_sub5	tagcgaactgagaagggccAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCctttgctgccacaataccgCgccccttctcag	36728
hPKU5_P10R24_sub5	tagcgaactgagaagggccAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCaactttgctgccacaataccgCgccccttctcag	36729
hPKU5_P10R8_sub5	tagcgaactgagaagggccAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCtaccgCgccccttctcag	36730

hPKU5_P11 R10_sub5	tagcgaactgagaagggccAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGA GTCGGTGCaataccgCgccccttctcagt	36731
hPKU5_P11 R12_sub5	tagcgaactgagaagggccAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGA GTCGGTGCacaataccgCgccccttctcagt	36732
hPKU5_P11 R14_sub5	tagcgaactgagaagggccAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGA GTCGGTGCccacaataccgCgccccttctcagt	36733
hPKU5_P11 R16_sub5	tagcgaactgagaagggccAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGA GTCGGTGCtgccacaataccgCgccccttctcagt	36734
hPKU5_P11 R18_sub5	tagcgaactgagaagggccAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGA GTCGGTGCgctgccacaataccgCgccccttctcagt	36735
hPKU5_P11 R20_sub5	tagcgaactgagaagggccAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGA GTCGGTGCttgctgccacaataccgCgccccttctcagt	36736
hPKU5_P11 R22_sub5	tagcgaactgagaagggccAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGA GTCGGTGCctttgctgccacaataccgCgccccttctcagt	36737
hPKU5_P11 R24_sub5	tagcgaactgagaagggccAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGA GTCGGTGCaactttgctgccacaataccgCgccccttctcagt	36738
hPKU5_P11 R8_sub5	tagcgaactgagaagggccAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGA GTCGGTGCtaccgCgccccttctcagt	36739
hPKU5_P12 R10_sub5	tagcgaactgagaagggccAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGA GTCGGTGCaataccgCgccccttctcagtt	36740
hPKU5_P12 R12_sub5	tagcgaactgagaagggccAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGA GTCGGTGCacaataccgCgccccttctcagtt	36741
hPKU5_P12 R14_sub5	tagcgaactgagaagggccAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGA GTCGGTGCccacaataccgCgccccttctcagtt	36742
hPKU5_P12 R16_sub5	tagcgaactgagaagggccAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGA GTCGGTGCtgccacaataccgCgccccttctcagtt	36743
hPKU5_P12 R18_sub5	tagcgaactgagaagggccAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGA GTCGGTGCgctgccacaataccgCgccccttctcagtt	36744
hPKU5_P12 R20_sub5	tagcgaactgagaagggccAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGA GTCGGTGCttgctgccacaataccgCgccccttctcagtt	36745
hPKU5_P12 R22_sub5	tagcgaactgagaagggccAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGA GTCGGTGCctttgctgccacaataccgCgccccttctcagtt	36746
hPKU5_P12 R24_sub5	tagcgaactgagaagggccAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGA GTCGGTGCaactttgctgccacaataccgCgccccttctcagtt	36747

hPKU5_P12R8_sub5	tagcgaactgagaagggccAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCtaccgCgccccttctcagtt	36748
hPKU5_P13R10_sub5	tagcgaactgagaagggccAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCaataccgCgccccttctcagttc	36749
hPKU5_P13R12_sub5	tagcgaactgagaagggccAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCacaataccgCgccccttctcagttc	36750
hPKU5_P13R14_sub5	tagcgaactgagaagggccAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCccacaataccgCgccccttctcagttc	36751
hPKU5_P13R16_sub5	tagcgaactgagaagggccAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCtgccacaataccgCgccccttctcagttc	36752
hPKU5_P13R18_sub5	tagcgaactgagaagggccAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCgctgccacaataccgCgccccttctcagttc	36753
hPKU5_P13R20_sub5	tagcgaactgagaagggccAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCttgctgccacaataccgCgccccttctcagttc	36754
hPKU5_P13R22_sub5	tagcgaactgagaagggccAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCctttgctgccacaataccgCgccccttctcagttc	36755
hPKU5_P13R24_sub5	tagcgaactgagaagggccAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCaactttgctgccacaataccgCgccccttctcagttc	36756
hPKU5_P13R8_sub5	tagcgaactgagaagggccAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCtaccgCgccccttctcagttc	36757
hPKU5_P14R10_sub5	tagcgaactgagaagggccAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCaataccgCgccccttctcagttcg	36758
hPKU5_P14R12_sub5	tagcgaactgagaagggccAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCacaataccgCgccccttctcagttcg	36759
hPKU5_P14R14_sub5	tagcgaactgagaagggccAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCccacaataccgCgccccttctcagttcg	36760
hPKU5_P14R16_sub5	tagcgaactgagaagggccAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCtgccacaataccgCgccccttctcagttcg	36761
hPKU5_P14R18_sub5	tagcgaactgagaagggccAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCgctgccacaataccgCgccccttctcagttcg	36762
hPKU5_P14R20_sub5	tagcgaactgagaagggccAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCttgctgccacaataccgCgccccttctcagttcg	36763
hPKU5_P14R22_sub5	tagcgaactgagaagggccAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCctttgctgccacaataccgCgccccttctcagttcg	36764

hPKU5_P14 R24_sub5	tagcgaactgagaagggccAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGA GTCGGTGCaactttgctgccacaataccgCgccccttctcagttcg	36765
hPKU5_P14 R8_sub5	tagcgaactgagaagggccAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGA GTCGGTGCtaccgCgccccttctcagttcg	36766
hPKU5_P15 R10_sub5	tagcgaactgagaagggccAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGA GTCGGTGCaataccgCgccccttctcagttcgc	36767
hPKU5_P15 R12_sub5	tagcgaactgagaagggccAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGA GTCGGTGCacaataccgCgccccttctcagttcgc	36768
hPKU5_P15 R14_sub5	tagcgaactgagaagggccAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGA GTCGGTGCccacaataccgCgccccttctcagttcgc	36769
hPKU5_P15 R16_sub5	tagcgaactgagaagggccAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGA GTCGGTGCtgccacaataccgCgccccttctcagttcgc	36770
hPKU5_P15 R18_sub5	tagcgaactgagaagggccAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGA GTCGGTGCgctgccacaataccgCgccccttctcagttcgc	36771
hPKU5_P15 R20_sub5	tagcgaactgagaagggccAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGA GTCGGTGCttgctgccacaataccgCgccccttctcagttcgc	36772
hPKU5_P15 R22_sub5	tagcgaactgagaagggccAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGA GTCGGTGCctttgctgccacaataccgCgccccttctcagttcgc	36773
hPKU5_P15 R24_sub5	tagcgaactgagaagggccAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGA GTCGGTGCaactttgctgccacaataccgCgccccttctcagttcgc	36774
hPKU5_P15 R8_sub5	tagcgaactgagaagggccAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGA GTCGGTGCtaccgCgccccttctcagttcgc	36775
hPKU5_P16 R10_sub5	tagcgaactgagaagggccAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGA GTCGGTGCaataccgCgccccttctcagttcgct	36776
hPKU5_P16 R12_sub5	tagcgaactgagaagggccAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGA GTCGGTGCacaataccgCgccccttctcagttcgct	36777
hPKU5_P16 R14_sub5	tagcgaactgagaagggccAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGA GTCGGTGCccacaataccgCgccccttctcagttcgct	36778
hPKU5_P16 R16_sub5	tagcgaactgagaagggccAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGA GTCGGTGCtgccacaataccgCgccccttctcagttcgct	36779
hPKU5_P16 R18_sub5	tagcgaactgagaagggccAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGA GTCGGTGCgctgccacaataccgCgccccttctcagttcgct	36780
hPKU5_P16 R20_sub5	tagcgaactgagaagggccAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGA GTCGGTGCttgctgccacaataccgCgccccttctcagttcgct	36781

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hPKU5_R20_P10_sub7	TAGCGAACTGAGAAGGGCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCttgctgccacgatacctCggcccttctcag	36889
hPKU5_R20_P8_sub0	TAGCGAACTGAGAAGGGCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCttgctgccacaatacctCggcccttctc	36890
hPKU5_R20_P8_sub1	TAGCGAACTGAGAAGGGCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCttgctgccacaataccgCggcccttctc	36891
hPKU5_R20_P8_sub2	TAGCGAACTGAGAAGGGCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCttgctgccacaatccctCggcccttctc	36892
hPKU5_R20_P8_sub3	TAGCGAACTGAGAAGGGCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCttgctgccacaatcccgCggcccttctc	36893
hPKU5_R20_P8_sub4	TAGCGAACTGAGAAGGGCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCttgctgccacaatacctCgccccttctc	36894
hPKU5_R20_P8_sub7	TAGCGAACTGAGAAGGGCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCttgctgccacgatacctCggcccttctc	36895
hPKU5_R20_P9_sub0	TAGCGAACTGAGAAGGGCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCttgctgccacaatacctCggcccttctca	36896
hPKU5_R20_P9_sub1	TAGCGAACTGAGAAGGGCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCttgctgccacaataccgCggcccttctca	36897
hPKU5_R20_P9_sub2	TAGCGAACTGAGAAGGGCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCttgctgccacaatccctCggcccttctca	36898
hPKU5_R20_P9_sub3	TAGCGAACTGAGAAGGGCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCttgctgccacaatcccgCggcccttctca	36899
hPKU5_R20_P9_sub4	TAGCGAACTGAGAAGGGCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCttgctgccacaatacctCgccccttctca	36900

hPKU5_R20_P9_sub7	TAGCGAACTGAGAAGGGCCAGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCttgctgccacgatacctCggcccttctca	36901

Table 8D. Exemplary template RNA sequences

Table 8D provides design of exemplary DNA components of gene modifying systems for correcting the pathogenic R408W mutation in PAH to the wild-type form. This table details the sequence of a complete template RNA comprising one or more silent substitutions described in Table 7A for use in a Cas-RT fusion gene modifying polypeptide. Templates in this table employ the hPKU6 spacer ACTTTGCTGCCACAATACCT (SEQ ID NO: 16032).

Name	tgRNA sequence	SEQ ID NO
hPKU6_P10R11_sub3	actttgctgccacaatacctGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCaagggacGgggtattgtggca	36902
hPKU6_P10R13_sub3	actttgctgccacaatacctGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCagaagggacGgggtattgtggca	36903
hPKU6_P10R15_sub3	actttgctgccacaatacctGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCtgagaagggacGgggtattgtggca	36904
hPKU6_P10R17_sub3	actttgctgccacaatacctGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCactgagaagggacGgggtattgtggca	36905
hPKU6_P10R19_sub3	actttgctgccacaatacctGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCgaactgagaagggacGgggtattgtggca	36906
hPKU6_P10R21_sub3	actttgctgccacaatacctGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCgcgaactgagaagggacGgggtattgtggca	36907
hPKU6_P10R23_sub3	actttgctgccacaatacctGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCtagcgaactgagaagggacGgggtattgtggca	36908
hPKU6_P10R25_sub3	actttgctgccacaatacctGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCcgtagcgaactgagaagggacGgggtattgtggca	36909
hPKU6_P10R9_sub3	actttgctgccacaatacctGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCgggacGgggtattgtggca	36910
hPKU6_P11R11_sub3	actttgctgccacaatacctGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCaagggacGgggtattgtggcag	36911

hPKU6_P11R13_sub3	actttgctgccacaatacctGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCagaagggacGgggtattgtggcag	36912
hPKU6_P11R15_sub3	actttgctgccacaatacctGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCtgagaagggacGgggtattgtggcag	36913
hPKU6_P11R17_sub3	actttgctgccacaatacctGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCactgagaagggacGgggtattgtggcag	36914
hPKU6_P11R19_sub3	actttgctgccacaatacctGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCgaactgagaagggacGgggtattgtggcag	36915
hPKU6_P11R21_sub3	actttgctgccacaatacctGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCgcgaactgagaagggacGgggtattgtggcag	36916
hPKU6_P11R23_sub3	actttgctgccacaatacctGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCtagcgaactgagaagggacGgggtattgtggcag	36917
hPKU6_P11R25_sub3	actttgctgccacaatacctGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCcgtagcgaactgagaagggacGgggtattgtggcag	36918
hPKU6_P11R9_sub3	actttgctgccacaatacctGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCgggacGgggtattgtggcag	36919
hPKU6_P12R11_sub3	actttgctgccacaatacctGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCaagggacGgggtattgtggcagc	36920
hPKU6_P12R13_sub3	actttgctgccacaatacctGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCagaagggacGgggtattgtggcagc	36921
hPKU6_P12R15_sub3	actttgctgccacaatacctGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCtgagaagggacGgggtattgtggcagc	36922
hPKU6_P12R17_sub3	actttgctgccacaatacctGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCactgagaagggacGgggtattgtggcagc	36923
hPKU6_P12R19_sub3	actttgctgccacaatacctGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCgaactgagaagggacGgggtattgtggcagc	36924
hPKU6_P12R21_sub3	actttgctgccacaatacctGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCgcgaactgagaagggacGgggtattgtggcagc	36925
hPKU6_P12R23_sub3	actttgctgccacaatacctGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCtagcgaactgagaagggacGgggtattgtggcagc	36926
hPKU6_P12R25_sub3	actttgctgccacaatacctGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCcgtagcgaactgagaagggacGgggtattgtggcagc	36927
hPKU6_P12R9_sub3	actttgctgccacaatacctGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCgggacGgggtattgtggcagc	36928

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hPKU6_P13R13_sub3	actttgctgccacaatacctGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCagaagggacGgggtattgtggcagca	36930
hPKU6_P13R15_sub3	actttgctgccacaatacctGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCtgagaagggacGgggtattgtggcagca	36931
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hPKU6_P13R21_sub3	actttgctgccacaatacctGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCgcgaactgagaagggacGgggtattgtggcagca	36934
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hPKU6_P13R25_sub3	actttgctgccacaatacctGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCcgtagcgaactgagaagggacGgggtattgtggcagca	36936
hPKU6_P13R9_sub3	actttgctgccacaatacctGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCgggacGgggtattgtggcagca	36937
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hPKU6_P14R17_sub3	actttgctgccacaatacctGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCactgagaagggacGgggtattgtggcagcaa	36941
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hPKU6_P14R23_sub3	actttgctgccacaatacctGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCtagcgaactgagaagggacGgggtattgtggcagcaa	36944
hPKU6_P14R25_sub3	actttgctgccacaatacctGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCcgtagcgaactgagaagggacGgggtattgtggcagcaa	36945

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hPKU6_P15R17_sub3	actttgctgccacaatacctGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCactgagaagggacGgggtattgtggcagcaaa	36950
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hPKU6_P16R11_sub3	actttgctgccacaatacctGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCaagggacGgggtattgtggcagcaaag	36956
hPKU6_P16R13_sub3	actttgctgccacaatacctGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCagaagggacGgggtattgtggcagcaaag	36957
hPKU6_P16R15_sub3	actttgctgccacaatacctGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCtgagaagggacGgggtattgtggcagcaaag	36958
hPKU6_P16R17_sub3	actttgctgccacaatacctGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCactgagaagggacGgggtattgtggcagcaaag	36959
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hPKU6_P16R23_sub3	actttgctgccacaatacctGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCtagcgaactgagaagggacGgggtattgtggcagcaaag	36962

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hPKU6_R12_P10_sub1	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCgaagggccGgggtattgtggca	36993
hPKU6_R12_P10_sub4	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCgaacggccGgggtattgtggca	36994
hPKU6_R12_P10_sub5	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCgaacggacGgggtattgtggca	36995
hPKU6_R12_P10_sub6	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCgaagggccGcggtattgtggca	36996

hPKU6_R12_P10_sub7	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCgaagggacGcggtattgtggca	36997
hPKU6_R12_P11_sub0	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCgaagggccGaggtattgtggcag	36998
hPKU6_R12_P11_sub1	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCgaagggccGgggtattgtggcag	36999
hPKU6_R12_P11_sub4	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCgaacggccGgggtattgtggcag	37000
hPKU6_R12_P11_sub5	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCgaacggacGgggtattgtggcag	37001
hPKU6_R12_P11_sub6	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCgaagggccGcggtattgtggcag	37002
hPKU6_R12_P11_sub7	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCgaagggacGcggtattgtggcag	37003
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hPKU6_R12_P9_sub1	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCgaagggccGgggtattgtggc	37005
hPKU6_R12_P9_sub4	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCgaacggccGgggtattgtggc	37006
hPKU6_R12_P9_sub5	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCgaacggacGgggtattgtggc	37007
hPKU6_R12_P9_sub6	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCgaagggccGcggtattgtggc	37008
hPKU6_R12_P9_sub7	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCgaagggacGcggtattgtggc	37009
hPKU6_R14_P10_sub0	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCgagaagggccGaggtattgtggca	37010
hPKU6_R14_P10_sub1	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCgagaagggccGgggtattgtggca	37011
hPKU6_R14_P10_sub4	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCgagaacggccGgggtattgtggca	37012
hPKU6_R14_P10_sub5	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCgagaacggacGgggtattgtggca	37013

hPKU6_R14_P10_sub6	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCgagaagggccGcggtattgtggca	37014
hPKU6_R14_P10_sub7	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCgagaagggacGcggtattgtggca	37015
hPKU6_R14_P11_sub0	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCgagaagggccGaggtattgtggcag	37016
hPKU6_R14_P11_sub1	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCgagaagggccGgggtattgtggcag	37017
hPKU6_R14_P11_sub4	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCgagaacggccGgggtattgtggcag	37018
hPKU6_R14_P11_sub5	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCgagaacggacGgggtattgtggcag	37019
hPKU6_R14_P11_sub6	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCgagaagggccGcggtattgtggcag	37020
hPKU6_R14_P11_sub7	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCgagaagggacGcggtattgtggcag	37021
hPKU6_R14_P9_sub0	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCgagaagggccGaggtattgtggc	37022
hPKU6_R14_P9_sub1	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCgagaagggccGgggtattgtggc	37023
hPKU6_R14_P9_sub4	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCgagaacggccGgggtattgtggc	37024
hPKU6_R14_P9_sub5	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCgagaacggacGgggtattgtggc	37025
hPKU6_R14_P9_sub6	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCgagaagggccGcggtattgtggc	37026
hPKU6_R14_P9_sub7	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCgagaagggacGcggtattgtggc	37027
hPKU6_R16_P10_sub0	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCctgagaagggccGaggtattgtggca	37028
hPKU6_R16_P10_sub1	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCctgagaagggccGgggtattgtggca	37029
hPKU6_R16_P10_sub4	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCctgagaacggccGgggtattgtggca	37030

hPKU6_R16_P10_sub5	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCctgagaacggacGgggtattgtggca	37031
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hPKU6_R16_P10_sub7	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCctgagaagggacGcggtattgtggca	37033
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hPKU6_R16_P11_sub7	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCctgagaagggacGcggtattgtggcag	37039
hPKU6_R16_P9_sub0	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCctgagaagggccGaggtattgtggc	37040
hPKU6_R16_P9_sub1	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCctgagaagggccGgggtattgtggc	37041
hPKU6_R16_P9_sub4	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCctgagaacggccGgggtattgtggc	37042
hPKU6_R16_P9_sub5	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCctgagaacggacGgggtattgtggc	37043
hPKU6_R16_P9_sub6	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCctgagaagggccGcggtattgtggc	37044
hPKU6_R16_P9_sub7	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCctgagaagggacGcggtattgtggc	37045
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hPKU6_R18_P10_sub1	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCaactgagaagggccGgggtattgtggca	37047

hPKU6_R18_P10_sub4	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCaactgagaacggccGgggtattgtggca	37048
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hPKU6_R18_P9_sub0	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCaactgagaagggccGaggtattgtggc	37058
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hPKU6_R18_P9_sub4	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCaactgagaacggccGgggtattgtggc	37060
hPKU6_R18_P9_sub5	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCaactgagaacggacGgggtattgtggc	37061
hPKU6_R18_P9_sub6	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCaactgagaagggccGcggtattgtggc	37062
hPKU6_R18_P9_sub7	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCaactgagaagggacGcggtattgtggc	37063
hPKU6_R20_P10_sub0	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCcgaactgagaagggccGaggtattgtggca	37064

hPKU6_R20_P10_sub1	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCcgaactgagaagggccGgggtattgtggca	37065
hPKU6_R20_P10_sub4	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCcgaactgagaacggccGgggtattgtggca	37066
hPKU6_R20_P10_sub5	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCcgaactgagaacggacGgggtattgtggca	37067
hPKU6_R20_P10_sub6	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCcgaactgagaagggccGcggtattgtggca	37068
hPKU6_R20_P10_sub7	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCcgaactgagaagggacGcggtattgtggca	37069
hPKU6_R20_P11_sub0	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCcgaactgagaagggccGaggtattgtggcag	37070
hPKU6_R20_P11_sub1	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCcgaactgagaagggccGgggtattgtggcag	37071
hPKU6_R20_P11_sub4	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCcgaactgagaacggccGgggtattgtggcag	37072
hPKU6_R20_P11_sub5	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCcgaactgagaacggacGgggtattgtggcag	37073
hPKU6_R20_P11_sub6	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCcgaactgagaagggccGcggtattgtggcag	37074
hPKU6_R20_P11_sub7	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCcgaactgagaagggacGcggtattgtggcag	37075
hPKU6_R20_P9_sub0	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCcgaactgagaagggccGaggtattgtggc	37076
hPKU6_R20_P9_sub1	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCcgaactgagaagggccGgggtattgtggc	37077
hPKU6_R20_P9_sub4	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCcgaactgagaacggccGgggtattgtggc	37078
hPKU6_R20_P9_sub5	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCcgaactgagaacggacGgggtattgtggc	37079
hPKU6_R20_P9_sub6	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCcgaactgagaagggccGcggtattgtggc	37080
hPKU6_R20_P9_sub7	ACTTTGCTGCCACAATACCTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCcgaactgagaagggacGcggtattgtggc	37081

gRNAs with inducible activity

In some embodiments, a gRNA described herein (e.g., a gRNA that is part of a template RNA or a gRNA used for second strand nicking) has inducible activity. Inducible activity may be achieved by the template nucleic acid, e.g., template RNA, further comprising (in addition to the gRNA) a blocking domain, wherein the sequence of a portion of or all of the blocking domain is at least partially complementary to a portion or all of the gRNA. The blocking domain is thus capable of hybridizing or substantially hybridizing to a portion of or all of the gRNA. In some embodiments, the blocking domain and inducibly active gRNA are disposed on the template nucleic acid, e.g., template RNA, such that the gRNA can adopt a first conformation where the blocking domain is hybridized or substantially hybridized to the gRNA, and a second conformation where the blocking domain is not hybridized or not substantially hybridized to the gRNA. In some embodiments, in the first conformation the gRNA is unable to bind to the gene modifying polypeptide (e.g., the template nucleic acid binding domain, DNA binding domain, or endonuclease domain (e.g., a CRISPR/Cas protein)) or binds with substantially decreased affinity compared to an otherwise similar template RNA lacking the blocking domain. In some embodiments, in the second conformation the gRNA is able to bind to the gene modifying polypeptide (e.g., the template nucleic acid binding domain, DNA binding domain, or endonuclease domain (e.g., a CRISPR/Cas protein)). In some embodiments, whether the gRNA is in the first or second conformation can influence whether the DNA binding or endonuclease activities of the gene modifying polypeptide (e.g., of the CRISPR/Cas protein the gene modifying polypeptide comprises) are active.

In some embodiments, the gRNA that coordinates the second nick has inducible activity. In some embodiments, the gRNA that coordinates the second nick is induced after the template is reverse transcribed. In some embodiments, hybridization of the gRNA to the blocking domain can be disrupted using an opener molecule. In some embodiments, an opener molecule comprises an agent that binds to a portion or all of the gRNA or blocking domain and inhibits hybridization of the gRNA to the blocking domain. In some embodiments, the opener molecule comprises a nucleic acid, e.g., comprising a sequence that is partially or wholly complementary to the gRNA, blocking domain, or both. By choosing or designing an appropriate opener molecule, providing the opener molecule can promote a change in the conformation of the gRNA such that it can associate with a CRISPR/Cas protein and provide the associated functions of the

CRISPR/Cas protein (e.g., DNA binding and/or endonuclease activity). Without wishing to be bound by theory, providing the opener molecule at a selected time and/or location may allow for spatial and temporal control of the activity of the gRNA, CRISPR/Cas protein, or gene modifying system comprising the same. In some embodiments, the opener molecule is exogenous to the cell comprising the gene modifying polypeptide and or template nucleic acid. In some embodiments, the opener molecule comprises an endogenous agent (e.g., endogenous to the cell comprising the gene modifying polypeptide and or template nucleic acid comprising the gRNA and blocking domain). For example, an inducible gRNA, blocking domain, and opener molecule may be chosen such that the opener molecule is an endogenous agent expressed in a target cell or tissue, e.g., thereby ensuring activity of a gene modifying system in the target cell or tissue. As a further example, an inducible gRNA, blocking domain, and opener molecule may be chosen such that the opener molecule is absent or not substantially expressed in one or more non-target cells or tissues, e.g., thereby ensuring that activity of a gene modifying system does not occur or substantially occur in the one or more non-target cells or tissues, or occurs at a reduced level compared to a target cell or tissue. Exemplary blocking domains, opener molecules, and uses thereof are described in PCT App. Publication WO2020044039A1, which is incorporated herein by reference in its entirety. In some embodiments, the template nucleic acid, e.g., template RNA, may comprise one or more sequences or structures for binding by one or more components of a gene modifying polypeptide, e.g., by a reverse transcriptase or RNA binding domain, and a gRNA. In some embodiments, the gRNA facilitates interaction with the template nucleic acid binding domain (e.g., RNA binding domain) of the gene modifying polypeptide. In some embodiments, the gRNA directs the gene modifying polypeptide to the matching target sequence, e.g., in a target cell genome.

Circular RNAs and Ribozymes in Gene Modifying Systems

It is contemplated that it may be useful to employ circular and/or linear RNA states during the formulation, delivery, or gene modifying reaction within the target cell. Thus, in some embodiments of any of the aspects described herein, a gene modifying system comprises one or more circular RNAs (circRNAs). In some embodiments of any of the aspects described herein, a gene modifying system comprises one or more linear RNAs. In some embodiments, a nucleic acid as described herein (e.g., a template nucleic acid, a nucleic acid molecule encoding a

gene modifying polypeptide, or both) is a circRNA. In some embodiments, a circular RNA molecule encodes the gene modifying polypeptide. In some embodiments, the circRNA molecule encoding the gene modifying polypeptide is delivered to a host cell. In some embodiments, a circular RNA molecule encodes a recombinase, e.g., as described herein. In some embodiments, the circRNA molecule encoding the recombinase is delivered to a host cell. In some embodiments, the circRNA molecule encoding the gene modifying polypeptide is linearized (e.g., in the host cell, e.g., in the nucleus of the host cell) prior to translation.

Circular RNAs (circRNAs) have been found to occur naturally in cells and have been found to have diverse functions, including both non-coding and protein coding roles in human cells. It has been shown that a circRNA can be engineered by incorporating a self-splicing intron into an RNA molecule (or DNA encoding the RNA molecule) that results in circularization of the RNA, and that an engineered circRNA can have enhanced protein production and stability (Wesselhoeft et al. *Nature Communications* 2018). In some embodiments, the gene modifying polypeptide is encoded as circRNA. In certain embodiments, the template nucleic acid is a DNA, such as a dsDNA or ssDNA. In certain embodiments, the circDNA comprises a template RNA.

In some embodiments, the circRNA comprises one or more ribozyme sequences. In some embodiments, the ribozyme sequence is activated for autocleavage, e.g., in a host cell, e.g., thereby resulting in linearization of the circRNA. In some embodiments, the ribozyme is activated when the concentration of magnesium reaches a sufficient level for cleavage, e.g., in a host cell. In some embodiments the circRNA is maintained in a low magnesium environment prior to delivery to the host cell. In some embodiments, the ribozyme is a protein-responsive ribozyme. In some embodiments, the ribozyme is a nucleic acid-responsive ribozyme. In some embodiments, the circRNA comprises a cleavage site. In some embodiments, the circRNA comprises a second cleavage site.

In some embodiments, the circRNA is linearized in the nucleus of a target cell. In some embodiments, linearization of a circRNA in the nucleus of a cell involves components present in the nucleus of the cell, e.g., to activate a cleavage event. In some embodiments, a ribozyme, e.g., a ribozyme from a B2 or ALU element, that is responsive to a nuclear element, e.g., a nuclear protein, e.g., a genome-interacting protein, e.g., an epigenetic modifier, e.g., EZH2, is

incorporated into a circRNA, e.g., of a gene modifying system. In some embodiments, nuclear localization of the circRNA results in an increase in autocatalytic activity of the ribozyme and linearization of the circRNA.

In some embodiments, the ribozyme is heterologous to one or more of the other components of the gene modifying system. In some embodiments, an inducible ribozyme (e.g., in a circRNA as described herein) is created synthetically, for example, by utilizing a protein ligand-responsive aptamer design. A system for utilizing the satellite RNA of tobacco ringspot virus hammerhead ribozyme with an MS2 coat protein aptamer has been described (Kennedy et al. Nucleic Acids Res 42(19):12306-12321 (2014), incorporated herein by reference in its entirety) that results in activation of the ribozyme activity in the presence of the MS2 coat protein. In embodiments, such a system responds to protein ligand localized to the cytoplasm or the nucleus. In some embodiments the protein ligand is not MS2. Methods for generating RNA aptamers to target ligands have been described, for example, based on the systematic evolution of ligands by exponential enrichment (SELEX) (Tuerk and Gold, Science 249(4968):505-510 (1990); Ellington and Szostak, Nature 346(6287):818-822 (1990); the methods of each of which are incorporated herein by reference) and have, in some instances, been aided by *in silico* design (Bell et al. PNAS 117(15):8486-8493, the methods of which are incorporated herein by reference). Thus, in some embodiments, an aptamer for a target ligand is generated and incorporated into a synthetic ribozyme system, e.g., to trigger ribozyme-mediated cleavage and circRNA linearization, e.g., in the presence of the protein ligand. In some embodiments, circRNA linearization is triggered in the cytoplasm, e.g., using an aptamer that associates with a ligand in the cytoplasm. In some embodiments, circRNA linearization is triggered in the nucleus, e.g., using an aptamer that associates with a ligand in the nucleus. In embodiments, the ligand in the nucleus comprises an epigenetic modifier or a transcription factor. In some embodiments the ligand that triggers linearization is present at higher levels in on-target cells than off-target cells.

It is further contemplated that a nucleic acid-responsive ribozyme system can be employed for circRNA linearization. For example, biosensors that sense defined target nucleic acid molecules to trigger ribozyme activation are described, e.g., in Penchovsky (Biotechnology Advances 32(5):1015-1027 (2014), incorporated herein by reference). By these methods, a ribozyme naturally folds into an inactive state and is only activated in the presence of a defined

target nucleic acid molecule (e.g., an RNA molecule). In some embodiments, a circRNA of a gene modifying system comprises a nucleic acid-responsive ribozyme that is activated in the presence of a defined target nucleic acid, e.g., an RNA, e.g., an mRNA, miRNA, guide RNA, gRNA, sgRNA, ncRNA, lncRNA, tRNA, snRNA, or mtRNA. In some embodiments the nucleic acid that triggers linearization is present at higher levels in on-target cells than off-target cells.

In some embodiments of any of the aspects herein, a gene modifying system incorporates one or more ribozymes with inducible specificity to a target tissue or target cell of interest, e.g., a ribozyme that is activated by a ligand or nucleic acid present at higher levels in a target tissue or target cell of interest. In some embodiments, the gene modifying system incorporates a ribozyme with inducible specificity to a subcellular compartment, e.g., the nucleus, nucleolus, cytoplasm, or mitochondria. In some embodiments, the ribozyme that is activated by a ligand or nucleic acid present at higher levels in the target subcellular compartment. In some embodiments, an RNA component of a gene modifying system is provided as circRNA, e.g., that is activated by linearization. In some embodiments, linearization of a circRNA encoding a gene modifying polypeptide activates the molecule for translation. In some embodiments, a signal that activates a circRNA component of a gene modifying system is present at higher levels in on-target cells or tissues, e.g., such that the system is specifically activated in these cells.

In some embodiments, an RNA component of a gene modifying system is provided as a circRNA that is inactivated by linearization. In some embodiments, a circRNA encoding the gene modifying polypeptide is inactivated by cleavage and degradation. In some embodiments, a circRNA encoding the gene modifying polypeptide is inactivated by cleavage that separates a translation signal from the coding sequence of the polypeptide. In some embodiments, a signal that inactivates a circRNA component of a gene modifying system is present at higher levels in off-target cells or tissues, such that the system is specifically inactivated in these cells.

Target Nucleic Acid Site

In some embodiments, after gene modification, the target site surrounding the edited sequence contains a limited number of insertions or deletions, for example, in less than about 50% or 10% of editing events, e.g., as determined by long-read amplicon sequencing of the target site, e.g., as described in Karst et al. (2020) *bioRxiv* doi.org/10.1101/645903 (incorporated by reference herein in its entirety). In some embodiments, the target site does not show multiple

consecutive editing events, e.g., head-to-tail or head-to-head duplications, e.g., as determined by long-read amplicon sequencing of the target site, e.g., as described in Karst et al. *bioRxiv* doi.org/10.1101/645903 (2020) (incorporated herein by reference in its entirety). In some embodiments, the target site contains an integrated sequence corresponding to the template RNA. In some embodiments, the target site does not contain insertions resulting from endogenous RNA in more than about 1% or 10% of events, e.g., as determined by long-read amplicon sequencing of the target site, e.g., as described in Karst et al. *bioRxiv* doi.org/10.1101/645903 (2020) (incorporated herein by reference in its entirety). In some embodiments, the target site contains the integrated sequence corresponding to the template RNA.

In certain aspects of the present invention, the host DNA-binding site integrated into by the gene modifying system can be in a gene, in an intron, in an exon, an ORF, outside of a coding region of any gene, in a regulatory region of a gene, or outside of a regulatory region of a gene. In other aspects, the polypeptide may bind to one or more than one host DNA sequence.

In some embodiments, a gene modifying system is used to edit a target locus in multiple alleles. In some embodiments, a gene modifying system is designed to edit a specific allele. For example, a gene modifying polypeptide may be directed to a specific sequence that is only present on one allele, e.g., comprises a template RNA with homology to a target allele, e.g., a gRNA or annealing domain, but not to a second cognate allele. In some embodiments, a gene modifying system can alter a haplotype-specific allele. In some embodiments, a gene modifying system that targets a specific allele preferentially targets that allele, e.g., has at least a 2, 4, 6, 8, or 10-fold preference for a target allele.

Second Strand Nicking

In some embodiments, a gene modifying system described herein comprises a nickase activity (e.g., in the gene modifying polypeptide) that nicks the first strand, and a nickase activity (e.g., in a polypeptide separate from the gene modifying polypeptide) that nicks the second strand of target DNA. As discussed herein, without wishing to be bound by theory, nicking of the first strand of the target site DNA is thought to provide a 3´ OH that can be used by an RT domain to reverse transcribe a sequence of a template RNA, e.g., a heterologous object sequence. Without wishing to be bound by theory, it is thought that introducing an additional nick to the second strand may bias the cellular DNA repair machinery to adopt the heterologous object

sequence-based sequence more frequently than the original genomic sequence. In some embodiments, the additional nick to the second strand is made by the same endonuclease domain (e.g., nickase domain) as the nick to the first strand. In some embodiments, the same gene modifying polypeptide performs both the nick to the first strand and the nick to the second strand. In some embodiments, the gene modifying polypeptide comprises a CRISPR/Cas domain and the additional nick to the second strand is directed by an additional nucleic acid, e.g., comprising a second gRNA directing the CRISPR/Cas domain to nick the second strand. In other embodiments, the additional second strand nick is made by a different endonuclease domain (e.g., nickase domain) than the nick to the first strand. In some embodiments, that different endonuclease domain is situated in an additional polypeptide (e.g., a system of the invention further comprises the additional polypeptide), separate from the gene modifying polypeptide. In some embodiments, the additional polypeptide comprises an endonuclease domain (e.g., nickase domain) described herein. In some embodiments, the additional polypeptide comprises a DNA binding domain, e.g., described herein.

It is contemplated herein that the position at which the second strand nick occurs relative to the first strand nick may influence the extent to which one or more of: desired gene modifying DNA modifications are obtained, undesired double-strand breaks (DSBs) occur, undesired insertions occur, or undesired deletions occur. Without wishing to be bound by theory, second strand nicking may occur in two general orientations: inward nicks and outward nicks.

In some embodiments, in the inward nick orientation, the RT domain polymerizes (e.g., using the template RNA (e.g., the heterologous object sequence)) away from the second strand nick. In some embodiments, in the inward nick orientation, the location of the nick to the first strand and the location of the nick to the second strand are positioned between the first PAM site and second PAM site (e.g., in a scenario wherein both nicks are made by a polypeptide (e.g., a gene modifying polypeptide) comprising a CRISPR/Cas domain). When there are two PAMs on the outside and two nicks on the inside, this inward nick orientation can also be referred to as "PAM-out". In some embodiments, in the inward nick orientation, the location of the nick to the first strand and the location of the nick to the second strand are between the sites where the polypeptide and the additional polypeptide bind to the target DNA. In some embodiments, in the inward nick orientation, the location of the nick to the second strand is positioned between the binding sites of the polypeptide and additional polypeptide, and the nick to the first strand is also

located between the binding sites of the polypeptide and additional polypeptide. In some embodiments, in the inward nick orientation, the location of the nick to the first strand and the location of the nick to the second strand are positioned between the PAM site and the binding site of the second polypeptide which is at a distance from the target site.

An example of a gene modifying system that provides an inward nick orientation comprises a gene modifying polypeptide comprising a CRISPR/Cas domain, a template RNA comprising a gRNA that directs nicking of the target site DNA on the first strand, and an additional nucleic acid comprising an additional gRNA that directs nicking at a site a distance from the location of the first nick, wherein the location of the first nick and the location of the second nick are between the PAM sites of the sites to which the two gRNAs direct the gene modifying polypeptide. As a further example, another gene modifying system that provides an inward nick orientation comprises a gene modifying polypeptide comprising a zinc finger molecule and a first nickase domain wherein the zinc finger molecule binds to the target DNA in a manner that directs the first nickase domain to nick the first strand of the target site; an additional polypeptide comprising a CRISPR/Cas domain, and an additional nucleic acid comprising a gRNA that directs the additional polypeptide to nick a site a distance from the target site DNA on the second strand, wherein the location of the first nick and the location of the second nick are between the PAM site and the site to which the zinc finger molecule binds. As a further example, another gene modifying system that provides an inward nick orientation comprises a gene modifying polypeptide comprising a zinc finger molecule and a first nickase domain wherein the zinc finger molecule binds to the target DNA in a manner that directs the first nickase domain to nick the first strand of the target site; an additional polypeptide comprising a TAL effector molecule and a second nickase domain wherein the TAL effector molecule binds to a site a distance from the target site in a manner that directs the additional polypeptide to nick the second strand, wherein the location of the first nick and the location of the second nick are between the site to which the TAL effector molecule binds and the site to which the zinc finger molecule binds.

In some embodiments, in the outward nick orientation, the RT domain polymerizes (e.g., using the template RNA (e.g., the heterologous object sequence)) toward the second strand nick. In some embodiments, in the outward nick orientation when both the first and second nicks are made by a polypeptide comprising a CRISPR/Cas domain (e.g., a gene modifying

polypeptide), the first PAM site and second PAM site are positioned between the location of the nick to the first strand and the location of the nick to the second strand. When there are two PAMs on the inside and two nicks on the outside, this outward nick orientation also can be referred to as "PAM-in". In some embodiments, in the outward nick orientation, the polypeptide (e.g., the gene modifying polypeptide) and the additional polypeptide bind to sites on the target DNA between the location of the nick to the first strand and the location of the nick to the second. In some embodiments, in the outward nick orientation, the location of the nick to the second strand is positioned on the opposite side of the binding sites of the polypeptide and additional polypeptide relative to the location of the nick to the first strand. In some embodiments, in the outward orientation, the PAM site and the binding site of the second polypeptide which is at a distance from the target site are positioned between the location of the nick to the first strand and the location of the nick to the second strand.

An example of a gene modifying system that provides an outward nick orientation comprises a gene modifying polypeptide comprising a CRISPR/Cas domain, a template RNA comprising a gRNA that directs nicking of the target site DNA on the first strand, and an additional nucleic acid comprising an additional gRNA that directs nicking at a site a distance from the location of the first nick, wherein the location of the first nick and the location of the second nick are outside of the PAM sites of the sites to which the two gRNAs direct the gene modifying polypeptide (i.e., the PAM sites are between the location of the first nick and the location of the second nick). As a further example, another gene modifying system that provides an outward nick orientation comprises a gene modifying polypeptide comprising a zinc finger molecule and a first nickase domain wherein the zinc finger molecule binds to the target DNA in a manner that directs the first nickase domain to nick the first strand of the target site; an additional polypeptide comprising a CRISPR/Cas domain, and an additional nucleic acid comprising a gRNA that directs the additional polypeptide to nick a site a distance from the target site DNA on the second strand, wherein the location of the first nick and the location of the second nick are outside the PAM site and the site to which the zinc finger molecule binds (i.e., the PAM site and the site to which the zinc finger molecule binds are between the location of the first nick and the location of the second nick). As a further example, another gene modifying system that provides an outward nick orientation comprises a gene modifying polypeptide comprising a zinc finger molecule and a first nickase domain wherein the zinc finger

molecule binds to the target DNA in a manner that directs the first nickase domain to nick the first strand of the target site; an additional polypeptide comprising a TAL effector molecule and a second nickase domain wherein the TAL effector molecule binds to a site a distance from the target site in a manner that directs the additional polypeptide to nick the second strand, wherein the location of the first nick and the location of the second nick are outside the site to which the TAL effector molecule binds and the site to which the zinc finger molecule binds (i.e., the site to which the TAL effector molecule binds and the site to which the zinc finger molecule binds are between the location of the first nick and the location of the second nick).

Without wishing to be bound by theory, it is thought that, for gene modifying systems where a second strand nick is provided, an outward nick orientation is preferred in some embodiments. As is described herein, an inward nick may produce a higher number of double-strand breaks (DSBs) than an outward nick orientation. DSBs may be recognized by the DSB repair pathways in the nucleus of a cell, which can result in undesired insertions and deletions. An outward nick orientation may provide a decreased risk of DSB formation, and a corresponding lower amount of undesired insertions and deletions. In some embodiments, undesired insertions and deletions are insertions and deletions not encoded by the heterologous object sequence, e.g., an insertion or deletion produced by the double-strand break repair pathway unrelated to the modification encoded by the heterologous object sequence. In some embodiments, a desired gene modification comprises a change to the target DNA (e.g., a substitution, insertion, or deletion) encoded by the heterologous object sequence (e.g., and achieved by the gene modifying writing the heterologous object sequence into the target site). In some embodiments, the first strand nick and the second strand nick are in an outward orientation.

In addition, the distance between the first strand nick and second strand nick may influence the extent to which one or more of: desired gene modifying system DNA modifications are obtained, undesired double-strand breaks (DSBs) occur, undesired insertions occur, or undesired deletions occur. Without wishing to be bound by theory, it is thought the second strand nick benefit, the biasing of DNA repair toward incorporation of the heterologous object sequence into the target DNA, increases as the distance between the first strand nick and second strand nick decreases. However, it is thought that the risk of DSB formation also increases as the distance between the first strand nick and second strand nick decreases. Correspondingly, it is thought that the number of undesired insertions and/or deletions may increase as the distance

between the first strand nick and second strand nick decreases. In some embodiments, the distance between the first strand nick and second strand nick is chosen to balance the benefit of biasing DNA repair toward incorporation of the heterologous object sequence into the target DNA and the risk of DSB formation and of undesired deletions and/or insertions. In some embodiments, a system where the first strand nick and the second strand nick are at least a threshold distance apart has an increased level of desired gene modifying system modification outcomes, a decreased level of undesired deletions, and/or a decreased level of undesired insertions relative to an otherwise similar inward nick orientation system where the first nick and the second nick are less than the a threshold distance apart. In some embodiments the threshold distance(s) is given below.

In some embodiments, the first nick and the second nick are at least 20, 25, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, 100, 110, 120, 130, 140, 150, 160, 170, 180, 190, or 200 nucleotides apart. In some embodiments, the first nick and the second nick are no more than 25, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, 100, 110, 120, 130, 140, 150, 160, 170, 180, 190, 200, or 250 nucleotides apart. In some embodiments, the first nick and the second nick are 20-200, 30-200, 40-200, 50-200, 60-200, 70-200, 80-200, 90-200, 100-200, 110-200, 120-200, 130-200, 140-200, 150-200, 160-200, 170-200, 180-200, 190-200, 20-190, 30-190, 40-190, 50-190, 60-190, 70-190, 80-190, 90-190, 100-190, 110-190, 120-190, 130-190, 140-190, 150-190, 160-190, 170-190, 180-190, 20-180, 30-180, 40-180, 50-180, 60-180, 70-180, 80-180, 90-180, 100-180, 110-180, 120-180, 130-180, 140-180, 150-180, 160-180, 170-180, 20-170, 30-170, 40-170, 50-170, 60-170, 70-170, 80-170, 90-170, 100-170, 110-170, 120-170, 130-170, 140-170, 150-170, 160-170, 20-160, 30-160, 40-160, 50-160, 60-160, 70-160, 80-160, 90-160, 100-160, 110-160, 120-160, 130-160, 140-160, 150-160, 20-150, 30-150, 40-150, 50-150, 60-150, 70-150, 80-150, 90-150, 100-150, 110-150, 120-150, 130-150, 140-150, 20-140, 30-140, 40-140, 50-140, 60-140, 70-140, 80-140, 90-140, 100-140, 110-140, 120-140, 130-140, 20-130, 30-130, 40-130, 50-130, 60-130, 70-130, 80-130, 90-130, 100-130, 110-130, 120-130, 20-120, 30-120, 40-120, 50-120, 60-120, 70-120, 80-120, 90-120, 100-120, 110-120, 20-110, 30-110, 40-110, 50-110, 60-110, 70-110, 80-110, 90-110, 100-110, 20-100, 30-100, 40-100, 50-100, 60-100, 70-100, 80-100, 90-100, 20-90, 30-90, 40-90, 50-90, 60-90, 70-90, 80-90, 20-80, 30-80, 40-80, 50-80, 60-80, 70-80, 20-70, 30-70, 40-70, 50-70, 60-70, 20-60, 30-60, 40-60, 50-60, 20-50, 30-

50, 40-50, 20-40, 30-40, or 20-30 nucleotides apart. In some embodiments, the first nick and the second nick are 40-100 nucleotides apart.

Without wishing to be bound by theory, it is thought that, for gene modifying systems where a second strand nick is provided and an inward nick orientation is selected, increasing the distance between the first strand nick and second strand nick may be preferred. As is described herein, an inward nick orientation may produce a higher number of DSBs than an outward nick orientation, and may result in a higher amount of undesired insertions and deletions than an outward nick orientation, but increasing the distance between the nicks may mitigate that increase in DSBs, undesired deletions, and/or undesired insertions. In some embodiments, an inward nick orientation wherein the first nick and the second nick are at least a threshold distance apart has an increased level of desired gene modifying system modification outcomes, a decreased level of undesired deletions, and/or a decreased level of undesired insertions relative to an otherwise similar inward nick orientation system where the first nick and the second nick are less than the a threshold distance apart. In some embodiments the threshold distance is given below.

In some embodiments, the first strand nick and the second strand nick are in an inward orientation. In some embodiments, the first strand nick and the second strand nick are in an inward orientation and the first strand nick and second strand nick are at least 100, 110, 120, 130, 140, 150, 160, 170, 180, 190, 200, 220, 240, 260, 280, 300, 350, 400, 450, or 500 nucleotides apart, e.g., at least 100 nucleotides apart, (and optionally no more than 500, 400, 300, 200, 190, 180, 170, 160, 150, 140, 130, or 120 nucleotides apart). In some embodiments, the first strand nick and the second strand nick are in an inward orientation and the first strand nick and second strand nick are 100-200, 110-200, 120-200, 130-200, 140-200, 150-200, 160-200, 170-200, 180-200, 190-200, 100-190, 110-190, 120-190, 130-190, 140-190, 150-190, 160-190, 170-190, 180-190, 100-180, 110-180, 120-180, 130-180, 140-180, 150-180, 160-180, 170-180, 100-170, 110-170, 120-170, 130-170, 140-170, 150-170, 160-170, 100-160, 110-160, 120-160, 130-160, 140-160, 150-160, 100-150, 110-150, 120-150, 130-150, 140-150, 100-140, 110-140, 120-140, 130-140, 100-130, 110-130, 120-130, 100-120, 110-120, or 100-110 nucleotides apart.

Chemically modified nucleic acids and nucleic acid end features

A nucleic acid described herein (e.g., a template nucleic acid, e.g., a template RNA; or a nucleic acid (e.g., mRNA) encoding a gene modifying polypeptide; or a gRNA) can comprise

unmodified or modified nucleobases. Naturally occurring RNAs are synthesized from four basic ribonucleotides: ATP, CTP, UTP and GTP, but may contain post-transcriptionally modified nucleotides. Further, approximately one hundred different nucleoside modifications have been identified in RNA (Rozenski, J, Crain, P, and McCloskey, J. (1999). The RNA Modification Database: 1999 update. Nucl Acids Res 27: 196-197). An RNA can also comprise wholly synthetic nucleotides that do not occur in nature.

In some embodiments, the chemical modification is one provided in WO/2016/183482, US Pat. Pub. No. 20090286852, of International Application No. WO/2012/019168, WO/2012/045075, WO/2012/135805, WO/2012/158736, WO/2013/039857, WO/2013/039861, WO/2013/052523, WO/2013/090648, WO/2013/096709, WO/2013/101690, WO/2013/106496, WO/2013/130161, WO/2013/151669, WO/2013/151736, WO/2013/151672, WO/2013/151664, WO/2013/151665, WO/2013/151668, WO/2013/151671, WO/2013/151667, WO/2013/151670, WO/2013/151666, WO/2013/151663, WO/2014/028429, WO/2014/081507, WO/2014/093924, WO/2014/093574, WO/2014/113089, WO/2014/144711, WO/2014/144767, WO/2014/144039, WO/2014/152540, WO/2014/152030, WO/2014/152031, WO/2014/152027, WO/2014/152211, WO/2014/158795, WO/2014/159813, WO/2014/164253, WO/2015/006747, WO/2015/034928, WO/2015/034925, WO/2015/038892, WO/2015/048744, WO/2015/051214, WO/2015/051173, WO/2015/051169, WO/2015/058069, WO/2015/085318, WO/2015/089511, WO/2015/105926, WO/2015/164674, WO/2015/196130, WO/2015/196128, WO/2015/196118, WO/2016/011226, WO/2016/011222, WO/2016/011306, WO/2016/014846, WO/2016/022914, WO/2016/036902, WO/2016/077125, or WO/2016/077123, each of which is herein incorporated by reference in its entirety. It is understood that incorporation of a chemically modified nucleotide into a polynucleotide can result in the modification being incorporated into a nucleobase, the backbone, or both, depending on the location of the modification in the nucleotide. In some embodiments, the backbone modification is one provided in EP 2813570, which is herein incorporated by reference in its entirety. In some embodiments, the modified cap is one provided in US Pat. Pub. No. 20050287539, which is herein incorporated by reference in its entirety.

In some embodiments, the chemically modified nucleic acid (e.g., RNA, e.g., mRNA) comprises one or more of ARCA: anti-reverse cap analog (m27.3´-OGP3G), GP3G (Unmethylated Cap Analog), m7GP3G (Monomethylated Cap Analog), m32.2.7GP3G (Trimethylated Cap Analog), m5CTP (5´-methyl-cytidine triphosphate), m6ATP (N6-methyl-

adenosine-5′-triphosphate), s2UTP (2-thio-uridine triphosphate), and Ψ (pseudouridine triphosphate).

In some embodiments, the chemically modified nucleic acid comprises a 5′ cap, e.g.: a 7-methylguanosine cap (e.g., a O-Me-m7G cap); a hypermethylated cap analog; an NAD+-derived cap analog (e.g., as described in Kiledjian, Trends in Cell Biology 28, 454-464 (2018)); or a modified, e.g., biotinylated, cap analog (e.g., as described in Bednarek et al., Phil Trans R Soc B 373, 20180167 (2018)).

In some embodiments, the chemically modified nucleic acid comprises a 3′ feature selected from one or more of: a polyA tail; a 16-nucleotide long stem-loop structure flanked by unpaired 5 nucleotides (e.g., as described by Mannironi et al., Nucleic Acid Research 17, 9113-9126 (1989)); a triple-helical structure (e.g., as described by Brown et al., PNAS 109, 19202-19207 (2012)); a tRNA, Y RNA, or vault RNA structure (e.g., as described by Labno et al., Biochemica et Biophysica Acta 1863, 3125-3147 (2016)); incorporation of one or more deoxyribonucleotide triphosphates (dNTPs), 2'O-Methylated NTPs, or phosphorothioate-NTPs; a single nucleotide chemical modification (e.g., oxidation of the 3′ terminal ribose to a reactive aldehyde followed by conjugation of the aldehyde-reactive modified nucleotide); or chemical ligation to another nucleic acid molecule.

In some embodiments, the nucleic acid (e.g., template nucleic acid) comprises one or more modified nucleotides, e.g., selected from dihydrouridine, inosine, 7-methylguanosine, 5-methylcytidine (5mC), 5′ Phosphate ribothymidine, 2′-O-methyl ribothymidine, 2′-O-ethyl ribothymidine, 2′-fluoro ribothymidine, C-5 propynyl-deoxycytidine (pdC), C-5 propynyl-deoxyuridine (pdU), C-5 propynyl-cytidine (pC), C-5 propynyl-uridine (pU), 5-methyl cytidine, 5-methyl uridine, 5-methyl deoxycytidine, 5-methyl deoxyuridine methoxy, 2,6-diaminopurine, 5′-Dimethoxytrityl-N4-ethyl-2′-deoxycytidine, C-5 propynyl-f-cytidine (pfC), C-5 propynyl-f-uridine (pfU), 5-methyl f-cytidine, 5-methyl f-uridine, C-5 propynyl-m-cytidine (pmC), C-5 propynyl-f-uridine (pmU), 5-methyl m-cytidine, 5-methyl m-uridine, LNA (locked nucleic acid), MGB (minor groove binder) pseudouridine (Ψ), 1-N-methylpseudouridine (1-Me-Ψ), or 5-methoxyuridine (5-MO-U).

In some embodiments, the nucleic acid comprises a backbone modification, e.g., a modification to a sugar or phosphate group in the backbone. In some embodiments, the nucleic acid comprises a nucleobase modification.

In some embodiments, the nucleic acid comprises one or more chemically modified nucleotides of Table 13, one or more chemical backbone modifications of Table 14, one or more chemically modified caps of Table 15. For instance, in some embodiments, the nucleic acid comprises two or more (e.g., 3, 4, 5, 6, 7, 8, 9, or 10 or more) different types of chemical modifications. As an example, the nucleic acid may comprise two or more (e.g., 3, 4, 5, 6, 7, 8, 9, or 10 or more) different types of modified nucleobases, e.g., as described herein, e.g., in Table 13. Alternatively or in combination, the nucleic acid may comprise two or more (e.g., 3, 4, 5, 6, 7, 8, 9, or 10 or more) different types of backbone modifications, e.g., as described herein, e.g., in Table 14. Alternatively or in combination, the nucleic acid may comprise one or more modified cap, e.g., as described herein, e.g., in Table 15. For instance, in some embodiments, the nucleic acid comprises one or more type of modified nucleobase and one or more type of backbone modification; one or more type of modified nucleobase and one or more modified cap; one or more type of modified cap and one or more type of backbone modification; or one or more type of modified nucleobase, one or more type of backbone modification, and one or more type of modified cap.

In some embodiments, the nucleic acid comprises one or more (e.g., 2, 3, 4, 5, 6, 7, 8, 9, 10, 20, 30, 40, 50, 60, 70, 80, 90, 100, 150, 200, 250, 300, 350, 400, 450, 500, 600, 700, 800, 900, 1000, or more) modified nucleobases. In some embodiments, all nucleobases of the nucleic acid are modified. In some embodiments, the nucleic acid is modified at one or more (e.g., 2, 3, 4, 5, 6, 7, 8, 9, 10, 20, 30, 40, 50, 60, 70, 80, 90, 100, 150, 200, 250, 300, 350, 400, 450, 500, 600, 700, 800, 900, 1000, or more) positions in the backbone. In some embodiments, all backbone positions of the nucleic acid are modified.

Table 13. Modified nucleotides

5-aza-uridine	N2-methyl-6-thio-guanosine
2-thio-5-aza-midine	N2,N2-dimethyl-6-thio-guanosine
2-thiouridine	pyridin-4-one ribonucleoside
4-thio-pseudouridine	2-thio-5-aza-uridine
2-thio-pseudouridine	2-thiomidine
5-hydroxyuridine	4-thio-pseudomidine
3-methyluridine	2-thio-pseudowidine
5-carboxymethyl-uridine	3-methylmidine
1-carboxymethyl-pseudouridine	1-propynyl-pseudomidine
5-propynyl-uridine	1-methyl-1-deaza-pseudomidine

1-propynyl-pseudouridine	2-thio-1-methyl-1-deaza-pseudouridine
5-taurinomethyluridine	4-methoxy-pseudomidine
1-taurinomethyl-pseudouridine	5'-O-(1-Thiophosphate)-Adenosine
5-taurinomethyl-2-thio-uridine	5'-O-(1-Thiophosphate)-Cytidine
1-taurinomethyl-4-thio-uridine	5'-O-(1-thiophosphate)-Guanosine
5-methyl-uridine	5'-O-(1-Thiophophate)-Uridine
1-methyl-pseudouridine	5'-O-(1-Thiophosphate)-Pseudouridine
4-thio-1-methyl-pseudouridine	2'-O-methyl-Adenosine
2-thio-1-methyl-pseudouridine	2'-O-methyl-Cytidine
1-methyl-1-deaza-pseudouridine	2'-O-methyl-Guanosine
2-thio-1-methyl-1-deaza-pseudomidine	2'-O-methyl-Uridine
dihydrouridine	2'-O-methyl-Pseudouridine
dihydropseudouridine	2'-O-methyl-Inosine
2-thio-dihydromidine	2-methyladenosine
2-thio-dihydropseudouridine	2-methylthio-N6-methyladenosine
2-methoxyuridine	2-methylthio-N6 isopentenyladenosine
2-methoxy-4-thio-uridine	2-methylthio-N6-(cis-hydroxyisopentenyl)adenosine
4-methoxy-pseudouridine	N6-methyl-N6-threonylcarbamoyladenosine
4-methoxy-2-thio-pseudouridine	N6-hydroxynorvalylcarbamoyladenosine
5-aza-cytidine	2-methylthio-N6-hydroxynorvalyl carbamoyladenosine
pseudoisocytidine	2'-O-ribosyladenosine (phosphate)
3-methyl-cytidine	1,2'-O-dimethylinosine
N4-acetylcytidine	5,2'-O-dimethylcytidine
5-formylcytidine	N4-acetyl-2'-O-methylcytidine
N4-methylcytidine	Lysidine
5-hydroxymethylcytidine	7-methylguanosine
1-methyl-pseudoisocytidine	N2,2'-O-dimethylguanosine
pyrrolo-cytidine	N2,N2,2'-O-trimethylguanosine
pyrrolo-pseudoisocytidine	2'-O-ribosylguanosine (phosphate)
2-thio-cytidine	Wybutosine
2-thio-5-methyl-cytidine	Peroxywybutosine
4-thio-pseudoisocytidine	Hydroxywybutosine
4-thio-1-methyl-pseudoisocytidine	undermodified hydroxywybutosine
4-thio-1-methyl-1-deaza-pseudoisocytidine	methylwyosine
1-methyl-1-deaza-pseudoisocytidine	queuosine
zebularine	epoxyqueuosine
5-aza-zebularine	galactosyl-queuosine
5-methyl-zebularine	mannosyl-queuosine
5-aza-2-thio-zebularine	7-cyano-7-deazaguanosine
2-thio-zebularine	7-aminomethyl-7-deazaguanosine
2-methoxy-cytidine	archaeosine
2-methoxy-5-methyl-cytidine	5,2'-O-dimethyluridine
4-methoxy-pseudoisocytidine	4-thiouridine
4-methoxy-1-methyl-pseudoisocytidine	5-methyl-2-thiouridine
2-aminopurine	
2,6-diaminopurine	

7-deaza-adenine	2-thio-2'-O-methyluridine
7-deaza-8-aza-adenine	3-(3-amino-3-carboxypropyl)uridine
7-deaza-2-aminopurine	5-methoxyuridine
7-deaza-8-aza-2-aminopurine	uridine 5-oxyacetic acid
7-deaza-2,6- diaminopurine	uridine 5-oxyacetic acid methyl ester
7-deaza-8-aza-2,6-diarninopurine	5-(carboxyhydroxymethyl)uridine)
1-methyladenosine	5-(carboxyhydroxymethyl)uridine methyl ester
N6-isopentenyladenosine	5-methoxycarbonylmethyluridine
N6-(cis-hydroxyisopentenyl)adenosine	5-methoxycarbonylmethyl-2'-O-methyluridine
2-methylthio-N6-(cis-hydroxyisopentenyl) adenosine	5-methoxycarbonylmethyl-2-thiouridine
N6-glycinylcarbamoyladenosine	5-aminomethyl-2-thiouridine
N6-threonylcarbamoyladenosine	5-methylaminomethyluridine
2-methylthio-N6-threonyl carbamoyladenosine	5-methylaminomethyl-2-thiouridine
N6,N6-dimethyladenosine	5-methylaminomethyl-2-selenouridine
7-methyladenine	5-carbamoylmethyluridine
2-methylthio-adenine	5-carbamoylmethyl-2'-O-methyluridine
2-methoxy-adenine	5-carboxymethylaminomethyluridine
inosine	5-carboxymethylaminomethyl-2'-O-methyluridine
1-methyl-inosine	5-carboxymethylaminomethyl-2-thiouridine
wyosine	N4,2'-O-dimethylcytidine
wybutosine	5-carboxymethyluridine
7-deaza-guanosine	N6,2'-O-dimethyladenosine
7-deaza-8-aza-guanosine	N,N6,O-2'-trimethyladenosine
6-thio-guanosine	N2,7-dimethylguanosine
6-thio-7-deaza-guanosine	N2,N2,7-trimethylguanosine
6-thio-7-deaza-8-aza-guanosine	3,2'-O-dimethyluridine
7-methyl-guanosine	5-methyldihydrouridine
6-thio-7-methyl-guanosine	5-formyl-2'-O-methylcytidine
7-methylinosine	1,2'-O-dimethylguanosine
6-methoxy-guanosine	4-demethylwyosine
1-methylguanosine	Isowyosine
N2-methylguanosine	N6-acetyladenosine
N2,N2-dimethylguanosine	
8-oxo-guanosine	
7-methyl-8-oxo-guanosine	
1-methyl-6-thio-guanosine	

Table 14. Backbone modifications

2’-O-Methyl backbone
Peptide Nucleic Acid (PNA) backbone
phosphorothioate backbone
morpholino backbone
carbamate backbone

siloxane backbone
sulfide backbone
sulfoxide backbone
sulfone backbone
formacetyl backbone
thioformacetyl backbone
methyleneformacetyl backbone
riboacetyl backbone
alkene containing backbone
sulfamate backbone
sulfonate backbone
sulfonamide backbone
methyleneimino backbone
methylenehydrazino backbone
amide backbone

Table 15. Modified caps

m7GpppA
m7GpppC
m2,7GpppG
m2,2,7GpppG
m7Gpppm7G
m7,2'OmeGpppG
m72'dGpppG
m7,3'OmeGpppG
m7,3'dGpppG
GppppG
m7GppppG
m7GppppA
m7GppppC
m2,7GppppG
m2,2,7GppppG
m7Gppppm7G
m7,2'OmeGppppG
m72'dGppppG
m7,3'OmeGppppG
m7,3'dGppppG

The nucleotides comprising the template of the gene modifying system can be natural or modified bases, or a combination thereof. For example, the template may contain pseudouridine, dihydrouridine, inosine, 7-methylguanosine, or other modified bases. In some embodiments, the template may contain locked nucleic acid nucleotides. In some embodiments, the modified bases used in the template do not inhibit the reverse transcription of the template. In some

embodiments, the modified bases used in the template may improve reverse transcription, e.g., specificity or fidelity.

In some embodiments, an RNA component of the system (e.g., a template RNA or a gRNA) comprises one or more nucleotide modifications. In some embodiments, the modification pattern of a gRNA can significantly affect *in vivo* activity compared to unmodified or end-modified guides (e.g., as shown in Figure 1D from Finn et al. *Cell Rep* 22(9):2227-2235 (2018); incorporated herein by reference in its entirety). Without wishing to be bound by theory, this process may be due, at least in part, to a stabilization of the RNA conferred by the modifications. Non-limiting examples of such modifications may include 2'-O-methyl (2'-O-Me), 2'-0-(2-methoxyethyl) (2'-0-MOE), 2'- fluoro (2'-F), phosphorothioate (PS) bond between nucleotides, G-C substitutions, and inverted abasic linkages between nucleotides and equivalents thereof.

In some embodiments, the template RNA (e.g., at the portion thereof that binds a target site) or the guide RNA comprises a 5´ terminus region. In some embodiments, the template RNA or the guide RNA does not comprise a 5´ terminus region. In some embodiments, the 5´ terminus region comprises a gRNA spacer region, e.g., as described with respect to sgRNA in Briner AE et al, Molecular Cell 56: 333-339 (2014) (incorporated herein by reference in its entirety; applicable herein, e.g., to all guide RNAs). In some embodiments, the 5´ terminus region comprises a 5´ end modification. In some embodiments, a 5´ terminus region with or without a spacer region may be associated with a crRNA, trRNA, sgRNA and/or dgRNA. The gRNA spacer region can, in some instances, comprise a guide region, guide domain, or targeting domain.

In some embodiments, the template RNAs (e.g., at the portion thereof that binds a target site) or guide RNAs described herein comprises any of the sequences shown in Table 4 of WO2018107028A1, incorporated herein by reference in its entirety. In some embodiments, where a sequence shows a guide and/or spacer region, the composition may comprise this region or not. In some embodiments, a guide RNA comprises one or more of the modifications of any of the sequences shown in Table 4 of WO2018107028A1, e.g., as identified therein by a SEQ ID NO. In embodiments, the nucleotides may be the same or different, and/or the modification pattern shown may be the same or similar to a modification pattern of a guide sequence as shown

in Table 4 of WO2018107028A1. In some embodiments, a modification pattern includes the relative position and identity of modifications of the gRNA or a region of the gRNA (e.g. 5´ terminus region, lower stem region, bulge region, upper stem region, nexus region, hairpin 1 region, hairpin 2 region, 3´ terminus region). In some embodiments, the modification pattern contains at least 50%, 55%, 60%, 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% of the modifications of any one of the sequences shown in the sequence column of Table 4 of WO2018107028A1, and/or over one or more regions of the sequence. In some embodiments, the modification pattern is at least 50%, 55%, 60%, 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the modification pattern of any one of the sequences shown in the sequence column of Table 4 of WO2018107028A1. In some embodiments, the modification pattern is at least 50%, 55%, 60%, 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical over one or more regions of the sequence shown in Table 4 of WO2018107028A1, e.g., in a 5 ' terminus region, lower stem region, bulge region, upper stem region, nexus region, hairpin 1 region, hairpin 2 region, and/or 3´ terminus region. In some embodiments, the modification pattern is least 50%, 55%, 60%, 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical to the modification pattern of a sequence over the 5 ' terminus region. In some embodiments, the modification pattern is least 50%, 55%, 60%, 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical over the lower stem. In some embodiments, the modification pattern is least 50%, 55%, 60%, 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical over the bulge. In some embodiments, the modification pattern is least 50%, 55%, 60%, 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical over the upper stem. In some embodiments, the modification pattern is least 50%, 55%, 60%, 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical over the nexus. In some embodiments, the modification pattern is least 50%, 55%, 60%, 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical over the hairpin 1. In some embodiments, the modification pattern is least 50%, 55%, 60%, 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical over the hairpin 2. In some embodiments, the modification pattern is least 50%, 55%, 60%, 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical over the 3 ' terminus. In some embodiments, the modification pattern differs from the modification pattern of a sequence of Table 4 of WO2018107028A1, or a region (e.g. 5´ terminus, lower stem, bulge, upper stem, nexus, hairpin

1, hairpin 2, 3´ terminus) of such a sequence, e.g., at 0, 1, 2, 3, 4, 5, 6, or more nucleotides. In some embodiments, the gRNA comprises modifications that differ from the modifications of a sequence of Table 4 of WO2018107028A1, e.g., at 0, 1, 2, 3, 4, 5, 6, or more nucleotides. In some embodiments, the gRNA comprises modifications that differ from modifications of a region (e.g. 5 ' terminus, lower stem, bulge, upper stem, nexus, hairpin 1, hairpin 2, 3´ terminus) of a sequence of Table 4 of WO2018107028A1, e.g., at 0, 1, 2, 3, 4, 5, 6, or more nucleotides.

In some embodiments, the template RNAs (e.g., at the portion thereof that binds a target site) or the gRNA comprises a 2'-O-methyl (2'-O-Me) modified nucleotide. In some embodiments, the gRNA comprises a 2'-O-(2-methoxy ethyl) (2'-O-moe) modified nucleotide. In some embodiments, the gRNA comprises a 2'-fluoro (2'- F) modified nucleotide. In some embodiments, the gRNA comprises a phosphorothioate (PS) bond between nucleotides. In some embodiments, the gRNA comprises a 5´ end modification, a 3´ end modification, or 5´ and 3´ end modifications. In some embodiments, the 5´ end modification comprises a phosphorothioate (PS) bond between nucleotides. In some embodiments, the 5´ end modification comprises a 2'-O-methyl (2'-O-Me), 2'-O-(2-methoxy ethyl) (2'-O-MOE), and/or 2'-fluoro (2'-F) modified nucleotide. In some embodiments, the 5´ end modification comprises at least one phosphorothioate (PS) bond and one or more of a 2'-O-methyl (2'-O- Me), 2'-O-(2-methoxyethyl) (2'-O-MOE), and/or 2'-fluoro (2'-F) modified nucleotide. The end modification may comprise a phosphorothioate (PS), 2'-O-methyl (2'-O-Me), 2'-O-(2- methoxyethyl) (2'-O-MOE), and/or 2'-fluoro (2'-F) modification. Equivalent end modifications are also encompassed by embodiments described herein. In some embodiments, the template RNA or gRNA comprises an end modification in combination with a modification of one or more regions of the template RNA or gRNA. Additional exemplary modifications and methods for protecting RNA, e.g., gRNA, and formulae thereof, are described in WO2018126176A1, which is incorporated herein by reference in its entirety.

In some embodiments, a template RNA described herein comprises three phosphorothioate linkages at the 5’ end and three phosphorothioate linkages at the 3’ end. In some embodiments, a template RNA described herein comprises three 2’-O-methyl ribonucleotides at the 5’ end and three 2’-O-methyl ribonucleotides at the 3’ end. In some embodiments, the 5’ most three nucleotides of the template RNA are 2’-O-methyl

ribonucleotides, the 5’ most three internucleotide linkages of the template RNA are phosphorothioate linkages, the 3’ most three nucleotides of the template RNA are 2’-O-methyl ribonucleotides, and the 3’ most three internucleotide linkages of the template RNA are phosphorothioate linkages. In some embodiments, the template RNA comprises alternating blocks of ribonucleotides and 2’-O-methyl ribonucleotides, for instance, blocks of between 12 and 28 nucleotides in length. In some embodiments, the central portion of the template RNA comprises the alternating blocks and the 5’ and 3’ ends each comprise three 2’-O-methyl ribonucleotides and three phosphorothioate linkages.

In some embodiments, structure-guided and systematic approaches are used to introduce modifications (e.g., 2′-OMe-RNA, 2′-F-RNA, and PS modifications) to a template RNA or guide RNA, for example, as described in Mir et al. *Nat Commun* 9:2641 (2018) (incorporated by reference herein in its entirety). In some embodiments, the incorporation of 2′-F-RNAs increases thermal and nuclease stability of RNA:RNA or RNA:DNA duplexes, e.g., while minimally interfering with C3′-endo sugar puckering. In some embodiments, 2′-F may be better tolerated than 2′-OMe at positions where the 2′-OH is important for RNA:DNA duplex stability. In some embodiments, a crRNA comprises one or more modifications that do not reduce Cas9 activity, e.g., C10, C20, or C21 (fully modified), e.g., as described in Supplementary Table 1 of Mir et al. *Nat Commun* 9:2641 (2018), incorporated herein by reference in its entirety. In some embodiments, a tracrRNA comprises one or more modifications that do not reduce Cas9 activity, e.g., T2, T6, T7, or T8 (fully modified) of Supplementary Table 1 of Mir et al. *Nat Commun* 9:2641 (2018). In some embodiments, a crRNA comprises one or more modifications (e.g., as described herein) may be paired with a tracrRNA comprising one or more modifications, e.g., C20 and T2. In some embodiments, a gRNA comprises a chimera, e.g., of a crRNA and a tracrRNA (e.g., Jinek et al. *Science* 337(6096):816-821 (2012)). In embodiments, modifications from the crRNA and tracrRNA are mapped onto the single-guide chimera, e.g., to produce a modified gRNA with enhanced stability.

In some embodiments, gRNA molecules may be modified by the addition or subtraction of the naturally occurring structural components, e.g., hairpins. In some embodiments, a gRNA may comprise a gRNA with one or more 3´ hairpin elements deleted, e.g., as described in WO2018106727, incorporated herein by reference in its entirety. In some embodiments, a

gRNA may contain an added hairpin structure, e.g., an added hairpin structure in the spacer region, which was shown to increase specificity of a CRISPR-Cas system in the teachings of Kocak et al. *Nat Biotechnol* 37(6):657-666 (2019). Additional modifications, including examples of shortened gRNA and specific modifications improving *in vivo* activity, can be found in US20190316121, incorporated herein by reference in its entirety.

In some embodiments, structure-guided and systematic approaches (e.g., as described in Mir et al. *Nat Commun* 9:2641 (2018); incorporated herein by reference in its entirety) are employed to find modifications for the template RNA. In embodiments, the modifications are identified with the inclusion or exclusion of a guide region of the template RNA. In some embodiments, a structure of polypeptide bound to template RNA is used to determine non-protein-contacted nucleotides of the RNA that may then be selected for modifications, e.g., with lower risk of disrupting the association of the RNA with the polypeptide. Secondary structures in a template RNA can also be predicted *in silico* by software tools, e.g., the RNAstructure tool available at rna.urmc.rochester.edu/RNAstructureWeb (Bellaousov et al. *Nucleic Acids Res* 41:W471-W474 (2013); incorporated by reference herein in its entirety), e.g., to determine secondary structures for selecting modifications, e.g., hairpins, stems, and/or bulges.

Production of Compositions and Systems

As will be appreciated by one of skill, methods of designing and constructing nucleic acid constructs and proteins or polypeptides (such as the systems, constructs and polypeptides described herein) are routine in the art. Generally, recombinant methods may be used. See, in general, Smales & James (Eds.), *Therapeutic Proteins: Methods and Protocols* (Methods in Molecular Biology), Humana Press (2005); and Crommelin, Sindelar & Meibohm (Eds.), *Pharmaceutical Biotechnology: Fundamentals and Applications*, Springer (2013). Methods of designing, preparing, evaluating, purifying and manipulating nucleic acid compositions are described in Green and Sambrook (Eds.), *Molecular Cloning: A Laboratory Manual* (Fourth Edition), Cold Spring Harbor Laboratory Press (2012).

The disclosure provides, in part, a nucleic acid, e.g., vector, encoding a gene modifying polypeptide described herein, a template nucleic acid described herein, or both. In some embodiments, a vector comprises a selective marker, e.g., an antibiotic resistance marker. In some embodiments, the antibiotic resistance marker is a kanamycin resistance marker. In some embodiments, the antibiotic resistance marker does not confer resistance to beta-lactam

antibiotics. In some embodiments, the vector does not comprise an ampicillin resistance marker. In some embodiments, the vector comprises a kanamycin resistance marker and does not comprise an ampicillin resistance marker. In some embodiments, a vector encoding a gene modifying polypeptide is integrated into a target cell genome (e.g., upon administration to a target cell, tissue, organ, or subject). In some embodiments, a vector encoding a gene modifying polypeptide is not integrated into a target cell genome (e.g., upon administration to a target cell, tissue, organ, or subject). In some embodiments, a vector encoding a template nucleic acid (e.g., template RNA) is not integrated into a target cell genome (e.g., upon administration to a target cell, tissue, organ, or subject). In some embodiments, if a vector is integrated into a target site in a target cell genome, the selective marker is not integrated into the genome. In some embodiments, if a vector is integrated into a target site in a target cell genome, genes or sequences involved in vector maintenance (e.g., plasmid maintenance genes) are not integrated into the genome. In some embodiments, if a vector is integrated into a target site in a target cell genome, transfer regulating sequences (e.g., inverted terminal repeats, e.g., from an AAV) are not integrated into the genome. In some embodiments, administration of a vector (e.g., encoding a gene modifying polypeptide described herein, a template nucleic acid described herein, or both) to a target cell, tissue, organ, or subject results in integration of a portion of the vector into one or more target sites in the genome(s) of said target cell, tissue, organ, or subject. In some embodiments, less than 99, 95, 90, 80, 70, 60, 50, 40, 30, 20, 10, 5, 4, 3, 2, or 1% of target sites (e.g., no target sites) comprising integrated material comprise a selective marker (e.g., an antibiotic resistance gene), a transfer regulating sequence (e.g., an inverted terminal repeat, e.g., from an AAV), or both from the vector.

Exemplary methods for producing a therapeutic pharmaceutical protein or polypeptide described herein involve expression in mammalian cells, although recombinant proteins can also be produced using insect cells, yeast, bacteria, or other cells under control of appropriate promoters. Mammalian expression vectors may comprise non-transcribed elements such as an origin of replication, a suitable promoter, and other 5' or 3' flanking non-transcribed sequences, and 5' or 3' non-translated sequences such as necessary ribosome binding sites, a polyadenylation site, splice donor and acceptor sites, and termination sequences. DNA sequences derived from the SV40 viral genome, for example, SV40 origin, early promoter, splice, and polyadenylation sites may be used to provide other genetic elements required for expression of a heterologous

DNA sequence. Appropriate cloning and expression vectors for use with bacterial, fungal, yeast, and mammalian cellular hosts are described in Green & Sambrook, *Molecular Cloning: A Laboratory Manual* (Fourth Edition), Cold Spring Harbor Laboratory Press (2012).

Various mammalian cell culture systems can be employed to express and manufacture recombinant protein. Examples of mammalian expression systems include CHO, COS, HEK293, HeLA, and BHK cell lines. Processes of host cell culture for production of protein therapeutics are described in Zhou and Kantardjieff (Eds.), *Mammalian Cell Cultures for Biologics Manufacturing (Advances in Biochemical Engineering/Biotechnology)*, Springer (2014). Compositions described herein may include a vector, such as a viral vector, e.g., a lentiviral vector, encoding a recombinant protein. In some embodiments, a vector, e.g., a viral vector, may comprise a nucleic acid encoding a recombinant protein.

Purification of protein therapeutics is described in Franks, Protein Biotechnology: *Isolation, Characterization, and Stabilization*, Humana Press (2013); and in Cutler, *Protein Purification Protocols (Methods in Molecular Biology)*, Humana Press (2010).

The disclosure also provides compositions and methods for the production of template nucleic acid molecules (e.g., template RNAs) with specificity for a gene modifying polypeptide and/or a genomic target site. In an aspect, the method comprises production of RNA segments including an upstream homology segment, a heterologous object sequence segment, a gene modifying polypeptide binding motif, and a gRNA segment.

Therapeutic Applications

In some embodiments, a gene modifying system as described herein can be used to modify a cell (e.g., an animal cell, plant cell, or fungal cell). In some embodiments, a gene modifying system as described herein can be used to modify a mammalian cell (e.g., a human cell). In some embodiments, a gene modifying system as described herein can be used to modify a cell from a livestock animal (e.g., a cow, horse, sheep, goat, pig, llama, alpaca, camel, yak, chicken, duck, goose, or ostrich). In some embodiments, a gene modifying system as described herein can be used as a laboratory tool or a research tool, or used in a laboratory method or research method, e.g., to modify an animal cell, e.g., a mammalian cell (e.g., a human cell), a plant cell, or a fungal cell.

By integrating coding genes into a RNA sequence template, the gene modifying system can address therapeutic needs, for example, by providing expression of a therapeutic transgene in individuals with loss-of-function mutations, by replacing gain-of-function mutations with normal transgenes, by providing regulatory sequences to eliminate gain-of-function mutation expression, and/or by controlling the expression of operably linked genes, transgenes and systems thereof. In certain embodiments, the RNA sequence template encodes a promotor region specific to the therapeutic needs of the host cell, for example a tissue specific promotor or enhancer. In still other embodiments, a promotor can be operably linked to a coding sequence.

Accordingly, provided herein are methods for treating phenylketonuria (PKU) or hyperphenylalaninemia (e.g., mild or severe hyperphenylalaninemia) in a subject in need thereof. In some embodiments, treatment results in amelioration of one or more symptoms associated with PKU or hyperphenylalaninemia.

In some embodiments, a system herein is used to treat a subject having a mutation in R408 (e.g., R408W), R261 (e.g., R261Q), R243 (e.g., R243Q), and/or IVS10-11G (e.g., IVS10-11G>A).

In some embodiments, treatment with a system disclosed herein results in correction of the R408W, R261Q, R243Q, and/or IVS10-11G>A mutation in between about 5-50% (e.g., about 5-10%, 10-20%, 20-30%, 30-40%, 40-50%, or about 10%) of cells. In some embodiments, treatment with a system disclosed herein results in correction of the R408W, R261Q, R243Q, and/or IVS10-11G>A mutation in between about 5-50% (e.g., about 5-10%, 10-20%, 20-30%, 30-40%, 40-50%, or about 10%) of DNA from the treated cells.

In some embodiments, treatment with a gene modifying system described herein results in one or more of:

(a) an increase in phenylalanine hydroxylase (PAH) activity, efficiency, and/or function;

(b) a decrease in the concentration of phenylalanine in the blood and/or cerebrospinal fluid;

(c) increase in the concentration of tyrosine in the blood

(d) a restoration of normal synthesis of dopamine, norepinephrine, and/or melanin;

(e) a reduction in ureagenesis; and/or

(f) an improvement in protein retention and/or Phe utilization

as compared to a subject having PKU that has not been treated with a gene modifying system described herein.

Administration and Delivery

The compositions and systems described herein may be used *in vitro* or *in vivo*. In some embodiments the system or components of the system are delivered to cells (e.g., mammalian cells, e.g., human cells), e.g., *in vitro* or *in vivo*. In some embodiments, the cells are eukaryotic cells, e.g., cells of a multicellular organism, e.g., an animal, e.g., a mammal (e.g., human, swine, bovine), a bird (e.g., poultry, such as chicken, turkey, or duck), or a fish. In some embodiments, the cells are non-human animal cells (e.g., a laboratory animal, a livestock animal, or a companion animal). In some embodiments, the cell is a stem cell (e.g., a hematopoietic stem cell), a fibroblast, or a T cell. In some embodiments, the cell is an immune cell, e.g., a T cell (e.g., a Treg, CD4, CD8, γδ, or memory T cell), B cell (e.g., memory B cell or plasma cell), or NK cell. In some embodiments, the cell is a non-dividing cell, e.g., a non-dividing fibroblast or non-dividing T cell. In some embodiments, the cell is an HSC and p53 is not upregulated or is upregulated by less than 10%, 5%, 2%, or 1%, e.g., as determined according to the method described in Example 30 of PCT/US2019/048607. The skilled artisan will understand that the components of the gene modifying system may be delivered in the form of polypeptide, nucleic acid (e.g., DNA, RNA), and combinations thereof.

In one embodiment the system and/or components of the system are delivered as nucleic acid. For example, the gene modifying polypeptide may be delivered in the form of a DNA or RNA encoding the polypeptide, and the template RNA may be delivered in the form of RNA or its complementary DNA to be transcribed into RNA. In some embodiments the system or components of the system are delivered on 1, 2, 3, 4, or more distinct nucleic acid molecules. In some embodiments the system or components of the system are delivered as a combination of DNA and RNA. In some embodiments the system or components of the system are delivered as a combination of DNA and protein. In some embodiments the system or components of the system are delivered as a combination of RNA and protein. In some embodiments the gene modifying polypeptide is delivered as a protein.

In some embodiments the system or components of the system are delivered to cells, e.g. mammalian cells or human cells, using a vector. The vector may be, e.g., a plasmid or a virus. In some embodiments, delivery is *in vivo, in vitro, ex vivo,* or *in situ.* In some embodiments the virus is an adeno associated virus (AAV), a lentivirus, or an adenovirus. In some embodiments the system or components of the system are delivered to cells with a viral-like particle or a virosome. In some embodiments the delivery uses more than one virus, viral-like particle or virosome.

In one embodiment, the compositions and systems described herein can be formulated in liposomes or other similar vesicles. Liposomes are spherical vesicle structures composed of a uni- or multilamellar lipid bilayer surrounding internal aqueous compartments and a relatively impermeable outer lipophilic phospholipid bilayer. Liposomes may be anionic, neutral or cationic. Liposomes are biocompatible, nontoxic, can deliver both hydrophilic and lipophilic drug molecules, protect their cargo from degradation by plasma enzymes, and transport their load across biological membranes and the blood brain barrier (BBB) (see, e.g., Spuch and Navarro, Journal of Drug Delivery, vol. 2011, Article ID 469679, 12 pages, 2011. doi:10.1155/2011/469679 for review).

Vesicles can be made from several different types of lipids; however, phospholipids are most commonly used to generate liposomes as drug carriers. Methods for preparation of multilamellar vesicle lipids are known in the art (see for example U.S. Pat. No. 6,693,086, the teachings of which relating to multilamellar vesicle lipid preparation are incorporated herein by reference). Although vesicle formation can be spontaneous when a lipid film is mixed with an aqueous solution, it can also be expedited by applying force in the form of shaking by using a homogenizer, sonicator, or an extrusion apparatus (see, e.g., Spuch and Navarro, Journal of Drug Delivery, vol. 2011, Article ID 469679, 12 pages, 2011. doi:10.1155/2011/469679 for review). Extruded lipids can be prepared by extruding through filters of decreasing size, as described in Templeton et al., Nature Biotech, 15:647-652, 1997, the teachings of which relating to extruded lipid preparation are incorporated herein by reference.

A variety of nanoparticles can be used for delivery, such as a liposome, a lipid nanoparticle, a cationic lipid nanoparticle, an ionizable lipid nanoparticle, a polymeric nanoparticle, a gold nanoparticle, a dendrimer, a cyclodextrin nanoparticle, a micelle, or a combination of the foregoing.

Lipid nanoparticles are an example of a carrier that provides a biocompatible and biodegradable delivery system for the pharmaceutical compositions described herein. Nanostructured lipid carriers (NLCs) are modified solid lipid nanoparticles (SLNs) that retain the characteristics of the SLN, improve drug stability and loading capacity, and prevent drug leakage. Polymer nanoparticles (PNPs) are an important component of drug delivery. These nanoparticles can effectively direct drug delivery to specific targets and improve drug stability and controlled drug release. Lipid–polymer nanoparticles (PLNs), a type of carrier that combines liposomes and polymers, may also be employed. These nanoparticles possess the complementary advantages of PNPs and liposomes. A PLN is composed of a core–shell structure; the polymer core provides a stable structure, and the phospholipid shell offers good biocompatibility. As such, the two components increase the drug encapsulation efficiency rate, facilitate surface modification, and prevent leakage of water-soluble drugs. For a review, see, e.g., Li et al. 2017, Nanomaterials 7, 122; doi:10.3390/nano7060122.

Exosomes can also be used as drug delivery vehicles for the compositions and systems described herein. For a review, see Ha et al. July 2016. Acta Pharmaceutica Sinica B. Volume 6, Issue 4, Pages 287-296; https://doi.org/10.1016/j.apsb.2016.02.001.

Fusosomes interact and fuse with target cells, and thus can be used as delivery vehicles for a variety of molecules. They generally consist of a bilayer of amphipathic lipids enclosing a lumen or cavity and a fusogen that interacts with the amphipathic lipid bilayer. The fusogen component has been shown to be engineerable in order to confer target cell specificity for the fusion and payload delivery, allowing the creation of delivery vehicles with programmable cell specificity (see for example Patent Application WO2020014209, the teachings of which relating to fusosome design, preparation, and usage are incorporated herein by reference).

In some embodiments, the protein component(s) of the gene modifying system may be pre-associated with the template nucleic acid (e.g., template RNA). For example, in some embodiments, the gene modifying polypeptide may be first combined with the template nucleic acid (e.g., template RNA) to form a ribonucleoprotein (RNP) complex. In some embodiments, the RNP may be delivered to cells via, e.g., transfection, nucleofection, virus, vesicle, LNP, exosome, fusosome.

A gene modifying system can be introduced into cells, tissues and multicellular organisms. In some embodiments the system or components of the system are delivered to the cells via mechanical means or physical means.

Formulation of protein therapeutics is described in Meyer (Ed.), *Therapeutic Protein Drug Products: Practical Approaches to formulation in the Laboratory, Manufacturing, and the Clinic*, Woodhead Publishing Series (2012).

Tissue Specific Activity/Administration

In some embodiments, a system described herein can make use of one or more feature (e.g., a promoter or microRNA binding site) to limit activity in off-target cells or tissues.

In some embodiments, a nucleic acid described herein (e.g., a template RNA or a DNA encoding a template RNA) comprises a promoter sequence, e.g., a tissue specific promoter sequence. In some embodiments, the tissue-specific promoter is used to increase the target-cell specificity of a gene modifying system. For instance, the promoter can be chosen on the basis that it is active in a target cell type but not active in (or active at a lower level in) a non-target cell type. Thus, even if the promoter integrated into the genome of a non-target cell, it would not drive expression (or only drive low level expression) of an integrated gene. A system having a tissue-specific promoter sequence in the template RNA may also be used in combination with a microRNA binding site, e.g., in the template RNA or a nucleic acid encoding a gene modifying protein, e.g., as described herein. A system having a tissue-specific promoter sequence in the template RNA may also be used in combination with a DNA encoding a gene modifying polypeptide, driven by a tissue-specific promoter, e.g., to achieve higher levels of gene modifying protein in target cells than in non-target cells. In some embodiments, e.g., for liver indications, a tissue-specific promoter is selected from Table 3 of WO2020014209, incorporated herein by reference.

In some embodiments, a nucleic acid described herein (e.g., a template RNA or a DNA encoding a template RNA) comprises a microRNA binding site. In some embodiments, the microRNA binding site is used to increase the target-cell specificity of a gene modifying system. For instance, the microRNA binding site can be chosen on the basis that is recognized by a miRNA that is present in a non-target cell type, but that is not present (or is present at a reduced level relative to the non-target cell) in a target cell type. Thus, when the template RNA is present

in a non-target cell, it would be bound by the miRNA, and when the template RNA is present in a target cell, it would not be bound by the miRNA (or bound but at reduced levels relative to the non-target cell). While not wishing to be bound by theory, binding of the miRNA to the template RNA may interfere with its activity, e.g., may interfere with insertion of the heterologous object sequence into the genome. Accordingly, the system would edit the genome of target cells more efficiently than it edits the genome of non-target cells, e.g., the heterologous object sequence would be inserted into the genome of target cells more efficiently than into the genome of non-target cells, or an insertion or deletion is produced more efficiently in target cells than in non-target cells. A system having a microRNA binding site in the template RNA (or DNA encoding it) may also be used in combination with a nucleic acid encoding a gene modifying polypeptide, wherein expression of the gene modifying polypeptide is regulated by a second microRNA binding site, e.g., as described herein. In some embodiments, e.g., for liver indications, a miRNA is selected from Table 4 of WO2020014209, incorporated herein by reference.

In some embodiments, the template RNA comprises a microRNA sequence, an siRNA sequence, a guide RNA sequence, or a piwi RNA sequence.

Promoters

In some embodiments, one or more promoter or enhancer elements are operably linked to a nucleic acid encoding a gene modifying protein or a template nucleic acid, e.g., that controls expression of the heterologous object sequence. In certain embodiments, the one or more promoter or enhancer elements comprise cell-type or tissue specific elements. In some embodiments, the promoter or enhancer is the same or derived from the promoter or enhancer that naturally controls expression of the heterologous object sequence. For example, the ornithine transcarbomylase promoter and enhancer may be used to control expression of the ornithine transcarbomylase gene in a system or method provided by the invention for correcting ornithine transcarbomylase deficiencies. In some embodiments, the promoter is a promoter of Table 16 or 17 or a functional fragment or variant thereof.

Exemplary tissue specific promoters that are commercially available can be found, for example, at a uniform resource locator (e.g., www.invivogen.com/tissue-specific-promoters). In some embodiments, a promoter is a native promoter or a minimal promoter, e.g., which consists

of a single fragment from the 5´ region of a given gene. In some embodiments, a native promoter comprises a core promoter and its natural 5´ UTR. In some embodiments, the 5´ UTR comprises an intron. In other embodiments, these include composite promoters, which combine promoter elements of different origins or were generated by assembling a distal enhancer with a minimal promoter of the same origin.

Exemplary cell or tissue specific promoters are provided in the tables, below, and exemplary nucleic acid sequences encoding them are known in the art and can be readily accessed using a variety of resources, such as the NCBI database, including RefSeq, as well as the Eukaryotic Promoter Database (//epd.epfl.ch//index.php).

Table 16. Exemplary cell or tissue-specific promoters

Promoter	**Target cells**
B29 Promoter	B cells
CD14 Promoter	Monocytic Cells
CD43 Promoter	Leukocytes and platelets
CD45 Promoter	Hematopoeitic cells
CD68 promoter	macrophages
Desmin promoter	muscle cells
Elastase-1 promoter	pancreatic acinar cells
Endoglin promoter	endothelial cells
fibronectin promoter	differentiating cells, healing tissue
Flt-1 promoter	endothelial cells
GFAP promoter	Astrocytes
GPIIB promoter	megakaryocytes
ICAM-2 Promoter	Endothelial cells
INF-Beta promoter	Hematopoeitic cells
Mb promoter	muscle cells
Nphs1 promoter	podocytes
OG-2 promoter	Osteoblasts, Odonblasts
SP-B promoter	Lung
Syn1 promoter	Neurons
WASP promoter	Hematopoeitic cells
SV40/bAlb promoter	Liver

SV40/bAlb promoter	Liver
SV40/Cd3 promoter	Leukocytes and platelets
SV40/CD45 promoter	hematopoeitic cells
NSE/RU5' promoter	Mature Neurons

Table 17. Additional exemplary cell or tissue-specific promoters

Promoter	**Gene Description**	**Gene Specificity**
APOA2	Apolipoprotein A-II	Hepatocytes (from hepatocyte progenitors)
SERPINA 1 (hAAT)	Serpin peptidase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 1 (also named alpha 1 anti-tryps in)	Hepatocytes (from definitive endoderm stage)
CYP3A	Cytochrome P450, family 3, subfamily A, polypeptide	Mature Hepatocytes
MIR122	MicroRNA 122	Hepatocytes (from early stage embryonic liver cells) and endoderm
Pancreatic specific promoters		
Promoter	**Gene Description**	**Gene Specificity**
INS	Insulin	Pancreatic beta cells (from definitive endoderm stage)
IRS2	Insulin receptor substrate 2	Pancreatic beta cells
Pdx1	Pancreatic and duodenal homeobox 1	Pancreas (from definitive endoderm stage)
Alx3	Aristaless-like homeobox 3	Pancreatic beta cells (from definitive endoderm stage)
Ppy	Pancreatic polypeptide	PP pancreatic cells (gamma cells)
Cardiac specific promoters		
Promoter	**Gene Description**	**Gene Specificity**
Myh6 (aMHC)	Myosin, heavy chain 6, cardiac muscle, alpha	Late differentiation marker of cardiac muscle cells (atrial specificity)
MYL2 (MLC-2v)	Myosin, light chain 2, regulatory, cardiac, slow	Late differentiation marker of cardiac muscle cells (ventricular specificity)

ITNNl3 (cTnl)	Troponin I type 3 (cardiac)	Cardiomyocytes (from immature state)
ITNNl3 (cTnl)	Troponin I type 3 (cardiac)	Cardiomyocytes (from immature state)
NPPA (ANF)	Natriuretic peptide precursor A (also named Atrial Natriuretic Factor)	Atrial specificity in adult cells
Slc8a1 (Ncx1)	Solute carrier family 8 (sodium/calcium exchanger), member 1	Cardiomyocytes from early developmental stages
CNS specific promoters		
Promoter	**Gene Description**	**Gene Specificity**
SYN1 (hSyn)	Synapsin I	Neurons
GFAP	Glial fibrillary acidic protein	Astrocytes
INA	lnternexin neuronal intermediate filament protein, alpha (a-internexin)	Neuroprogenitors
NES	Nestin	Neuroprogenitors and ectoderm
MOBP	Myelin-associated oligodendrocyte basic protein	Oligodendrocytes
MBP	Myelin basic protein	Oligodendrocytes
TH	Tyrosine hydroxylase	Dopaminergic neurons
FOXA2 (HNF3 beta)	Forkhead box A2	Dopaminergic neurons (also used as a marker of endoderm)
Skin specific promoters		
Promoter	**Gene Description**	**Gene Specificity**
FLG	Filaggrin	Keratinocytes from granular layer
K14	Keratin 14	Keratinocytes from granular and basal layers
TGM3	Transglutaminase 3	Keratinocytes from granular layer
Immune cell specific promoters		
Promoter	**Gene Description**	**Gene Specificity**
ITGAM (CD11B)	lntegrin, alpha M (complement component 3 receptor 3 subunit)	Monocytes, macrophages , granulocytes , natural killer cells
Urogential cell specific promoters		
Promoter	**Gene Description**	**Gene Specificity**
Pbsn	Probasin	Prostatic epithelium

Upk2	Uroplakin 2	Bladder
Sbp	Spermine binding protein	Prostate
Fer1l4	Fer-1-like 4	Bladder
Endothelial cell specific promoters		
Promoter	**Gene Description**	**Gene Specificity**
ENG	Endoglin	Endothelial cells
Pluripotent and embryonic cell specific promoters		
Promoter	**Gene Description**	**Gene Specificity**
Oct4 (POU5F1)	POU class 5 homeobox 1	Pluripotent cells (germ cells, ES cells, iPS cells)
NANOG	Nanog homeobox	Pluripotent cells (ES cells, iPS cells)
Synthetic Oct4	Synthetic promoter based on a Oct-4 core enhancer element	Pluripotent cells (ES cells, iPS cells)
T brachyury	Brachyury	Mesoderm
NES	Nestin	Neuroprogenitors and Ectoderm
SOX17	SRY (sex determining region Y)-box 17	Endoderm
FOXA2 (HNFJ beta)	Forkhead box A2	Endoderm (also used as a marker of dopaminergic neurons)
MIR122	MicroRNA 122	Endoderm and hepatocytes (from early stage embryonic liver cells~

Depending on the host/vector system utilized, any of a number of suitable transcription and translation control elements, including constitutive and inducible promoters, transcription enhancer elements, transcription terminators, etc. may be used in the expression vector (see e.g., Bitter et al. (1987) *Methods in Enzymology*, 153:516-544; incorporated herein by reference in its entirety).

In some embodiments, a nucleic acid encoding a gene modifying protein or template nucleic acid is operably linked to a control element, e.g., a transcriptional control element, such as a promoter. The transcriptional control element may, in some embodiment, be functional in either a eukaryotic cell, e.g., a mammalian cell; or a prokaryotic cell (e.g., bacterial or archaeal cell). In some embodiments, a nucleotide sequence encoding a polypeptide is operably linked to

multiple control elements, e.g., that allow expression of the nucleotide sequence encoding the polypeptide in both prokaryotic and eukaryotic cells.

For illustration purposes, examples of spatially restricted promoters include, but are not limited to, neuron-specific promoters, adipocyte-specific promoters, cardiomyocyte-specific promoters, smooth muscle-specific promoters, photoreceptor-specific promoters, etc. Neuron-specific spatially restricted promoters include, but are not limited to, a neuron-specific enolase (NSE) promoter (see, e.g., EMBL HSENO2, X51956); an aromatic amino acid decarboxylase (AADC) promoter, a neurofilament promoter (see, e.g., GenBank HUMNFL, L04147); a synapsin promoter (see, e.g., GenBank HUMSYNIB, M55301); a thy-1 promoter (see, e.g., Chen et al. (1987) Cell 51:7-19; and Llewellyn, et al. (2010) Nat. Med. 16(10):1161-1166); a serotonin receptor promoter (see, e.g., GenBank S62283); a tyrosine hydroxylase promoter (TH) (see, e.g., Oh et al. (2009) Gene Ther 16:437; Sasaoka et al. (1992) Mol. Brain Res. 16:274; Boundy et al. (1998) J. Neurosci. 18:9989; and Kaneda et al. (1991) Neuron 6:583-594); a GnRH promoter (see, e.g., Radovick et al. (1991) Proc. Natl. Acad. Sci. USA 88:3402-3406); an L7 promoter (see, e.g., Oberdick et al. (1990) Science 248:223-226); a DNMT promoter (see, e.g., Bartge et al. (1988) Proc. Natl. Acad. Sci. USA 85:3648-3652); an enkephalin promoter (see, e.g., Comb et al. (1988) EMBO J. 17:3793-3805); a myelin basic protein (MBP) promoter; a Ca2+-calmodulin-dependent protein kinase II-alpha (CamKIIα) promoter (see, e.g., Mayford et al. (1996) Proc. Natl. Acad. Sci. USA 93:13250; and Casanova et al. (2001) Genesis 31:37); a CMV enhancer/platelet-derived growth factor-β promoter (see, e.g., Liu et al. (2004) Gene Therapy 11:52-60); and the like.

Adipocyte-specific spatially restricted promoters include, but are not limited to, the aP2 gene promoter/enhancer, e.g., a region from −5.4 kb to +21 bp of a human aP2 gene (see, e.g., Tozzo et al. (1997) Endocrinol. 138:1604; Ross et al. (1990) Proc. Natl. Acad. Sci. USA 87:9590; and Pavjani et al. (2005) Nat. Med. 11:797); a glucose transporter-4 (GLUT4) promoter (see, e.g., Knight et al. (2003) Proc. Natl. Acad. Sci. USA 100:14725); a fatty acid translocase (FAT/CD36) promoter (see, e.g., Kuriki et al. (2002) Biol. Pharm. Bull. 25:1476; and Sato et al. (2002) J. Biol. Chem. 277:15703); a stearoyl-CoA desaturase-1 (SCD1) promoter (Tabor et al. (1999) J. Biol. Chem. 274:20603); a leptin promoter (see, e.g., Mason et al. (1998) Endocrinol. 139:1013; and Chen et al. (1999) Biochem. Biophys. Res. Comm. 262:187); an adiponectin promoter (see, e.g., Kita et al. (2005) Biochem. Biophys. Res. Comm. 331:484; and Chakrabarti

(2010) Endocrinol. 151:2408); an adipsin promoter (see, e.g., Platt et al. (1989) Proc. Natl. Acad. Sci. USA 86:7490); a resistin promoter (see, e.g., Seo et al. (2003) Molec. Endocrinol. 17:1522); and the like.

Cardiomyocyte-specific spatially restricted promoters include, but are not limited to, control sequences derived from the following genes: myosin light chain-2, α-myosin heavy chain, AE3, cardiac troponin C, cardiac actin, and the like. Franz et al. (1997) Cardiovasc. Res. 35:560-566; Robbins et al. (1995) Ann. N.Y. Acad. Sci. 752:492-505; Linn et al. (1995) Circ. Res. 76:584-591; Parmacek et al. (1994) Mol. Cell. Biol. 14:1870-1885; Hunter et al. (1993) Hypertension 22:608-617; and Sartorelli et al. (1992) Proc. Natl. Acad. Sci. USA 89:4047-4051.

Smooth muscle-specific spatially restricted promoters include, but are not limited to, an SM22α promoter (see, e.g., Akyürek et al. (2000) Mol. Med. 6:983; and U.S. Pat. No. 7,169,874); a smoothelin promoter (see, e.g., WO 2001/018048); an α-smooth muscle actin promoter; and the like. For example, a 0.4 kb region of the SM22α promoter, within which lie two CArG elements, has been shown to mediate vascular smooth muscle cell-specific expression (see, e.g., Kim, et al. (1997) Mol. Cell. Biol. 17, 2266-2278; Li, et al., (1996) J. Cell Biol. 132, 849-859; and Moessler, et al. (1996) Development 122, 2415-2425).

Photoreceptor-specific spatially restricted promoters include, but are not limited to, a rhodopsin promoter; a rhodopsin kinase promoter (Young et al. (2003) Ophthalmol. Vis. Sci. 44:4076); a beta phosphodiesterase gene promoter (Nicoud et al. (2007) J. Gene Med. 9:1015); a retinitis pigmentosa gene promoter (Nicoud et al. (2007) supra); an interphotoreceptor retinoid-binding protein (IRBP) gene enhancer (Nicoud et al. (2007) supra); an IRBP gene promoter (Yokoyama et al. (1992) Exp Eye Res. 55:225); and the like.

In some embodiments, a gene modifying system, e.g., DNA encoding a gene modifying polypeptide, DNA encoding a template RNA, or DNA or RNA encoding a heterologous object sequence, is designed such that one or more elements is operably linked to a tissue-specific promoter, e.g., a promoter that is active in T-cells. In further embodiments, the T-cell active promoter is inactive in other cell types, e.g., B-cells, NK cells. In some embodiments, the T-cell active promoter is derived from a promoter for a gene encoding a component of the T-cell receptor, e.g., TRAC, TRBC, TRGC, TRDC. In some embodiments, the T-cell active promoter is derived from a promoter for a gene encoding a component of a T-cell-specific cluster of differentiation protein, e.g., CD3, e.g., CD3D, CD3E, CD3G, CD3Z. In some embodiments, T-

cell-specific promoters in gene modifying systems are discovered by comparing publicly available gene expression data across cell types and selecting promoters from the genes with enhanced expression in T-cells. In some embodiments, promoters may be selecting depending on the desired expression breadth, e.g., promoters that are active in T-cells only, promoters that are active in NK cells only, promoters that are active in both T-cells and NK cells.

Cell-specific promoters known in the art may be used to direct expression of a gene modifying protein, e.g., as described herein. Nonlimiting exemplary mammalian cell-specific promoters have been characterized and used in mice expressing Cre recombinase in a cell-specific manner. Certain nonlimiting exemplary mammalian cell-specific promoters are listed in Table 1 of US9845481, incorporated herein by reference.

In some embodiments, a vector as described herein comprises an expression cassette. Typically, an expression cassette comprises the nucleic acid molecule of the instant invention operatively linked to a promoter sequence. For example, a promoter is operatively linked with a coding sequence when it is capable of affecting the expression of that coding sequence (e.g., the coding sequence is under the transcriptional control of the promoter). Encoding sequences can be operatively linked to regulatory sequences in sense or antisense orientation. In certain embodiments, the promoter is a heterologous promoter. In certain embodiments, an expression cassette may comprise additional elements, for example, an intron, an enhancer, a polyadenylation site, a woodchuck response element (WRE), and/or other elements known to affect expression levels of the encoding sequence. A promoter typically controls the expression of a coding sequence or functional RNA. In certain embodiments, a promoter sequence comprises proximal and more distal upstream elements and can further comprise an enhancer element. An enhancer can typically stimulate promoter activity and may be an innate element of the promoter or a heterologous element inserted to enhance the level or tissue-specificity of a promoter. In certain embodiments, the promoter is derived in its entirety from a native gene. In certain embodiments, the promoter is composed of different elements derived from different naturally occurring promoters. In certain embodiments, the promoter comprises a synthetic nucleotide sequence. It will be understood by those skilled in the art that different promoters will direct the expression of a gene in different tissues or cell types, or at different stages of development, or in response to different environmental conditions or to the presence or the absence of a drug or transcriptional co-factor. Ubiquitous, cell-type-specific, tissue-specific,

developmental stage-specific, and conditional promoters, for example, drug-responsive promoters (e.g., tetracycline-responsive promoters) are well known to those of skill in the art. Exemplary promoters include, but are not limited to, the phosphoglycerate kinase (PKG) promoter, CAG (composite of the CMV enhancer the chicken beta actin promoter (CBA) and the rabbit beta globin intron), NSE (neuronal specific enolase), synapsin or NeuN promoters, the SV40 early promoter, mouse mammary tumor virus LTR promoter; adenovirus major late promoter (Ad MLP), a herpes simplex virus (HSV) promoter, a cytomegalovirus (CMV) promoter such as the CMV immediate early promoter region (CMVIE), SFFV promoter, rous sarcoma virus (RSV) promoter, synthetic promoters, hybrid promoters, and the like. Other promoters can be of human origin or from other species, including from mice. Common promoters include, e.g., the human cytomegalovirus (CMV) immediate early gene promoter, the SV40 early promoter, the Rous sarcoma virus long terminal repeat, [beta]- actin, rat insulin promoter, the phosphoglycerate kinase promoter, the human alpha-1 antitrypsin (hAAT) promoter, the transthyretin promoter, the TBG promoter and other liver-specific promoters, the desmin promoter and similar muscle-specific promoters, the EF1 -alpha promoter, hybrid promoters with multi-tissue specificity, promoters specific for neurons like synapsin and glyceraldehyde-3 -phosphate dehydrogenase promoter, all of which are promoters well known and readily available to those of skill in the art, can be used to obtain high-level expression of the coding sequence of interest. In addition, sequences derived from non-viral genes, such as the murine metallothionein gene, will also find use herein. Such promoter sequences are commercially available from, e.g., Stratagene (San Diego, CA). Additional exemplary promoter sequences are described, for example, in WO2018213786A1 (incorporated by reference herein in its entirety).

In some embodiments, the apolipoprotein E enhancer (ApoE) or a functional fragment thereof is used, e.g., to drive expression in the liver. In some embodiments, two copies of the ApoE enhancer or a functional fragment thereof are used. In some embodiments, the ApoE enhancer or functional fragment thereof is used in combination with a promoter, e.g., the human alpha-1 antitrypsin (hAAT) promoter.

In some embodiments, the regulatory sequences impart tissue-specific gene expression capabilities. In some cases, the tissue-specific regulatory sequences bind tissue-specific transcription factors that induce transcription in a tissue specific manner. Various tissue-specific

regulatory sequences (e.g., promoters, enhancers, etc.) are known in the art. Exemplary tissue-specific regulatory sequences include, but are not limited to, the following tissue-specific promoters: a liver-specific thyroxin binding globulin (TBG) promoter, a insulin promoter, a glucagon promoter, a somatostatin promoter, a pancreatic polypeptide (PPY) promoter, a synapsin-1 (Syn) promoter, a creatine kinase (MCK) promoter, a mammalian desmin (DES) promoter, a α-myosin heavy chain (a-MHC) promoter, or a cardiac Troponin T (cTnT) promoter. Other exemplary promoters include Beta-actin promoter, hepatitis B virus core promoter, Sandig et al., Gene Ther., 3:1002-9 (1996); alpha-fetoprotein (AFP) promoter, Arbuthnot et al., Hum. Gene Ther., 7:1503-14 (1996)), bone osteocalcin promoter (Stein et al., Mol. Biol. Rep., 24:185-96 (1997)); bone sialoprotein promoter (Chen et al., J. Bone Miner. Res., 11:654-64 (1996)), CD2 promoter (Hansal et al., J. Immunol., 161:1063-8 (1998); immunoglobulin heavy chain promoter; T cell receptor α-chain promoter, neuronal such as neuron-specific enolase (NSE) promoter (Andersen et al., Cell. Mol. Neurobiol., 13:503-15 (1993)), neurofilament light-chain gene promoter (Piccioli et al., Proc. Natl. Acad. Sci. USA, 88:5611-5 (1991)), and the neuron-specific vgf gene promoter (Piccioli et al., Neuron, 15:373-84 (1995)), and others. Additional exemplary promoter sequences are described, for example, in U.S. Patent No. 10300146 (incorporated herein by reference in its entirety). In some embodiments, a tissue-specific regulatory element, e.g., a tissue-specific promoter, is selected from one known to be operably linked to a gene that is highly expressed in a given tissue, e.g., as measured by RNA-seq or protein expression data, or a combination thereof. Methods for analyzing tissue specificity by expression are taught in Fagerberg et al. *Mol Cell Proteomics* 13(2):397-406 (2014), which is incorporated herein by reference in its entirety.

In some embodiments, a vector described herein is a multicistronic expression construct. Multicistronic expression constructs include, for example, constructs harboring a first expression cassette, e.g. comprising a first promoter and a first encoding nucleic acid sequence, and a second expression cassette, e.g. comprising a second promoter and a second encoding nucleic acid sequence. Such multicistronic expression constructs may, in some instances, be particularly useful in the delivery of non-translated gene products, such as hairpin RNAs, together with a polypeptide, for example, a gene modifying polypeptide and gene modifying template. In some embodiments, multicistronic expression constructs may exhibit reduced expression levels of one or more of the included transgenes, for example, because of promoter interference or the

presence of incompatible nucleic acid elements in close proximity. If a multicistronic expression construct is part of a viral vector, the presence of a self-complementary nucleic acid sequence may, in some instances, interfere with the formation of structures necessary for viral reproduction or packaging.

In some embodiments, the sequence encodes an RNA with a hairpin. In some embodiments, the hairpin RNA is a guide RNA, a template RNA, a shRNA, or a microRNA. In some embodiments, the first promoter is an RNA polymerase I promoter. In some embodiments, the first promoter is an RNA polymerase II promoter. In some embodiments, the second promoter is an RNA polymerase III promoter. In some embodiments, the second promoter is a U6 or H1 promoter.

Without wishing to be bound by theory, multicistronic expression constructs may not achieve optimal expression levels as compared to expression systems containing only one cistron. One of the suggested causes of lower expression levels achieved with multicistronic expression constructs comprising two or more promoter elements is the phenomenon of promoter interference (see, e.g., Curtin J A, Dane A P, Swanson A, Alexander I E, Ginn S L. *Bidirectional promoter interference between two widely used internal heterologous promoters in a late-generation lentiviral construct*. Gene Ther. 2008 March; 15(5):384-90; and Martin-Duque P, Jezzard S, Kaftansis L, Vassaux G. *Direct comparison of the insulating properties of two genetic elements in an adenoviral vector containing two different expression cassettes.* Hum Gene Ther. 2004 October; 15(10):995-1002; both references incorporated herein by reference for disclosure of promoter interference phenomenon). In some embodiments, the problem of promoter interference may be overcome, e.g., by producing multicistronic expression constructs comprising only one promoter driving transcription of multiple encoding nucleic acid sequences separated by internal ribosomal entry sites, or by separating cistrons comprising their own promoter with transcriptional insulator elements. In some embodiments, single-promoter driven expression of multiple cistrons may result in uneven expression levels of the cistrons. In some embodiments, a promoter cannot efficiently be isolated and isolation elements may not be compatible with some gene transfer vectors, for example, some retroviral vectors.

MicroRNAs

MicroRNAs (miRNAs) and other small interfering nucleic acids generally regulate gene expression via target RNA transcript cleavage/degradation or translational repression of the target messenger RNA (mRNA). miRNAs may, in some instances, be natively expressed, typically as final 19-25 non-translated RNA products. miRNAs generally exhibit their activity through sequence-specific interactions with the 3′ untranslated regions (UTR) of target mRNAs. These endogenously expressed miRNAs may form hairpin precursors that are subsequently processed into an miRNA duplex, and further into a mature single stranded miRNA molecule This mature miRNA generally guides a multiprotein complex, miRISC, which identifies target 3′ UTR regions of target mRNAs based upon their complementarity to the mature miRNA. Useful transgene products may include, for example, miRNAs or miRNA binding sites that regulate the expression of a linked polypeptide. A non-limiting list of miRNA genes; the products of these genes and their homologues are useful as transgenes or as targets for small interfering nucleic acids (e.g., miRNA sponges, antisense oligonucleotides), e.g., in methods such as those listed in US10300146, 22:25-25:48, are herein incorporated by reference. In some embodiments, one or more binding sites for one or more of the foregoing miRNAs are incorporated in a transgene, e.g., a transgene delivered by a rAAV vector, e.g., to inhibit the expression of the transgene in one or more tissues of an animal harboring the transgene. In some embodiments, a binding site may be selected to control the expression of a transgene in a tissue specific manner. For example, binding sites for the liver-specific miR-122 may be incorporated into a transgene to inhibit expression of that transgene in the liver. Additional exemplary miRNA sequences are described, for example, in U.S. Patent No. 10,300,146 (incorporated herein by reference in its entirety).

An miR inhibitor or miRNA inhibitor is generally an agent that blocks miRNA expression and/or processing. Examples of such agents include, but are not limited to, microRNA antagonists, microRNA specific antisense, microRNA sponges, and microRNA oligonucleotides (double-stranded, hairpin, short oligonucleotides) that inhibit miRNA interaction with a Drosha complex. MicroRNA inhibitors, e.g., miRNA sponges, can be expressed in cells from transgenes (e.g., as described in Ebert, M. S. Nature Methods, Epub Aug. 12, 2007; incorporated by reference herein in its entirety). In some embodiments, microRNA sponges, or other miR inhibitors, are used with the AAVs. microRNA sponges generally

specifically inhibit miRNAs through a complementary heptameric seed sequence. In some embodiments, an entire family of miRNAs can be silenced using a single sponge sequence. Other methods for silencing miRNA function (derepression of miRNA targets) in cells will be apparent to one of ordinary skill in the art.

In some embodiments, a gene modifying system, template RNA, or polypeptide described herein is administered to or is active in (e.g., is more active in) a target tissue, e.g., a first tissue. In some embodiments, the gene modifying system, template RNA, or polypeptide is not administered to or is less active in (e.g., not active in) a non-target tissue. In some embodiments, a gene modifying system, template RNA, or polypeptide described herein is useful for modifying DNA in a target tissue, e.g., a first tissue, (e.g., and not modifying DNA in a non-target tissue).

In some embodiments, a gene modifying system comprises (a) a polypeptide described herein or a nucleic acid encoding the same, (b) a template nucleic acid (e.g., template RNA) described herein, and (c) one or more first tissue-specific expression-control sequences specific to the target tissue, wherein the one or more first tissue-specific expression-control sequences specific to the target tissue are in operative association with (a), (b), or (a) and (b), wherein, when associated with (a), (a) comprises a nucleic acid encoding the polypeptide.

In some embodiments, the nucleic acid in (b) comprises RNA.

In some embodiments, the nucleic acid in (b) comprises DNA.

In some embodiments, the nucleic acid in (b): (i) is single-stranded or comprises a single-stranded segment, e.g., is single-stranded DNA or comprises a single-stranded segment and one or more double stranded segments; (ii) has inverted terminal repeats; or (iii) both (i) and (ii).

In some embodiments, the nucleic acid in (b) is double-stranded or comprises a double-stranded segment.

In some embodiments, (a) comprises a nucleic acid encoding the polypeptide.

In some embodiments, the nucleic acid in (a) comprises RNA.

In some embodiments, the nucleic acid in (a) comprises DNA.

In some embodiments, the nucleic acid in (a): (i) is single-stranded or comprises a single-stranded segment, e.g., is single-stranded DNA or comprises a single-stranded segment and one or more double stranded segments; (ii) has inverted terminal repeats; or (iii) both (i) and (ii).

In some embodiments, the nucleic acid in (a) is double-stranded or comprises a double-stranded segment.

In some embodiments, the nucleic acid in (a), (b), or (a) and (b) is linear.

In some embodiments, the nucleic acid in (a), (b), or (a) and (b) is circular, e.g., a plasmid or minicircle.

In some embodiments, the heterologous object sequence is in operative association with a first promoter.

In some embodiments, the one or more first tissue-specific expression-control sequences comprises a tissue specific promoter.

In some embodiments, the tissue-specific promoter comprises a first promoter in operative association with: (i) the heterologous object sequence, (ii) a nucleic acid encoding the retroviral RT, or (iii) (i) and (ii).

In some embodiments, the one or more first tissue-specific expression-control sequences comprises a tissue-specific microRNA recognition sequence in operative association with: (i) the heterologous object sequence, (ii) a nucleic acid encoding the retroviral RT domain, or (iii) (i) and (ii).

In some embodiments, a system comprises a tissue-specific promoter, and the system further comprises one or more tissue-specific microRNA recognition sequences, wherein: (i) the tissue specific promoter is in operative association with: (I) the heterologous object sequence, (II) a nucleic acid encoding the retroviral RT domain, or (III) (I) and (II); and/or (ii) the one or more tissue-specific microRNA recognition sequences are in operative association with: (I) the heterologous object sequence, (II) a nucleic acid encoding the retroviral RT, or (III) (I) and (II).

In some embodiments, wherein (a) comprises a nucleic acid encoding the polypeptide, the nucleic acid comprises a promoter in operative association with the nucleic acid encoding the polypeptide.

In some embodiments, the nucleic acid encoding the polypeptide comprises one or more second tissue-specific expression-control sequences specific to the target tissue in operative association with the polypeptide coding sequence.

In some embodiments, the one or more second tissue-specific expression-control sequences comprises a tissue specific promoter.

In some embodiments, the tissue-specific promoter is the promoter in operative association with the nucleic acid encoding the polypeptide.

In some embodiments, the one or more second tissue-specific expression-control sequences comprises a tissue-specific microRNA recognition sequence.

In some embodiments, the promoter in operative association with the nucleic acid encoding the polypeptide is a tissue-specific promoter, the system further comprising one or more tissue-specific microRNA recognition sequences.

In some embodiments, a nucleic acid component of a system provided by the invention is a sequence (e.g., encoding the polypeptide or comprising a heterologous object sequence) flanked by untranslated regions (UTRs) that modify protein expression levels. Various 5′ and 3′ UTRs can affect protein expression. For example, in some embodiments, the coding sequence may be preceded by a 5′ UTR that modifies RNA stability or protein translation. In some embodiments, the sequence may be followed by a 3′ UTR that modifies RNA stability or translation. In some embodiments, the sequence may be preceded by a 5′ UTR and followed by a 3′ UTR that modify RNA stability or translation. In some embodiments, the 5′ and/or 3′ UTR may be selected from the 5′ and 3′ UTRs of complement factor 3 (C3) (CACTCCTCCCCATCCTCTCCCTCTGTCCCTCTGTCCCTCTGACCCTGCACTGTCCCAG CACC; SEQ ID NO: 11,004) or orosomucoid 1 (ORM1) (CAGGACACAGCCTTGGATCAGGACAGAGACTTGGGGGCCATCCTGCCCCTCCAACC CGACATGTGTACCTCAGCTTTTTCCCTCACTTGCATCAATAAAGCTTCTGTGTTTGGA ACAGCTAA; SEQ ID NO: 11,005) (Asrani et al. RNA Biology 2018). In certain embodiments, the 5′ UTR is the 5′ UTR from C3 and the 3′ UTR is the 3′ UTR from ORM1. In certain embodiments, a 5′ UTR and 3′ UTR for protein expression, e.g., mRNA (or DNA encoding the RNA) for a gene modifying polypeptide or heterologous object sequence, comprise optimized expression sequences. In some embodiments, the 5′ UTR comprises GGGAAAUAAGAGAGAAAAGAAGAGUAAGAAGAAAUAUAAGAGCCACC (SEQ ID NO: 11,006) and/or the 3′ UTR comprising UGAUAAUAGGCUGGAGCCUCGGUGGCCAUGCUUCUUGCCCCUUGGGCCUCCCCCC AGCCCCUCCUCCCCUUCCUGCACCCGUACCCCCGUGGUCUUUGAAUAAAGUCUGA (SEQ ID NO: 11,007), e.g., as described in Richner et al. *Cell* 168(6): P1114-1125 (2017), the sequences of which are incorporated herein by reference.In some embodiments, a 5′ and/or 3′

UTR may be selected to enhance protein expression. In some embodiments, a 5′ and/or 3′ UTR may be selected to modify protein expression such that overproduction inhibition is minimized. In some embodiments, UTRs are around a coding sequence, e.g., outside the coding sequence and in other embodiments proximal to the coding sequence. In some embodiments, additional regulatory elements (e.g., miRNA binding sites, cis-regulatory sites) are included in the UTRs.

In some embodiments, an open reading frame of a gene modifying system, e.g., an ORF of an mRNA (or DNA encoding an mRNA) encoding a gene modifying polypeptide or one or more ORFs of an mRNA (or DNA encoding an mRNA) of a heterologous object sequence, is flanked by a 5′ and/or 3′ untranslated region (UTR) that enhances the expression thereof. In some embodiments, the 5′ UTR of an mRNA component (or transcript produced from a DNA component) of the system comprises the sequence 5′-GGGAAAUAAGAGAGAAAAGAAGAGUAAGAAGAAAUAUAAGAGCCACC-3′; SEQ ID NO: 11,008). In some embodiments, the 3′ UTR of an mRNA component (or transcript produced from a DNA component) of the system comprises the sequence 5′-UGAUAAUAGGCUGGAGCCUCGGUGGCCAUGCUUCUUGCCCCUUGGGCCUCCCCCCAGCCCCUCCUCCCCUUCCUGCACCCGUACCCCCGUGGUCUUUGAAUAAAGUCUGA-3′ (SEQ ID NO: 11,009). This combination of 5′ UTR and 3′ UTR has been shown to result in desirable expression of an operably linked ORF by Richner et al. *Cell* 168(6): P1114-1125 (2017), the teachings and sequences of which are incorporated herein by reference. In some embodiments, a system described herein comprises a DNA encoding a transcript, wherein the DNA comprises the corresponding 5′ UTR and 3′ UTR sequences, with T substituting for U in the above-listed sequence). In some embodiments, a DNA vector used to produce an RNA component of the system further comprises a promoter upstream of the 5′ UTR for initiating *in vitro* transcription, e.g, a T7, T3, or SP6 promoter. The 5′ UTR above begins with GGG, which is a suitable start for optimizing transcription using T7 RNA polymerase. For tuning transcription levels and altering the transcription start site nucleotides to fit alternative 5′ UTRs, the teachings of Davidson et al. *Pac Symp Biocomput* 433-443 (2010) describe T7 promoter variants, and the methods of discovery thereof, that fulfill both of these traits.

Viral vectors and components thereof

Viruses are a useful source of delivery vehicles for the systems described herein, in addition to a source of relevant enzymes or domains as described herein, e.g., as sources of polymerases and polymerase functions used herein, e.g., DNA-dependent DNA polymerase, RNA-dependent RNA polymerase, RNA-dependent DNA polymerase, DNA-dependent RNA polymerase, reverse transcriptase. Some enzymes, e.g., reverse transcriptases, may have multiple activities, e.g., be capable of both RNA-dependent DNA polymerization and DNA-dependent DNA polymerization, e.g., first and second strand synthesis. In some embodiments, the virus used as a gene modifying delivery system or a source of components thereof may be selected from a group as described by Baltimore *Bacteriol Rev* 35(3):235-241 (1971).

In some embodiments, the virus is selected from a Group I virus, e.g., is a DNA virus and packages dsDNA into virions. In some embodiments, the Group I virus is selected from, e.g., Adenoviruses, Herpesviruses, Poxviruses.

In some embodiments, the virus is selected from a Group II virus, e.g., is a DNA virus and packages ssDNA into virions. In some embodiments, the Group II virus is selected from, e.g., Parvoviruses. In some embodiments, the parvovirus is a dependoparvovirus, e.g., an adeno-associated virus (AAV).

In some embodiments, the virus is selected from a Group III virus, e.g., is an RNA virus and packages dsRNA into virions. In some embodiments, the Group III virus is selected from, e.g., Reoviruses. In some embodiments, one or both strands of the dsRNA contained in such virions is a coding molecule able to serve directly as mRNA upon transduction into a host cell, e.g., can be directly translated into protein upon transduction into a host cell without requiring any intervening nucleic acid replication or polymerization steps.

In some embodiments, the virus is selected from a Group IV virus, e.g., is an RNA virus and packages ssRNA(+) into virions. In some embodiments, the Group IV virus is selected from, e.g., Coronaviruses, Picornaviruses, Togaviruses. In some embodiments, the ssRNA(+) contained in such virions is a coding molecule able to serve directly as mRNA upon transduction into a host cell, e.g., can be directly translated into protein upon transduction into a host cell without requiring any intervening nucleic acid replication or polymerization steps.

In some embodiments, the virus is selected from a Group V virus, e.g., is an RNA virus and packages ssRNA(-) into virions. In some embodiments, the Group V virus is selected from, e.g., Orthomyxoviruses, Rhabdoviruses. In some embodiments, an RNA virus with an ssRNA(-)

genome also carries an enzyme inside the virion that is transduced to host cells with the viral genome, e.g., an RNA-dependent RNA polymerase, capable of copying the ssRNA(-) into ssRNA(+) that can be translated directly by the host.

In some embodiments, the virus is selected from a Group VI virus, e.g., is a retrovirus and packages ssRNA(+) into virions. In some embodiments, the Group VI virus is selected from, e.g., retroviruses. In some embodiments, the retrovirus is a lentivirus, e.g., HIV-1, HIV-2, SIV, BIV. In some embodiments, the retrovirus is a spumavirus, e.g., a foamy virus, e.g., HFV, SFV, BFV. In some embodiments, the ssRNA(+) contained in such virions is a coding molecule able to serve directly as mRNA upon transduction into a host cell, e.g., can be directly translated into protein upon transduction into a host cell without requiring any intervening nucleic acid replication or polymerization steps. In some embodiments, the ssRNA(+) is first reverse transcribed and copied to generate a dsDNA genome intermediate from which mRNA can be transcribed in the host cell. In some embodiments, an RNA virus with an ssRNA(+) genome also carries an enzyme inside the virion that is transduced to host cells with the viral genome, e.g., an RNA-dependent DNA polymerase, capable of copying the ssRNA(+) into dsDNA that can be transcribed into mRNA and translated by the host. In some embodiments, the reverse transcriptase from a Group VI retrovirus is incorporated as the reverse transcriptase domain of a gene modifying polypeptide.

In some embodiments, the virus is selected from a Group VII virus, e.g., is a retrovirus and packages dsRNA into virions. In some embodiments, the Group VII virus is selected from, e.g., Hepadnaviruses. In some embodiments, one or both strands of the dsRNA contained in such virions is a coding molecule able to serve directly as mRNA upon transduction into a host cell, e.g., can be directly translated into protein upon transduction into a host cell without requiring any intervening nucleic acid replication or polymerization steps. In some embodiments, one or both strands of the dsRNA contained in such virions is first reverse transcribed and copied to generate a dsDNA genome intermediate from which mRNA can be transcribed in the host cell. In some embodiments, an RNA virus with a dsRNA genome also carries an enzyme inside the virion that is transduced to host cells with the viral genome, e.g., an RNA-dependent DNA polymerase, capable of copying the dsRNA into dsDNA that can be transcribed into mRNA and translated by the host. In some embodiments, the reverse

transcriptase from a Group VII retrovirus is incorporated as the reverse transcriptase domain of a gene modifying polypeptide.

In some embodiments, virions used to deliver nucleic acid in this invention may also carry enzymes involved in the process of gene modification. For example, a retroviral virion may contain a reverse transcriptase domain that is delivered into a host cell along with the nucleic acid. In some embodiments, an RNA template may be associated with a gene modifying polypeptide within a virion, such that both are co-delivered to a target cell upon transduction of the nucleic acid from the viral particle. In some embodiments, the nucleic acid in a virion may comprise DNA, e.g., linear ssDNA, linear dsDNA, circular ssDNA, circular dsDNA, minicircle DNA, dbDNA, ceDNA. In some embodiments, the nucleic acid in a virion may comprise RNA, e.g., linear ssRNA, linear dsRNA, circular ssRNA, circular dsRNA. In some embodiments, a viral genome may circularize upon transduction into a host cell, e.g., a linear ssRNA molecule may undergo a covalent linkage to form a circular ssRNA, a linear dsRNA molecule may undergo a covalent linkage to form a circular dsRNA or one or more circular ssRNA. In some embodiments, a viral genome may replicate by rolling circle replication in a host cell. In some embodiments, a viral genome may comprise a single nucleic acid molecule, e.g., comprise a non-segmented genome. In some embodiments, a viral genome may comprise two or more nucleic acid molecules, e.g., comprise a segmented genome. In some embodiments, a nucleic acid in a virion may be associated with one or proteins. In some embodiments, one or more proteins in a virion may be delivered to a host cell upon transduction. In some embodiments, a natural virus may be adapted for nucleic acid delivery by the addition of virion packaging signals to the target nucleic acid, wherein a host cell is used to package the target nucleic acid containing the packaging signals.

In some embodiments, a virion used as a delivery vehicle may comprise a commensal human virus. In some embodiments, a virion used as a delivery vehicle may comprise an anellovirus, the use of which is described in WO2018232017A1, which is incorporated herein by reference in its entirety.

AAV Administration

In some embodiments, an adeno-associated virus (AAV) is used in conjunction with the system, template nucleic acid, and/or polypeptide described herein. In some embodiments, an

AAV is used to deliver, administer, or package the system, template nucleic acid, and/or polypeptide described herein. In some embodiments, the AAV is a recombinant AAV (rAAV).

In some embodiments, a system comprises (a) a polypeptide described herein or a nucleic acid encoding the same, (b) a template nucleic acid (e.g., template RNA) described herein, and (c) one or more first tissue-specific expression-control sequences specific to the target tissue, wherein the one or more first tissue-specific expression-control sequences specific to the target tissue are in operative association with (a), (b), or (a) and (b), wherein, when associated with (a), (a) comprises a nucleic acid encoding the polypeptide.

In some embodiments, a system described herein further comprises a first recombinant adeno-associated virus (rAAV) capsid protein; wherein the at least one of (a) or (b) is associated with the first rAAV capsid protein, wherein at least one of (a) or (b) is flanked by AAV inverted terminal repeats (ITRs).

In some embodiments, (a) and (b) are associated with the first rAAV capsid protein.

In some embodiments, (a) and (b) are on a single nucleic acid.

In some embodiments, the system further comprises a second rAAV capsid protein, wherein at least one of (a) or (b) is associated with the second rAAV capsid protein, and wherein the at least one of (a) or (b) associated with the second rAAV capsid protein is different from the at least one of (a) or (b) is associated with the first rAAV capsid protein.

In some embodiments, the at least one of (a) or (b) is associated with the first or second rAAV capsid protein is dispersed in the interior of the first or second rAAV capsid protein, which first or second rAAV capsid protein is in the form of an AAV capsid particle.

In some embodiments, the system further comprises a nanoparticle, wherein the nanoparticle is associated with at least one of (a) or (b).

In some embodiments, (a) and (b), respectively are associated with: a) a first rAAV capsid protein and a second rAAV capsid protein; b) a nanoparticle and a first rAAV capsid protein; c) a first rAAV capsid protein; d) a first adenovirus capsid protein; e) a first nanoparticle and a second nanoparticle; or f) a first nanoparticle.

Viral vectors are useful for delivering all or part of a system provided by the invention, e.g., for use in methods provided by the invention. Systems derived from different viruses have been employed for the delivery of polypeptides or nucleic acids; for example: integrase-deficient lentivirus, adenovirus, adeno-associated virus (AAV), herpes simplex virus, and baculovirus

(reviewed in Hodge et al. Hum Gene Ther 2017; Narayanavari et al. Crit Rev Biochem Mol Biol 2017; Boehme et al. Curr Gene Ther 2015).

Adenoviruses are common viruses that have been used as gene delivery vehicles given well-defined biology, genetic stability, high transduction efficiency, and ease of large-scale production (see, for example, review by Lee et al. Genes & Diseases 2017). They possess linear dsDNA genomes and come in a variety of serotypes that differ in tissue and cell tropisms. In order to prevent replication of infectious virus in recipient cells, adenovirus genomes used for packaging are deleted of some or all endogenous viral proteins, which are provided in trans in viral production cells. This renders the genomes helper-dependent, meaning they can only be replicated and packaged into viral particles in the presence of the missing components provided by so-called helper functions. A helper-dependent adenovirus system with all viral ORFs removed may be compatible with packaging foreign DNA of up to ~37 kb (Parks et al. J Virol 1997). In some embodiments, an adenoviral vector is used to deliver DNA corresponding to the polypeptide or template component of the gene modifying system, or both are contained on separate or the same adenoviral vector. In some embodiments, the adenovirus is a helper-dependent adenovirus (HD-AdV) that is incapable of self-packaging. In some embodiments, the adenovirus is a high-capacity adenovirus (HC-AdV) that has had all or a substantial portion of endogenous viral ORFs deleted, while retaining the necessary sequence components for packaging into adenoviral particles. For this type of vector, the only adenoviral sequences required for genome packaging are noncoding sequences: the inverted terminal repeats (ITRs) at both ends and the packaging signal at the 5′-end (Jager et al. Nat Protoc 2009). In some embodiments, the adenoviral genome also comprises stuffer DNA to meet a minimal genome size for optimal production and stability (see, for example, Hausl et al. Mol Ther 2010). In some embodiments, an adenovirus is used to deliver a gene modifying system to the liver.

In some embodiments, an adenovirus is used to deliver a gene modifying system to HSCs, e.g., HDAd5/35++. HDAd5/35++ is an adenovirus with modified serotype 35 fibers that de-target the vector from the liver (Wang et al. Blood Adv 2019). In some embodiments, the adenovirus that delivers a gene modifying system to HSCs utilizes a receptor that is expressed specifically on primitive HSCs, e.g., CD46.

Adeno-associated viruses (AAV) belong to the parvoviridae family and more specifically constitute the dependoparvovirus genus. The AAV genome is composed of a linear single-

stranded DNA molecule which contains approximately 4.7 kilobases (kb) and consists of two major open reading frames (ORFs) encoding the non-structural Rep (replication) and structural Cap (capsid) proteins. A second ORF within the cap gene was identified that encodes the assembly-activating protein (AAP). The DNAs flanking the AAV coding regions are two cis-acting inverted terminal repeat (ITR) sequences, approximately 145 nucleotides in length, with interrupted palindromic sequences that can be folded into energetically stable hairpin structures that function as primers of DNA replication. In addition to their role in DNA replication, the ITR sequences have been shown to be involved in viral DNA integration into the cellular genome, rescue from the host genome or plasmid, and encapsidation of viral nucleic acid into mature virions (Muzyczka, (1992) Curr. Top. Micro. Immunol. 158:97-129). In some embodiments, one or more gene modifying nucleic acid components is flanked by ITRs derived from AAV for viral packaging. See, e.g., WO2019113310.

In some embodiments, one or more components of the gene modifying system are carried via at least one AAV vector. In some embodiments, the at least one AAV vector is selected for tropism to a particular cell, tissue, organism. In some embodiments, the AAV vector is pseudotyped, e.g., AAV2/8, wherein AAV2 describes the design of the construct but the capsid protein is replaced by that from AAV8. It is understood that any of the described vectors could be pseudotype derivatives, wherein the capsid protein used to package the AAV genome is derived from that of a different AAV serotype. Without wishing to be limited in vector choice, a list of exemplary AAV serotypes can be found in Table 18. In some embodiments, an AAV to be employed for gene modifying may be evolved for novel cell or tissue tropism as has been demonstrated in the literature (e.g., Davidsson et al. Proc Natl Acad Sci U S A 2019).

In some embodiments, the AAV delivery vector is a vector which has two AAV inverted terminal repeats (ITRs) and a nucleotide sequence of interest (for example, a sequence coding for a gene modifying polypeptideor a DNA template, or both), each of said ITRs having an interrupted (or noncontiguous) palindromic sequence, i.e., a sequence composed of three segments: a first segment and a last segment that are identical when read 5'→ 3' but hybridize when placed against each other, and a segment that is different that separates the identical segments. See, for example, WO2012123430.

Conventionally, AAV virions with capsids are produced by introducing a plasmid or plasmids encoding the rAAV or scAAV genome, Rep proteins, and Cap proteins (Grimm et al,

1998). Upon introduction of these helper plasmids in trans, the AAV genome is "rescued" (i.e., released and subsequently recovered) from the host genome, and is further encapsidated to produce infectious AAV. In some embodiments, one or more gene modifying nucleic acids are packaged into AAV particles by introducing the ITR-flanked nucleic acids into a packaging cell in conjunction with the helper functions.

In some embodiments, the AAV genome is a so called self-complementary genome (referred to as scAAV), such that the sequence located between the ITRs contains both the desired nucleic acid sequence (e.g., DNA encoding the gene modifying polypeptide or template, or both) in addition to the reverse complement of the desired nucleic acid sequence, such that these two components can fold over and self-hybridize. In some embodiments, the self-complementary modules are separated by an intervening sequence that permits the DNA to fold back on itself, e.g., forms a stem-loop. An scAAV has the advantage of being poised for transcription upon entering the nucleus, rather than being first dependent on ITR priming and second-strand synthesis to form dsDNA. In some embodiments, one or more gene modifying components is designed as an scAAV, wherein the sequence between the AAV ITRs contains two reverse complementing modules that can self-hybridize to create dsDNA.

In some embodiments, nucleic acid (e.g., encoding a polypeptide, or a template, or both) delivered to cells is closed-ended, linear duplex DNA (CELiD DNA or ceDNA). In some embodiments, ceDNA is derived from the replicative form of the AAV genome (Li et al. PLoS One 2013). In some embodiments, the nucleic acid (e.g., encoding a polypeptide, or a template DNA, or both) is flanked by ITRs, e.g., AAV ITRs, wherein at least one of the ITRs comprises a terminal resolution site and a replication protein binding site (sometimes referred to as a replicative protein binding site). In some embodiments, the ITRs are derived from an adeno-associated virus, e.g., AAV1, AAV2, AAV3, AAV4, AAV5, AAV6, AAV7, AAV8, AAV9, AAV10, AAV11, AAV12, or a combination thereof. In some embodiments, the ITRs are symmetric. In some embodiments, the ITRs are asymmetric. In some embodiments, at least one Rep protein is provided to enable replication of the construct. In some embodiments, the at least one Rep protein is derived from an adeno-associated virus, e.g., AAV1, AAV2, AAV3, AAV4, AAV5, AAV6, AAV7, AAV8, AAV9, AAV10, AAV11, AAV12, or a combination thereof. In some embodiments, ceDNA is generated by providing a production cell with (i) DNA flanked by

ITRs, e.g., AAV ITRs, and (ii) components required for ITR-dependent replication, e.g., AAV proteins Rep78 and Rep52 (or nucleic acid encoding the proteins). In some embodiments, ceDNA is free of any capsid protein, e.g., is not packaged into an infectious AAV particle. In some embodiments, ceDNA is formulated into LNPs (see, for example, WO2019051289A1).

In some embodiments, the ceDNA vector consists of two self-complementary sequences, e.g., asymmetrical or symmetrical or substantially symmetrical ITRs as defined herein, flanking said expression cassette, wherein the ceDNA vector is not associated with a capsid protein. In some embodiments, the ceDNA vector comprises two self-complementary sequences found in an AAV genome, where at least one ITR comprises an operative Rep-binding element (RBE) (also sometimes referred to herein as "RBS") and a terminal resolution site (trs) of AAV or a functional variant of the RBE. See, for example, WO2019113310.

In some embodiments, the AAV genome comprises two genes that encode four replication proteins and three capsid proteins, respectively. In some embodiments, the genes are flanked on either side by 145-bp inverted terminal repeats (ITRs). In some embodiments, the virion comprises up to three capsid proteins (Vp1, Vp2, and/or Vp3), e.g., produced in a 1:1:10 ratio. In some embodiments, the capsid proteins are produced from the same open reading frame and/or from differential splicing (Vp1) and alternative translational start sites (Vp2 and Vp3, respectively). Generally, Vp3 is the most abundant subunit in the virion and participates in receptor recognition at the cell surface defining the tropism of the virus. In some embodiments, Vp1 comprises a phospholipase domain, e.g., which functions in viral infectivity, in the N-terminus of Vp1.

In some embodiments, packaging capacity of the viral vectors limits the size of the gene modifying system that can be packaged into the vector. For example, the packaging capacity of the AAVs can be about 4.5 kb (e.g., about 3.0, 3.5, 4.0, 4.5, 5.0, 5.5, or 6.0 kb), e.g., including one or two inverted terminal repeats (ITRs), e.g., 145 base ITRs.

In some embodiments, recombinant AAV (rAAV) comprises cis-acting 145-bp ITRs flanking vector transgene cassettes, e.g., providing up to 4.5 kb for packaging of foreign DNA. Subsequent to infection, rAAV can, in some instances, express a fusion protein of the invention and persist without integration into the host genome by existing episomally in circular head-to-tail concatemers. rAAV can be used, for example, *in vitro* and *in vivo*. In some embodiments,

AAV-mediated gene delivery requires that the length of the coding sequence of the gene is equal or greater in size than the wild-type AAV genome.

AAV delivery of genes that exceed this size and/or the use of large physiological regulatory elements can be accomplished, for example, by dividing the protein(s) to be delivered into two or more fragments. In some embodiments, the N-terminal fragment is fused to an intein-N sequence. In some embodiments, the C- terminal fragment is fused to an intein-C sequence. In embodiments, the fragments are packaged into two or more AAV vectors.

In some embodiments, dual AAV vectors are generated by splitting a large transgene expression cassette in two separate halves (5′ and 3′ ends, or head and tail), e.g., wherein each half of the cassette is packaged in a single AAV vector (of <5 kb). The re-assembly of the full-length transgene expression cassette can, in some embodiments, then be achieved upon co-infection of the same cell by both dual AAV vectors. In some embodiments, co-infection is followed by one or more of: (1) homologous recombination (HR) between 5′ and 3′ genomes (dual AAV overlapping vectors); (2) ITR-mediated tail-to-head concatemerization of 5′ and 3′ genomes (dual AAV trans-splicing vectors); and/or (3) a combination of these two mechanisms (dual AAV hybrid vectors). In some embodiments, the use of dual AAV vectors *in vivo* results in the expression of full-length proteins. In some embodiments, the use of the dual AAV vector platform represents an efficient and viable gene transfer strategy for transgenes of greater than about 4.0, 4.1, 4.2, 4.3, 4.4, 4.5, 4.6, 4.7, 4.8, 4.9, or 5.0 kb in size. In some embodiments, AAV vectors can also be used to transduce cells with target nucleic acids, e.g., in the *in vitro* production of nucleic acids and peptides. In some embodiments, AAV vectors can be used for *in vivo* and *ex vivo* gene therapy procedures (see, e.g., West et al., Virology 160:38-47 (1987); U.S. Patent No. 4,797,368; WO 93/24641; Kotin, Human Gene Therapy 5:793-801 (1994); Muzyczka, J. Clin. Invest.94:1351 (1994); each of which is incorporated herein by reference in their entirety). The construction of recombinant AAV vectors is described in a number of publications, including U.S. Patent No.5,173,414; Tratschin et al., Mol. Cell. Biol.5:3251- 3260 (1985); Tratschin, et al., Mol. Cell. Biol.4:2072-2081 (1984); Hermonat & Muzyczka, PNAS 81:6466-6470 (1984); and Samulski et al., J. Virol.63:03822-3828 (1989) (incorporated by reference herein in their entirety).

In some embodiments, a gene modifying polypeptide described herein (e.g., with or without one or more guide nucleic acids) can be delivered using AAV, lentivirus, adenovirus or

other plasmid or viral vector types, in particular, using formulations and doses from, for example, U.S. Patent No. 8,454,972 (formulations, doses for adenovirus), U.S. Patent No.8,404,658 (formulations, doses for AAV) and U.S. Patent No.5,846,946 (formulations, doses for DNA plasmids) and from clinical trials and publications regarding the clinical trials involving lentivirus, AAV and adenovirus. For example, for AAV, the route of administration, formulation and dose can be as described in U.S. Patent No.8,454,972 and as in clinical trials involving AAV. For adenovirus, the route of administration, formulation and dose can be as described in U.S. Patent No.8,404,658 and as in clinical trials involving adenovirus. For plasmid delivery, the route of administration, formulation and dose can be as described in U.S. Patent No.5,846,946 and as in clinical studies involving plasmids. Doses can be based on or extrapolated to an average 70 kg individual (e.g. a male adult human), and can be adjusted for patients, subjects, mammals of different weight and species. Frequency of administration is within the ambit of the medical or veterinary practitioner (e.g., physician, veterinarian), depending on usual factors including the age, sex, general health, other conditions of the patient or subject and the particular condition or symptoms being addressed. In some embodiments, the viral vectors can be injected into the tissue of interest. For cell-type specific gene modifying, the expression of the gene modifying polypeptide and optional guide nucleic acid can, in some embodiments, be driven by a cell-type specific promoter.

In some embodiments, AAV allows for low toxicity, for example, due to the purification method not requiring ultracentrifugation of cell particles that can activate the immune response. In some embodiments, AAV allows low probability of causing insertional mutagenesis, for example, because it does not substantially integrate into the host genome.

In some embodiments, AAV has a packaging limit of about 4.4, 4.5, 4.6, 4.7, or 4.75 kb. In some embodiments, a gene modifying polypeptide-encoding sequence, promoter, and transcription terminator can fit into a single viral vector. SpCas9 (4.1 kb) may, in some instances, be difficult to package into AAV. Therefore, in some embodiments, a gene modifying polypeptide coding sequence is used that is shorter in length than other gene modifying polypeptide coding sequences or base editors. In some embodiments, the gene modifying polypeptide encoding sequences are less than about 4.5 kb, 4.4 kb, 4.3 kb, 4.2 kb, 4.1 kb, 4 kb, 3.9 kb, 3.8 kb, 3.7 kb, 3.6 kb, 3.5 kb, 3.4 kb, 3.3 kb, 3.2 kb, 3.1 kb, 3 kb, 2.9 kb, 2.8 kb, 2.7 kb, 2.6 kb, 2.5 kb, 2 kb, or 1.5 kb.

An AAV can be AAV1, AAV2, AAV5 or any combination thereof. In some embodiments, the type of AAV is selected with respect to the cells to be targeted; e.g., AAV serotypes 1, 2, 5 or a hybrid capsid AAV1, AAV2, AAV5 or any combination thereof can be selected for targeting brain or neuronal cells; or AAV4 can be selected for targeting cardiac tissue. In some embodiments, AAV8 is selected for delivery to the liver. Exemplary AAV serotypes as to these cells are described, for example, in Grimm, D. et al, J. Virol.82: 5887-5911 (2008) (incorporated herein by reference in its entirety). In some embodiments, AAV refers all serotypes, subtypes, and naturally-occurring AAV as well as recombinant AAV. AAV may be used to refer to the virus itself or a derivative thereof. In some embodiments, AAV includes AAV1, AAV2, AAV3, AAV3B, AAV4, AAV5, AAV6, AAV6.2, AAV7, AAVrh.64Rl, AAVhu.37, AAVrh.8, AAVrh.32.33, AAV8, AAV9, AAV-DJ, AAV2/8, AAVrhlO, AAVLK03, AV10, AAV11, AAV 12, rhlO, and hybrids thereof, avian AAV, bovine AAV, canine AAV, equine AAV, primate AAV, non-primate AAV, and ovine AAV. The genomic sequences of various serotypes of AAV, as well as the sequences of the native terminal repeats (TRs), Rep proteins, and capsid subunits are known in the art. Such sequences may be found in the literature or in public databases such as GenBank. Additional exemplary AAV serotypes are listed in Table 18.

Table 18. Exemplary AAV serotypes.

Target Tissue	Vehicle	Reference
Liver	AAV (AAV8[1], AAVrh.8[1], AAVhu.37[1], AAV2/8, AAV2/rh10[2], AAV9, AAV2, NP40[3], NP59[2,3], AAV3B[5], AAV-DJ[4], AAV-LK01[4], AAV-LK02[4], AAV-LK03[4], AAV-LK19[4], AAV5[7] Adenovirus (Ad5, HC-AdV[6])	1. Wang *et al.*, *Mol. Ther.* **18**, 118–25 (2010) 2. Ginn *et al.*, *JHEP Reports*, 100065 (2019) 3. Paulk *et al.*, *Mol. Ther.* **26**, 289–303 (2018). 4. L. Lisowski *et al.*, *Nature*. **506**, 382–6 (2014).

		5. L. Wang *et al.*, *Mol. Ther.* **23**, 1877–87 (2015). 6. Hausl *Mol Ther* (2010) 7. Davidoff *et al.*, *Mol. Ther.* 11, 875-88 (2005)
Lung	AAV (AAV4, AAV5, AAV6[1], AAV9, H22[2]) Adenovirus (Ad5, Ad3, Ad21, Ad14)[3]	1. Duncan *et al.*, *Mol Ther Methods Clin Dev* (2018) 2. Cooney *et al.*, Am J Respir Cell Mol Biol (2019) 3. Li *et al.*, *Mol Ther Methods Clin Dev* (2019)
Skin	AAV (AAV6[1], AAV-LK19[2])	1. Petek et al., *Mol. Ther.* (2010) 2. L. Lisowski *et al.*, *Nature.* **506**, 382–6 (2014).
HSCs	Adenovirus (HDAd5/35^{++})	Wang et al. *Blood Adv* (2019)

In some embodiments, a pharmaceutical composition (e.g., comprising an AAV as described herein) has less than 10% empty capsids, less than 8% empty capsids, less than 7% empty capsids, less than 5% empty capsids, less than 3% empty capsids, or less than 1 % empty capsids. In some embodiments, the pharmaceutical composition has less than about 5% empty capsids. In some embodiments, the number of empty capsids is below the limit of detection. In some embodiments, it is advantageous for the pharmaceutical composition to have low amounts of empty capsids, e.g., because empty capsids may generate an adverse response (e.g., immune response, inflammatory response, liver response, and/or cardiac response), e.g., with little or no substantial therapeutic benefit.

In some embodiments, the residual host cell protein (rHCP) in the pharmaceutical composition is less than or equal to 100 ng/ml rHCP per 1 x 10^{13} vg/ml, e.g., less than or equal to

40 ng/ml rHCP per 1 x 10^{13} vg/ml or 1-50 ng/ml rHCP per 1 x 10^{13} vg/ml. In some embodiments, the pharmaceutical composition comprises less than 10 ng rHCP per l.0 x 10^{13} vg, or less than 5 ng rHCP per 1.0 x 10^{13} vg, less than 4 ng rHCP per 1.0 x 10^{13} vg, or less than 3 ng rHCP per 1.0 x 10^{13} vg, or any concentration in between. In some embodiments, the residual host cell DNA (hcDNA) in the pharmaceutical composition is less than or equal to 5 x 10^{6} pg/ml hcDNA per 1 x 10^{13} vg/ml, less than or equal to 1.2 x 10^{6} pg/ml hcDNA per 1 x 10^{13} vg/ml, or 1 x 10^{5} pg/ml hcDNA per 1 x 10^{13} vg/ml. In some embodiments, the residual host cell DNA in said pharmaceutical composition is less than 5.0 x 10^{5} pg per 1 x 10^{13} vg, less than 2.0 x 10^{5} pg per l.0 x 10^{13} vg, less than 1.1 x 10^{5} pg per 1.0 x 10^{13} vg, less than 1.0 x 10^{5} pg hcDNA per 1.0 x 10^{13} vg, less than 0.9 x 10^{5} pg hcDNA per 1.0 x 10^{13} vg, less than 0.8 x 10^{5} pg hcDNA per 1.0 x 10^{13} vg, or any concentration in between.

In some embodiments, the residual plasmid DNA in the pharmaceutical composition is less than or equal to 1.7 x 10^{5} pg/ml per 1.0 x 10^{13} vg/ml, or 1 x 10^{5} pg/ml per 1 x 1.0 x 10^{13} vg/ml, or 1.7 x 10^{6} pg/ml per 1.0 x 10^{13} vg/ml. In some embodiments, the residual DNA plasmid in the pharmaceutical composition is less than 10.0 x 10^{5} pg by 1.0 x 10^{13} vg, less than 8.0 x 10^{5} pg by 1.0 x 10^{13} vg or less than 6.8 x 10^{5} pg by 1.0 x 10^{13} vg. In embodiments, the pharmaceutical composition comprises less than 0.5 ng per 1.0 x 10^{13} vg, less than 0.3 ng per 1.0 x 10^{13} vg, less than 0.22 ng per 1.0 x 10^{13} vg or less than 0.2 ng per 1.0 x 10^{13} vg or any intermediate concentration of bovine serum albumin (BSA). In embodiments, the benzonase in the pharmaceutical composition is less than 0.2 ng by 1.0 x 10^{13} vg, less than 0.1 ng by 1.0 x 10^{13} vg, less than 0.09 ng by 1.0 x 10^{13} vg, less than 0.08 ng by 1.0 x 10^{13} vg or any intermediate concentration. In embodiments, Poloxamer 188 in the pharmaceutical composition is about 10 to 150 ppm, about 15 to 100 ppm or about 20 to 80 ppm. In embodiments, the cesium in the pharmaceutical composition is less than 50 pg / g (ppm), less than 30 pg / g (ppm) or less than 20 pg / g (ppm) or any intermediate concentration.

In embodiments, the pharmaceutical composition comprises total impurities, e.g., as determined by SDS-PAGE, of less than 10%, less than 8%, less than 7%, less than 6%, less than 5%, less than 4%, less than 3%, less than 2%, or any percentage in between. In embodiments, the total purity, e.g., as determined by SDS-PAGE, is greater than 90%, greater than 92%, greater than 93%, greater than 94%, greater than 95%, greater than 96%, greater than 97%, greater than 98%, or any percentage in between. In embodiments, no single unnamed related impurity, e.g.,

as measured by SDS-PAGE, is greater than 5%, greater than 4%, greater than 3% or greater than 2%, or any percentage in between. In embodiments, the pharmaceutical composition comprises a percentage of filled capsids relative to total capsids (e.g., peak 1 + peak 2 as measured by analytical ultracentrifugation) of greater than 85%, greater than 86%, greater than 87%, greater than 88%, greater than 89%, greater than 90%, greater than 91%, greater than 91.9%, greater than 92%, greater than 93%, or any percentage in between. In embodiments of the pharmaceutical composition, the percentage of filled capsids measured in peak 1 by analytical ultracentrifugation is 20-80%, 25-75%, 30-75%, 35-75%, or 37.4-70.3%. In embodiments of the pharmaceutical composition, the percentage of filled capsids measured in peak 2 by analytical ultracentrifugation is 20-80%, 20-70%, 22-65%, 24-62%, or 24.9-60.1%.

In one embodiment, the pharmaceutical composition comprises a genomic titer of 1.0 to 5.0 x 10^{13} vg / mL, 1.2 to 3.0 x 10^{13} vg / mL or 1.7 to 2.3 x 10^{13} vg / ml. In one embodiment, the pharmaceutical composition exhibits a biological load of less than 5 CFU / mL, less than 4 CFU / mL, less than 3 CFU / mL, less than 2 CFU / mL or less than 1 CFU / mL or any intermediate contraction. In embodiments, the amount of endotoxin according to USP, for example, USP <85> (incorporated by reference in its entirety) is less than 1.0 EU / mL, less than 0.8 EU / mL or less than 0.75 EU / mL. In embodiments, the osmolarity of a pharmaceutical composition according to USP, for example, USP <785> (incorporated by reference in its entirety) is 350 to 450 mOsm / kg, 370 to 440 mOsm / kg or 390 to 430 mOsm / kg. In embodiments, the pharmaceutical composition contains less than 1200 particles that are greater than 25 μm per container, less than 1000 particles that are greater than 25 μm per container, less than 500 particles that are greater than 25 μm per container or any intermediate value. In embodiments, the pharmaceutical composition contains less than 10,000 particles that are greater than 10 μm per container, less than 8000 particles that are greater than 10 μm per container or less than 600 particles that are greater than 10 pm per container.

In one embodiment, the pharmaceutical composition has a genomic titer of 0.5 to 5.0 x 10^{13} vg / mL, 1.0 to 4.0 x 10^{13} vg / mL, 1.5 to 3.0 x 10^{13} vg / ml or 1.7 to 2.3 x 10^{13} vg / ml. In one embodiment, the pharmaceutical composition described herein comprises one or more of the following: less than about 0.09 ng benzonase per 1.0 x 10^{13} vg, less than about 30 pg / g (ppm) of cesium, about 20 to 80 ppm Poloxamer 188, less than about 0.22 ng BSA per 1.0 x 10^{13} vg, less than about 6.8 x 10^{5} pg of residual DNA plasmid per 1.0 x 10^{13} vg, less than about 1.1 x

10^{5} pg of residual hcDNA per 1.0 x 10^{13} vg, less than about 4 ng of rHCP per 1.0 x 10^{13} vg, pH 7.7 to 8.3, about 390 to 430 mOsm / kg, less than about 600 particles that are > 25 μm in size per container, less than about 6000 particles that are > 10 μm in size per container, about 1.7 x 10^{13} - 2.3 x 10^{13} vg / mL genomic titer, infectious titer of about 3.9 x 10^{8} to 8.4 x 10^{10} IU per 1.0 x 10^{13} vg, total protein of about 100-300 pg per 1.0 x 10^{13} vg, mean survival of >24 days in A7SMA mice with about 7.5 x 10^{13} vg / kg dose of viral vector, about 70 to 130% relative potency based on an *in vitro* cell based assay and / or less than about 5% empty capsid. In various embodiments, the pharmaceutical compositions described herein comprise any of the viral particles discussed here, retain a potency of between ± 20%, between ± 15%, between ± 10% or within ± 5% of a reference standard. In some embodiments, potency is measured using a suitable *in vitro* cell assay or *in vivo* animal model.

Additional methods of preparation, characterization, and dosing AAV particles are taught in WO2019094253, which is incorporated herein by reference in its entirety.

Additional rAAV constructs that can be employed consonant with the invention include those described in Wang et al 2019, available at: //doi.org/10.1038/s41573-019-0012-9, including Table 1 thereof, which is incorporated by reference in its entirety.

Lipid Nanoparticles

The methods and systems provided herein may employ any suitable carrier or delivery modality, including, in certain embodiments, lipid nanoparticles (LNPs). Lipid nanoparticles, in some embodiments, comprise one or more ionic lipids, such as non-cationic lipids (e.g., neutral or anionic, or zwitterionic lipids); one or more conjugated lipids (such as PEG-conjugated lipids or lipids conjugated to polymers described in Table 5 of WO2019217941; incorporated herein by reference in its entirety); one or more sterols (e.g., cholesterol); and, optionally, one or more targeting molecules (e.g., conjugated receptors, receptor ligands, antibodies); or combinations of the foregoing.

Lipids that can be used in nanoparticle formations (e.g., lipid nanoparticles) include, for example those described in Table 4 of WO2019217941, which is incorporated by reference—e.g., a lipid-containing nanoparticle can comprise one or more of the lipids in Table 4 of WO2019217941. Lipid nanoparticles can include additional elements, such as polymers, such as the polymers described in Table 5 of WO2019217941, incorporated by reference.

In some embodiments, conjugated lipids, when present, can include one or more of PEG-diacylglycerol (DAG) (such as l-(monomethoxy-polyethyleneglycol)-2,3- dimyristoylglycerol (PEG-DMG)), PEG-dialkyloxypropyl (DAA), PEG-phospholipid, PEG- ceramide (Cer), a pegylated phosphatidylethanoloamine (PEG-PE), PEG succinate diacylglycerol (PEGS-DAG) (such as 4-0-(2',3'-di(tetradecanoyloxy)propyl-l-0-(w- methoxy(polyethoxy)ethyl) butanedioate (PEG-S-DMG)), PEG dialkoxypropylcarbam, N- (carbonyl-methoxypoly ethylene glycol 2000)-1 ,2-distearoyl-sn-glycero-3-phosphoethanolamine sodium salt, and those described in Table 2 of WO2019051289 (incorporated by reference), and combinations of the foregoing.

In some embodiments, sterols that can be incorporated into lipid nanoparticles include one or more of cholesterol or cholesterol derivatives, such as those in W02009/127060 or US2010/0130588, which are incorporated by reference. Additional exemplary sterols include phytosterols, including those described in Eygeris et al (2020), dx.doi.org/10.1021/acs.nanolett.0c01386, incorporated herein by reference.

In some embodiments, the lipid particle comprises an ionizable lipid, a non-cationic lipid, a conjugated lipid that inhibits aggregation of particles, and a sterol. The amounts of these components can be varied independently and to achieve desired properties. For example, in some embodiments, the lipid nanoparticle comprises an ionizable lipid is in an amount from about 20 mol % to about 90 mol % of the total lipids (in other embodiments it may be 20-70% (mol), 30-60% (mol) or 40-50% (mol); about 50 mol % to about 90 mol % of the total lipid present in the lipid nanoparticle), a non-cationic lipid in an amount from about 5 mol % to about 30 mol % of the total lipids, a conjugated lipid in an amount from about 0.5 mol % to about 20 mol % of the total lipids, and a sterol in an amount from about 20 mol % to about 50 mol % of the total lipids. The ratio of total lipid to nucleic acid (e.g., encoding the gene modifying polypeptide or template nucleic acid) can be varied as desired. For example, the total lipid to nucleic acid (mass or weight) ratio can be from about 10: 1 to about 30: 1.

In some embodiments, an ionizable lipid may be a cationic lipid, an ionizable cationic lipid, e.g., a cationic lipid that can exist in a positively charged or neutral form depending on pH, or an amine-containing lipid that can be readily protonated. In some embodiments, the cationic lipid is a lipid capable of being positively charged, e.g., under physiological conditions. Exemplary cationic lipids include one or more amine group(s) which bear the positive charge. In some embodiments, the lipid particle comprises a cationic lipid in formulation with one or more

of neutral lipids, ionizable amine-containing lipids, biodegradable alkyn lipids, steroids, phospholipids including polyunsaturated lipids, structural lipids (e.g., sterols), PEG, cholesterol and polymer conjugated lipids. In some embodiments, the cationic lipid may be an ionizable cationic lipid. An exemplary cationic lipid as disclosed herein may have an effective pKa over 6.0. In embodiments, a lipid nanoparticle may comprise a second cationic lipid having a different effective pKa (e.g., greater than the first effective pKa), than the first cationic lipid. A lipid nanoparticle may comprise between 40 and 60 mol percent of a cationic lipid, a neutral lipid, a steroid, a polymer conjugated lipid, and a therapeutic agent, e.g., a nucleic acid (e.g., RNA) described herein (e.g., a template nucleic acid or a nucleic acid encoding a gene modifying polypeptide), encapsulated within or associated with the lipid nanoparticle. In some embodiments, the nucleic acid is co-formulated with the cationic lipid. The nucleic acid may be adsorbed to the surface of an LNP, e.g., an LNP comprising a cationic lipid. In some embodiments, the nucleic acid may be encapsulated in an LNP, e.g., an LNP comprising a cationic lipid. In some embodiments, the lipid nanoparticle may comprise a targeting moiety, e.g., coated with a targeting agent. In embodiments, the LNP formulation is biodegradable. In some embodiments, a lipid nanoparticle comprising one or more lipid described herein, e.g., Formula (i), (ii), (ii), (vii) and/or (ix) encapsulates at least 1%, at least 5%, at least 10%, at least 20%, at least 30%, at least 40%, at least 50%, at least 60%, at least 70%, at least 80%, at least 90%, at least 92%, at least 95%, at least 97%, at least 98% or 100% of an RNA molecule, e.g., template RNA and/or a mRNA encoding the gene modifying polypeptide.

In some embodiments, the lipid to nucleic acid ratio (mass/mass ratio; w/w ratio) can be in the range of from about 1 : 1 to about 25: 1, from about 10: 1 to about 14: 1, from about 3 : 1 to about 15: 1, from about 4: 1 to about 10: 1, from about 5: 1 to about 9: 1, or about 6: 1 to about 9: 1. The amounts of lipids and nucleic acid can be adjusted to provide a desired N/P ratio, for example, N/P ratio of 3, 4, 5, 6, 7, 8, 9, 10 or higher. Generally, the lipid nanoparticle formulation’s overall lipid content can range from about 5 mg/ml to about 30 mg/mL.

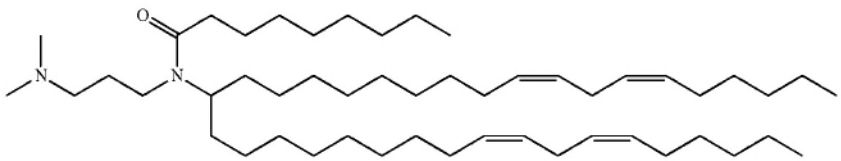
Exemplary ionizable lipids that can be used in lipid nanoparticle formulations include, without limitation, those listed in Table 1 of WO2019051289, incorporated herein by reference. Additional exemplary lipids include, without limitation, one or more of the following formulae: X of US2016/0311759; I of US20150376115 or in US2016/0376224; I, II or III of US20160151284; I, IA, II, or IIA of US20170210967; I-c of US20150140070; A of

US2013/0178541; I of US2013/0303587 or US2013/0123338; I of US2015/0141678; II, III, IV, or V of US2015/0239926; I of US2017/0119904; I or II of WO2017/117528; A of US2012/0149894; A of US2015/0057373; A of WO2013/116126; A of US2013/0090372; A of US2013/0274523; A of US2013/0274504; A of US2013/0053572; A of W02013/016058; A of W02012/162210; I of US2008/042973; I, II, III, or IV of US2012/01287670; I or II of US2014/0200257; I, II, or III of US2015/0203446; I or III of US2015/0005363; I, IA, IB, IC, ID, II, IIA, IIB, IIC, IID, or III-XXIV of US2014/0308304; of US2013/0338210; I, II, III, or IV of W02009/132131; A of US2012/01011478; I or XXXV of US2012/0027796; XIV or XVII of US2012/0058144; of US2013/0323269; I of US2011/0117125; I, II, or III of US2011/0256175; I, II, III, IV, V, VI, VII, VIII, IX, X, XI, XII of US2012/0202871; I, II, III, IV, V, VI, VII, VIII, X, XII, XIII, XIV, XV, or XVI of US2011/0076335; I or II of US2006/008378; I of US2013/0123338; I or X-A-Y-Z of US2015/0064242; XVI, XVII, or XVIII of US2013/0022649; I, II, or III of US2013/0116307; I, II, or III of US2013/0116307; I or II of US2010/0062967; I-X of US2013/0189351; I of US2014/0039032; V of US2018/0028664; I of US2016/0317458; I of US2013/0195920; 5, 6, or 10 of US10,221,127; III-3 of WO2018/081480; I-5 or I-8 of WO2020/081938; 18 or 25 of US9,867,888; A of US2019/0136231; II of WO2020/219876; 1 of US2012/0027803; OF-02 of US2019/0240349; 23 of US10,086,013; cKK-E12/A6 of Miao et al (2020); C12-200 of WO2010/053572; 7C1 of Dahlman et al (2017); 304-O13 or 503-O13 of Whitehead et al; TS-P4C2 of US9,708,628; I of WO2020/106946; I of WO2020/106946.

In some embodiments, the ionizable lipid is MC3 (6Z,9Z,28Z,3 lZ)-heptatriaconta-6,9,28,3 l-tetraen-l9-yl-4-(dimethylamino) butanoate (DLin-MC3-DMA or MC3), e.g., as described in Example 9 of WO2019051289A9 (incorporated by reference herein in its entirety). In some embodiments, the ionizable lipid is the lipid ATX-002, e.g., as described in Example 10 of WO2019051289A9 (incorporated by reference herein in its entirety). In some embodiments, the ionizable lipid is (l3Z,l6Z)-A,A-dimethyl-3- nonyldocosa-l3, l6-dien-l-amine (Compound 32), e.g., as described in Example 11 of WO2019051289A9 (incorporated by reference herein in its entirety). In some embodiments, the ionizable lipid is Compound 6 or Compound 22, e.g., as described in Example 12 of WO2019051289A9 (incorporated by reference herein in its entirety). In some embodiments, the ionizable lipid is heptadecan-9-yl 8-((2-hydroxyethyl)(6-oxo-6-(undecyloxy)hexyl)amino)octanoate (SM-102); e.g., as described in Example 1 of

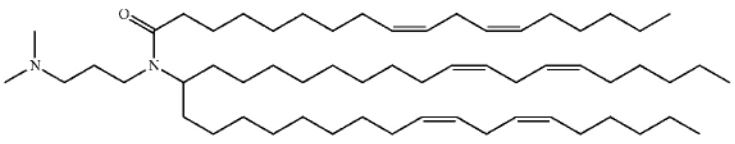
US9,867,888(incorporated by reference herein in its entirety). In some embodiments, the ionizable lipid is 9Z,12Z)-3-((4,4-bis(octyloxy)butanoyl)oxy)-2-((((3-(diethylamino)propoxy)carbonyl)oxy)methyl)propyl octadeca-9,12-dienoate (LP01) e.g., as synthesized in Example 13 of WO2015/095340(incorporated by reference herein in its entirety). In some embodiments, the ionizable lipid is Di((Z)-non-2-en-1-yl) 9-((4-dimethylamino)butanoyl)oxy)heptadecanedioate (L319), e.g. as synthesized in Example 7, 8, or 9 of US2012/0027803(incorporated by reference herein in its entirety). In some embodiments, the ionizable lipid is 1,1'-((2-(4-(2-((2-(Bis(2-hydroxydodecyl)amino)ethyl)(2-hydroxydodecyl) amino)ethyl)piperazin-1-yl)ethyl)azanediyl)bis(dodecan-2-ol) (C12-200), e.g., as synthesized in Examples 14 and 16 of WO2010/053572(incorporated by reference herein in its entirety). In some embodiments, the ionizable lipid is; Imidazole cholesterol ester (ICE) lipid (3S, 10R, 13R, 17R)-10, 13-dimethyl-17- ((R)-6-methylheptan-2-yl)-2, 3, 4, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17-tetradecahydro-lH- cyclopenta[a]phenanthren-3-yl 3-(1H-imidazol-4-yl)propanoate, e.g., Structure (I) from WO2020/106946 (incorporated by reference herein in its entirety).

Some non-limiting examples of lipid compounds that may be used (e.g., in combination with other lipid components) to form lipid nanoparticles for the delivery of compositions described herein, e.g., nucleic acid (e.g., RNA) described herein (e.g., a template nucleic acid or a nucleic acid encoding a gene modifying polypeptide) includes,



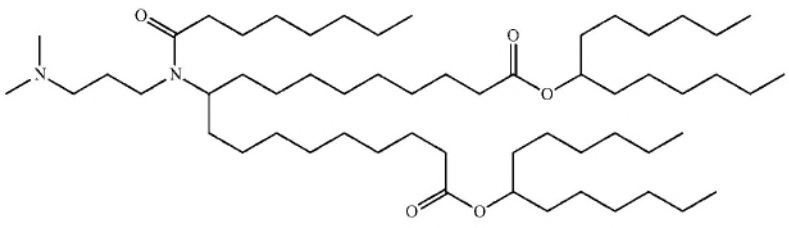
(i)

In some embodiments an LNP comprising Formula (i) is used to deliver a gene modifying composition described herein to the liver and/or hepatocyte cells.



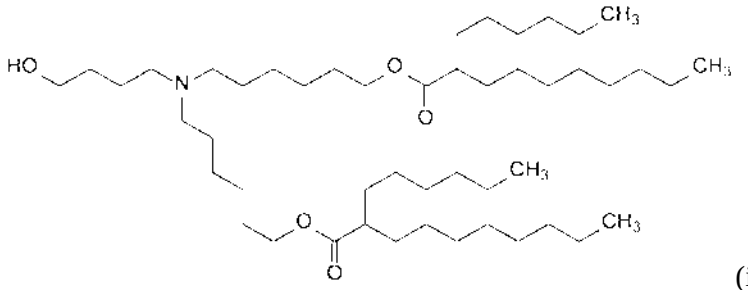
(ii)

In some embodiments an LNP comprising Formula (ii) is used to deliver a gene modifying composition described herein to the liver and/or hepatocyte cells.

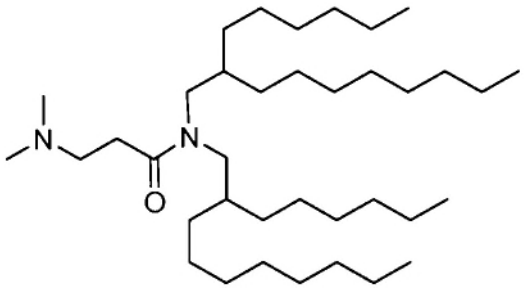


(iii)

In some embodiments an LNP comprising Formula (iii) is used to deliver a gene modifying composition described herein to the liver and/or hepatocyte cells.

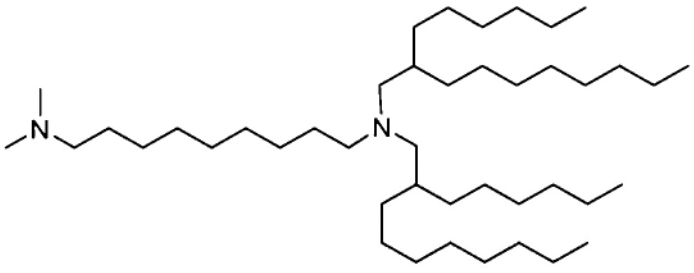


(iv)



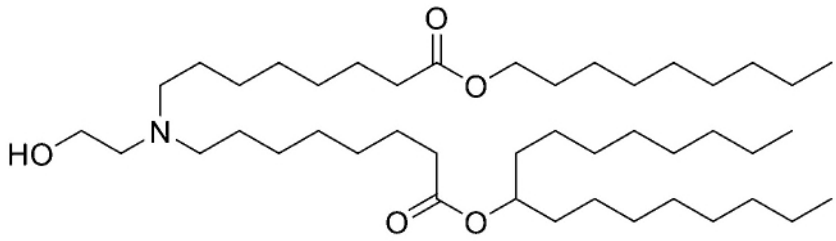
(v)

In some embodiments an LNP comprising Formula (v) is used to deliver a gene modifying composition described herein to the liver and/or hepatocyte cells.

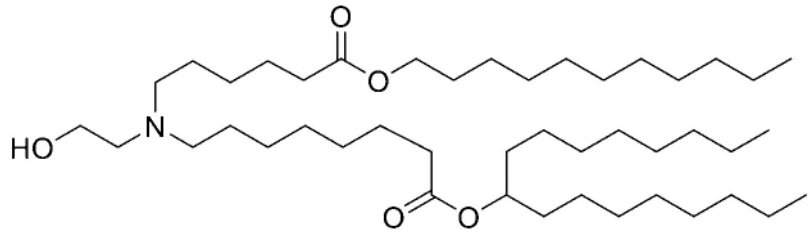


(vi)

In some embodiments an LNP comprising Formula (vi) is used to deliver a gene modifying composition described herein to the liver and/or hepatocyte cells.

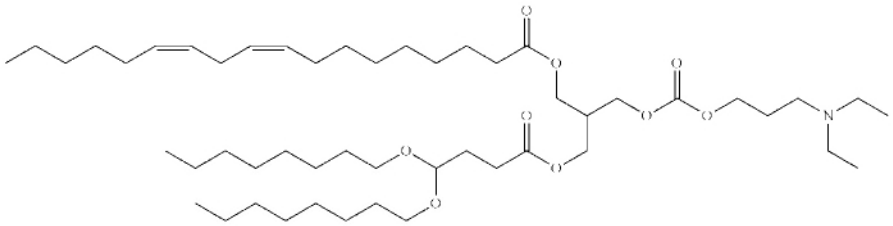


(vii)



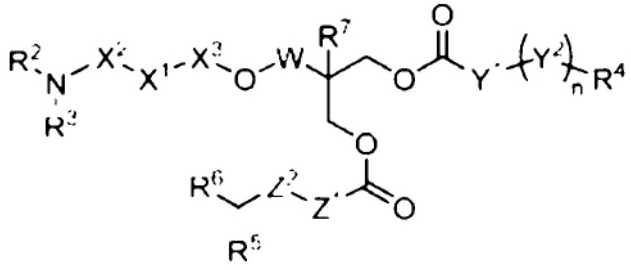
(viii)

In some embodiments an LNP comprising Formula (viii) is used to deliver a gene modifying composition described herein to the liver and/or hepatocyte cells.



(ix)

In some embodiments an LNP comprising Formula (ix) is used to deliver a gene modifying composition described herein to the liver and/or hepatocyte cells.

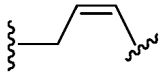
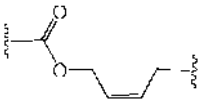
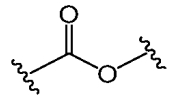


(x)

wherein

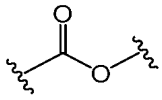
X^1 is O, NR^1, or a direct bond, X^2 is C2-5 alkylene, X^3 is C(=0) or a direct bond, R^1 is H or Me, R^3 is Ci-3 alkyl, R^2 is Ci-3 alkyl, or R^2 taken together with the nitrogen atom to which it is

attached and 1-3 carbon atoms of X^2 form a 4-, 5-, or 6-membered ring, or X^1 is NR^1, R^1 and R^2 taken together with the nitrogen atoms to which they are attached form a 5- or 6-membered ring, or R^2 taken together with R^3 and the nitrogen atom to which they are attached form a 5-, 6-, or 7-membered ring, Y^1 is C2-12 alkylene, Y^2 is selected from

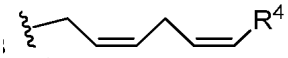
(in either orientation), (in either orientation), (in either orientation),

n is 0 to 3, R^4 is Ci-15 alkyl, Z^1 is Ci-6 alkylene or a direct bond,

Z^2 is 

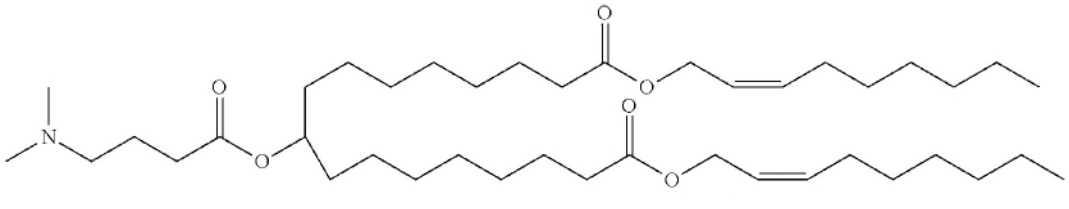
(in either orientation) or absent, provided that if Z^1 is a direct bond, Z^2 is absent;

R^5 is C5-9 alkyl or C6-10 alkoxy, R^6 is C5-9 alkyl or C6-10 alkoxy, W is methylene or a direct bond, and R^7 is H or Me, or a salt thereof, provided that if R^3 and R^2 are C2 alkyls, X^1 is O, X^2 is linear C3 alkylene, X^3 is C(=0), Y^1 is linear Ce alkylene, (Y^2)n-R^4 is



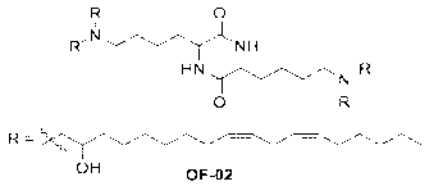
, R^4 is linear C5 alkyl, Z^1 is C2 alkylene, Z^2 is absent, W is methylene, and R^7 is H, then R^5 and R^6 are not Cx alkoxy.

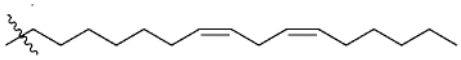
In some embodiments an LNP comprising Formula (xii) is used to deliver a gene modifying composition described herein to the liver and/or hepatocyte cells.

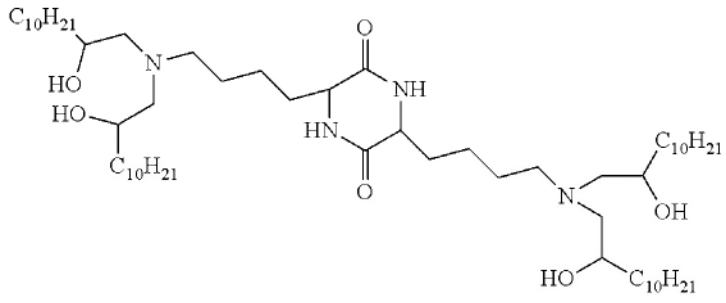


(xi)

In some embodiments an LNP comprising Formula (xi) is used to deliver a gene modifying composition described herein to the liver and/or hepatocyte cells.

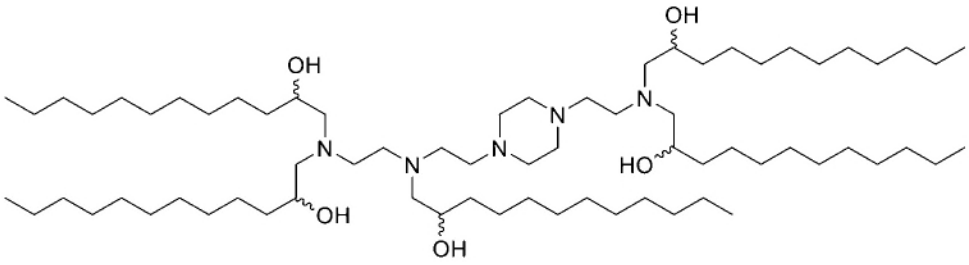


where R=  (xii)

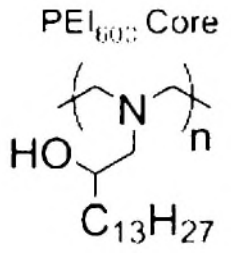
 (xiii)

 (xiv)

In some embodiments an LNP comprises a compound of Formula (xiii) and a compound of Formula (xiv).

 (xv)

In some embodiments an LNP comprising Formula (xv) is used to deliver a gene modifying composition described herein to the liver and/or hepatocyte cells.

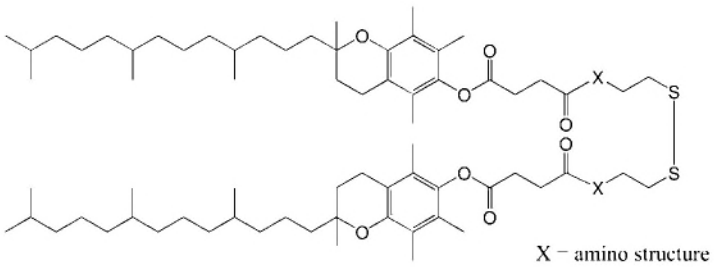


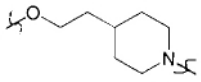
(xvi)

In some embodiments an LNP comprising a formulation of Formula (xvi) is used to deliver a gene modifying composition described herein to the lung endothelial cells.

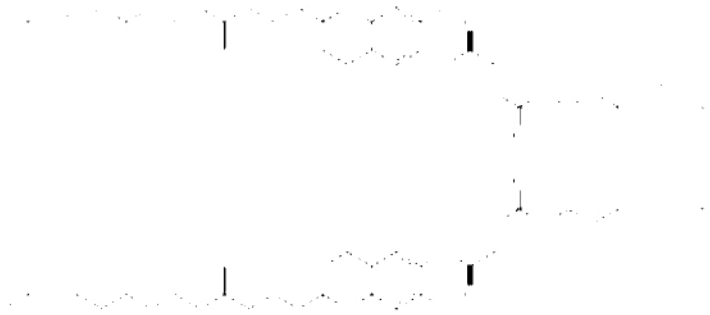


(xvii)

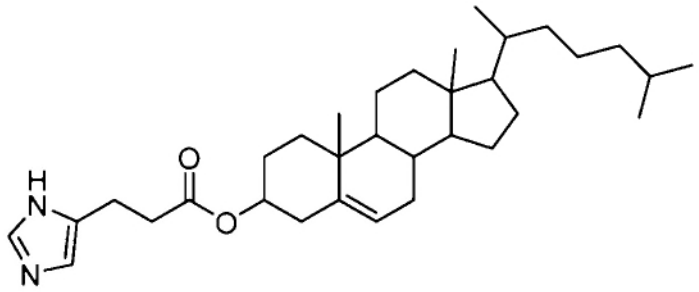


where X= 

(xviii) (a)

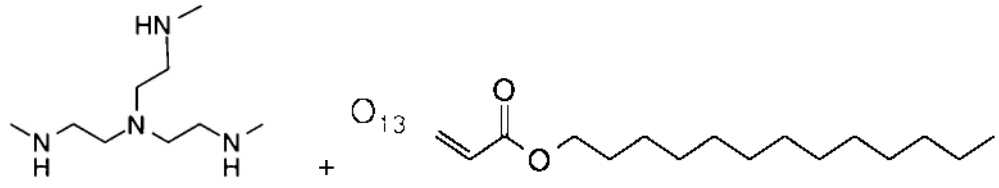


(xviii)(b)

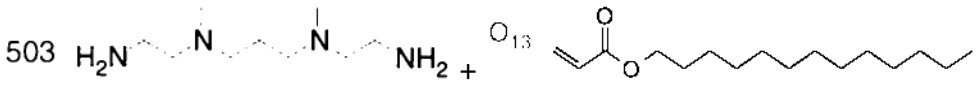


(xix)

In some embodiments, a lipid compound used to form lipid nanoparticles for the delivery of compositions described herein, e.g., nucleic acid (e.g., RNA) described herein (e.g., a template nucleic acid or a nucleic acid encoding a gene modifying polypeptide) is made by one of the following reactions:



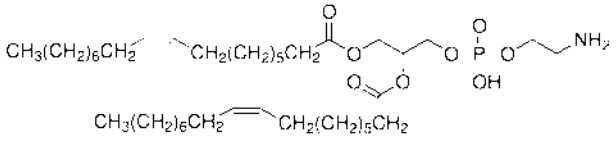
(xx) (a)



(xx)(b)

Exemplary non-cationic lipids include, but are not limited to, distearoyl-sn-glycero-phosphoethanolamine, distearoylphosphatidylcholine (DSPC), dioleoylphosphatidylcholine (DOPC), dipalmitoylphosphatidylcholine (DPPC), dioleoylphosphatidylglycerol (DOPG), dipalmitoylphosphatidylglycerol (DPPG), dioleoyl-phosphatidylethanolamine (DOPE), 1,2-dioleoyl-sn-glycero-3-phosphoethanolamine (DOPE), palmitoyloleoylphosphatidylcholine (POPC), palmitoyloleoylphosphatidylethanolamine (POPE), dioleoyl-phosphatidylethanolamine 4-(N-maleimidomethyl)-cyclohexane- 1 - carboxylate (DOPE-mal), dipalmitoyl phosphatidyl ethanolamine (DPPE), dimyristoylphosphoethanolamine (DMPE), distearoyl-phosphatidyl-ethanolamine (DSPE), monomethyl-phosphatidylethanolamine (such as 16-O-monomethyl PE), dimethyl- phosphatidylethanolamine (such as 16-O-dimethyl PE), l8-l-trans PE, l-stearoyl-2-oleoyl- phosphatidyethanolamine (SOPE), hydrogenated soy phosphatidylcholine (HSPC), egg

phosphatidylcholine (EPC), dioleoylphosphatidylserine (DOPS), sphingomyelin (SM), dimyristoyl phosphatidylcholine (DMPC), dimyristoyl phosphatidylglycerol (DMPG), distearoylphosphatidylglycerol (DSPG), dierucoylphosphatidylcholine (DEPC), palmitoyloleyolphosphatidylglycerol (POPG), dielaidoyl-phosphatidylethanolamine (DEPE), lecithin, phosphatidylethanolamine, lysolecithin, lysophosphatidylethanolamine, phosphatidylserine, phosphatidylinositol, sphingomyelin, egg sphingomyelin (ESM), cephalin, cardiolipin, phosphatidicacid,cerebrosides, dicetylphosphate, lysophosphatidylcholine, dilinoleoylphosphatidylcholine, or mixtures thereof. It is understood that other diacylphosphatidylcholine and diacylphosphatidylethanolamine phospholipids can also be used. The acyl groups in these lipids are preferably acyl groups derived from fatty acids having C10-C24 carbon chains, e.g., lauroyl, myristoyl, paimitoyl, stearoyl, or oleoyl. Additional exemplary lipids, in certain embodiments, include, without limitation, those described in Kim et al. (2020) dx.doi.org/10.1021/acs.nanolett.0c01386, incorporated herein by reference. Such lipids include, in some embodiments, plant lipids found to improve liver transfection with mRNA (e.g., DGTS). In some embodiments, the non-cationic lipid may have the following structure,



(xxi)

Other examples of non-cationic lipids suitable for use in the lipid nanopartieles include, without limitation, nonphosphorous lipids such as, e.g., stearylamine, dodeeylamine, hexadecylamine, acetyl palmitate, glycerol ricinoleate, hexadecyl stereate, isopropyl myristate, amphoteric acrylic polymers, triethanolamine-lauryl sulfate, alkyl-aryl sulfate polyethyloxylated fatty acid amides, dioctadecyl dimethyl ammonium bromide, ceramide, sphingomyelin, and the like. Other non-cationic lipids are described in WO2017/099823 or US patent publication US2018/0028664, the contents of which is incorporated herein by reference in their entirety.

In some embodiments, the non-cationic lipid is oleic acid or a compound of Formula I, II, or IV of US2018/0028664, incorporated herein by reference in its entirety. The non-cationic lipid can comprise, for example, 0-30% (mol) of the total lipid present in the lipid nanoparticle. In some embodiments, the non-cationic lipid content is 5-20% (mol) or 10-15% (mol) of the total

lipid present in the lipid nanoparticle. In embodiments, the molar ratio of ionizable lipid to the neutral lipid ranges from about 2:1 to about 8:1 (e.g., about 2:1, 3:1, 4:1, 5:1, 6:1, 7:1, or 8:1).

In some embodiments, the lipid nanoparticles do not comprise any phospholipids.

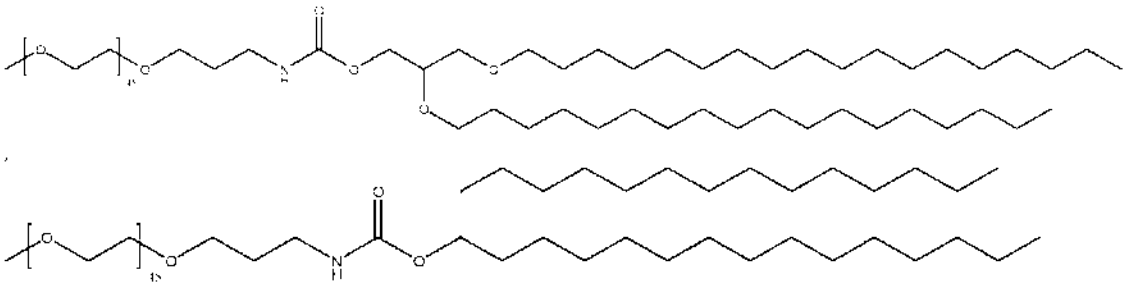
In some aspects, the lipid nanoparticle can further comprise a component, such as a sterol, to provide membrane integrity. One exemplary sterol that can be used in the lipid nanoparticle is cholesterol and derivatives thereof. Non-limiting examples of cholesterol derivatives include polar analogues such as 5a-choiestanol, 53-coprostanol, choiesteryl-(2'-hydroxy)-ethyl ether, choiesteryl-(4'- hydroxy)-butyl ether, and 6-ketocholestanol; non-polar analogues such as 5a-cholestane, cholestenone, 5a-cholestanone, 5p-cholestanone, and cholesteryl decanoate; and mixtures thereof. In some embodiments, the cholesterol derivative is a polar analogue, e.g., choiesteryl-(4'-hydroxy)-buty1 ether. Exemplary cholesterol derivatives are described in PCT publication W02009/127060 and US patent publication US2010/0130588, each of which is incorporated herein by reference in its entirety.

In some embodiments, the component providing membrane integrity, such as a sterol, can comprise 0-50% (mol) (e.g., 0-10%, 10-20%, 20-30%, 30-40%, or 40-50%) of the total lipid present in the lipid nanoparticle. In some embodiments, such a component is 20-50% (mol) 30-40% (mol) of the total lipid content of the lipid nanoparticle.

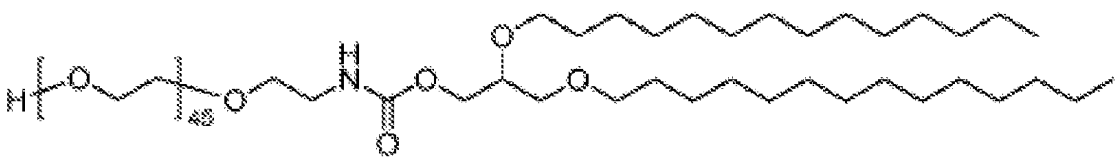
In some embodiments, the lipid nanoparticle can comprise a polyethylene glycol (PEG) or a conjugated lipid molecule. Generally, these are used to inhibit aggregation of lipid nanoparticles and/or provide steric stabilization. Exemplary conjugated lipids include, but are not limited to, PEG-lipid conjugates, polyoxazoline (POZ)-lipid conjugates, polyamide-lipid conjugates (such as ATTA-lipid conjugates), cationic-polymer lipid (CPL) conjugates, and mixtures thereof. In some embodiments, the conjugated lipid molecule is a PEG-lipid conjugate, for example, a (methoxy polyethylene glycol)-conjugated lipid.

Exemplary PEG-lipid conjugates include, but are not limited to, PEG-diacylglycerol (DAG) (such as l-(monomethoxy-polyethyleneglycol)-2,3-dimyristoylglycerol (PEG-DMG)), PEG-dialkyloxypropyl (DAA), PEG-phospholipid, PEG-ceramide (Cer), a pegylated phosphatidylethanoloamine (PEG-PE), 1,2-dimyristoyl-sn-glycerol, methoxypoly ethylene glycol (DMG-PEG-2K), PEG succinate diacylglycerol (PEGS-DAG) (such as 4-0-(2',3'-di(tetradecanoyloxy)propyl-l-0-(w-methoxy(polyethoxy)ethyl) butanedioate (PEG-S-DMG)), PEG dialkoxypropylcarbam, N-(carbonyl-methoxypolyethylene glycol 2000)-l,2-distearoyl-sn-

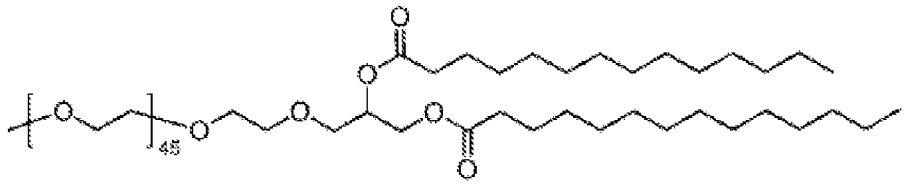
glycero-3-phosphoethanolamine sodium salt, or a mixture thereof. Additional exemplary PEG-lipid conjugates are described, for example, in US5,885,6l3, US6,287,59l, US2003/0077829, US2003/0077829, US2005/0175682, US2008/0020058, US2011/0117125, US2010/0130588, US2016/0376224, US2017/0119904, and US/099823, the contents of all of which are incorporated herein by reference in their entirety. In some embodiments, a PEG-lipid is a compound of Formula III, III-a-I, III-a-2, III-b-1, III-b-2, or V of US2018/0028664, the content of which is incorporated herein by reference in its entirety. In some embodiments, a PEG-lipid is of Formula II of US20150376115 or US2016/0376224, the content of both of which is incorporated herein by reference in its entirety. In some embodiments, the PEG-DAA conjugate can be, for example, PEG-dilauryloxypropyl, PEG- dimyristyloxypropyl, PEG-dipalmityloxypropyl, or PEG-distearyloxypropyl. The PEG-lipid can be one or more of PEG-DMG, PEG-dilaurylglycerol, PEG-dipalmitoylglycerol, PEG- disterylglycerol, PEG-dilaurylglycamide, PEG-dimyristylglycamide, PEG- dipalmitoylglycamide, PEG-disterylglycamide, PEG-cholesterol (l-[8'-(Cholest-5-en-3[beta]- oxy)carboxamido-3',6'-dioxaoctanyl] carbamoyl-[omega]-methyl-poly(ethylene glycol), PEG- DMB (3,4-Ditetradecoxylbenzyl- [omega]-methyl-poly(ethylene glycol) ether), and 1,2- dimyristoyl-sn-glycero-3-phosphoethanolamine-N-[methoxy(polyethylene glycol)-2000]. In some embodiments, the PEG-lipid comprises PEG-DMG, 1,2- dimyristoyl-sn-glycero-3-phosphoethanolamine-N-[methoxy(polyethylene glycol)-2000]. In some embodiments, the PEG-lipid comprises a structure selected from:



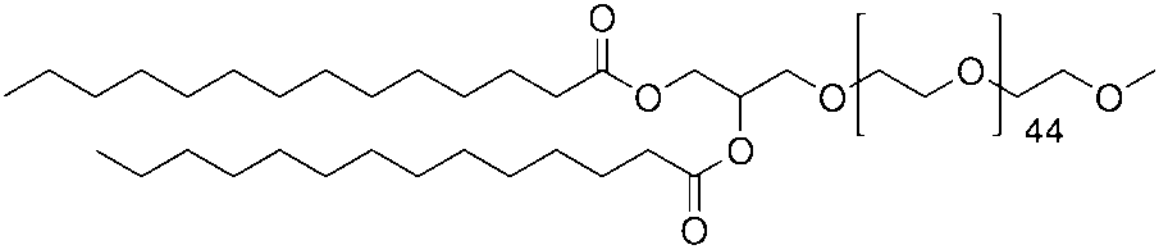
(xxii),



(xxiii),



(xxiv), and



(xxv).

In some embodiments, lipids conjugated with a molecule other than a PEG can also be used in place of PEG-lipid. For example, polyoxazoline (POZ)-lipid conjugates, polyamide-lipid conjugates (such as ATTA-lipid conjugates), and cationic-polymer lipid (GPL) conjugates can be used in place of or in addition to the PEG-lipid.

Exemplary conjugated lipids, i.e., PEG-lipids, (POZ)-lipid conjugates, ATTA-lipid conjugates and cationic polymer-lipids are described in the PCT and LIS patent applications listed in Table 2 of WO2019051289A9 and in WO2020106946A1, the contents of all of which are incorporated herein by reference in their entirety.

In some embodiments an LNP comprises a compound of Formula (xix), a compound of Formula (xxi) and a compound of Formula (xxv). In some embodiments an LNP comprising a formulation of Formula (xix), Formula (xxi) and Formula (xxv)is used to deliver a gene modifying composition described herein to the lung or pulmonary cells.

In some embodiments, a lipid nanoparticle may comprise one or more cationic lipids selected from Formula (i), Formula (ii), Formula (iii), Formula (vii), and Formula (ix). In some embodiments, the LNP may further comprise one or more neutral lipid, e.g., DSPC, DPPC, DMPC, DOPC, POPC, DOPE, SM, a steroid, e.g., cholesterol, and/or one or more polymer conjugated lipid, e.g., a pegylated lipid, e.g., PEG-DAG, PEG-PE, PEG-S-DAG, PEG-cer or a PEG dialkyoxypropylcarbamate.

In some embodiments, the PEG or the conjugated lipid can comprise 0-20% (mol) of the total lipid present in the lipid nanoparticle. In some embodiments, PEG or the conjugated lipid content is 0.5- 10% or 2-5% (mol) of the total lipid present in the lipid nanoparticle. Molar ratios of the ionizable lipid, non-cationic-lipid, sterol, and PEG/conjugated lipid can be varied as needed. For example, the lipid particle can comprise 30-70% ionizable lipid by mole or by total weight of the composition, 0-60% cholesterol by mole or by total weight of the composition, 0-30% non-cationic-lipid by mole or by total weight of the composition and 1-10% conjugated lipid by mole or by total weight of the composition. Preferably, the composition comprises 30-40% ionizable lipid by mole or by total weight of the composition, 40-50% cholesterol by mole or by total weight of the composition, and 10- 20% non-cationic-lipid by mole or by total weight of the composition. In some other embodiments, the composition is 50-75% ionizable lipid by mole or by total weight of the composition, 20-40% cholesterol by mole or by total weight of the composition, and 5 to 10% non-cationic-lipid, by mole or by total weight of the composition and 1-10% conjugated lipid by mole or by total weight of the composition. The composition may contain 60-70% ionizable lipid by mole or by total weight of the composition, 25-35% cholesterol by mole or by total weight of the composition, and 5-10% non-cationic-lipid by mole or by total weight of the composition. The composition may also contain up to 90% ionizable lipid by mole or by total weight of the composition and 2 to 15% non-cationic lipid by mole or by total weight of the composition. The formulation may also be a lipid nanoparticle formulation, for example comprising 8-30% ionizable lipid by mole or by total weight of the composition, 5-30% non- cationic lipid by mole or by total weight of the composition, and 0-20% cholesterol by mole or by total weight of the composition; 4-25% ionizable lipid by mole or by total weight of the composition, 4-25% non-cationic lipid by mole or by total weight of the composition, 2 to 25% cholesterol by mole or by total weight of the composition, 10 to 35% conjugate lipid by mole or by total weight of the composition, and 5% cholesterol by mole or by total weight of the composition; or 2-30% ionizable lipid by mole or by total weight of the composition, 2-30% non-cationic lipid by mole or by total weight of the composition, 1 to 15% cholesterol by mole or by total weight of the composition, 2 to 35% conjugate lipid by mole or by total weight of the composition, and 1-20% cholesterol by mole or by total weight of the composition; or even up to 90% ionizable lipid by mole or by total weight of the composition and 2-10% non-cationic lipids by mole or by total weight of the composition, or even 100% cationic lipid by mole or by total

weight of the composition. In some embodiments, the lipid particle formulation comprises ionizable lipid, phospholipid, cholesterol and a PEG-ylated lipid in a molar ratio of 50: 10:38.5: 1.5. In some other embodiments, the lipid particle formulation comprises ionizable lipid, cholesterol and a PEG-ylated lipid in a molar ratio of 60:38.5: 1.5.

In some embodiments, the lipid particle comprises ionizable lipid, non-cationic lipid (e.g. phospholipid), a sterol (e.g., cholesterol) and a PEG-ylated lipid, where the molar ratio of lipids ranges from 20 to 70 mole percent for the ionizable lipid, with a target of 40-60, the mole percent of non-cationic lipid ranges from 0 to 30, with a target of 0 to 15, the mole percent of sterol ranges from 20 to 70, with a target of 30 to 50, and the mole percent of PEG-ylated lipid ranges from 1 to 6, with a target of 2 to 5.

In some embodiments, the lipid particle comprises ionizable lipid / non-cationic- lipid / sterol / conjugated lipid at a molar ratio of 50: 10:38.5: 1.5.

In an aspect, the disclosure provides a lipid nanoparticle formulation comprising phospholipids, lecithin, phosphatidylcholine and phosphatidylethanolamine.

In some embodiments, one or more additional compounds can also be included. Those compounds can be administered separately or the additional compounds can be included in the lipid nanoparticles of the invention. In other words, the lipid nanoparticles can contain other compounds in addition to the nucleic acid or at least a second nucleic acid, different than the first. Without limitations, other additional compounds can be selected from the group consisting of small or large organic or inorganic molecules, monosaccharides, disaccharides, trisaccharides, oligosaccharides, polysaccharides, peptides, proteins, peptide analogs and derivatives thereof, peptidomimetics, nucleic acids, nucleic acid analogs and derivatives, an extract made from biological materials, or any combinations thereof.

In some embodiments, a lipid nanoparticle (or a formulation comprising lipid nanoparticles) lacks reactive impurities (e.g., aldehydes or ketones), or comprises less than a preselected level of reactive impurities (e.g., aldehydes or ketones). While not wishing to be bound by theory, in some embodiments, a lipid reagent is used to make a lipid nanoparticle formulation, and the lipid reagent may comprise a contaminating reactive impurity (e.g., an aldehyde or ketone). A lipid regent may be selected for manufacturing based on having less than a preselected level of reactive impurities (e.g., aldehydes or ketones). Without wishing to be bound by theory, in some embodiments, aldehydes can cause modification and damage of RNA,

e.g., cross-linking between bases and/or covalently conjugating lipid to RNA (e.g., forming lipid-RNA adducts). This may, in some instances, lead to failure of a reverse transcriptase reaction and/or incorporation of inappropriate bases, e.g., at the site(s) of lesion(s), e.g., a mutation in a newly synthesized target DNA.

In some embodiments, a lipid nanoparticle formulation is produced using a lipid reagent comprising less than 5%, 4%, 3%, 2%, 1%, 0.9%, 0.8%, 0.7%, 0.6%, 0.5%, 0.4%, 0.3%, 0.2%, or 0.1% total reactive impurity (e.g., aldehyde) content. In some embodiments, a lipid nanoparticle formulation is produced using a lipid reagent comprising less than 5%, 4%, 3%, 2%, 1%, 0.9%, 0.8%, 0.7%, 0.6%, 0.5%, 0.4%, 0.3%, 0.2%, or 0.1% of any single reactive impurity (e.g., aldehyde) species. In some embodiments, a lipid nanoparticle formulation is produced using a lipid reagent comprising: (i) less than 5%, 4%, 3%, 2%, 1%, 0.9%, 0.8%, 0.7%, 0.6%, 0.5%, 0.4%, 0.3%, 0.2%, or 0.1% total reactive impurity (e.g., aldehyde) content; and (ii) less than 5%, 4%, 3%, 2%, 1%, 0.9%, 0.8%, 0.7%, 0.6%, 0.5%, 0.4%, 0.3%, 0.2%, or 0.1% of any single reactive impurity (e.g., aldehyde) species. In some embodiments, the lipid nanoparticle formulation is produced using a plurality of lipid reagents, and each lipid reagent of the plurality independently meets one or more criterion described in this paragraph. In some embodiments, each lipid reagent of the plurality meets the same criterion, e.g., a criterion of this paragraph.

In some embodiments, the lipid nanoparticle formulation comprises less than 5%, 4%, 3%, 2%, 1%, 0.9%, 0.8%, 0.7%, 0.6%, 0.5%, 0.4%, 0.3%, 0.2%, or 0.1% total reactive impurity (e.g., aldehyde) content. In some embodiments, the lipid nanoparticle formulation comprises less than 5%, 4%, 3%, 2%, 1%, 0.9%, 0.8%, 0.7%, 0.6%, 0.5%, 0.4%, 0.3%, 0.2%, or 0.1% of any single reactive impurity (e.g., aldehyde) species. In some embodiments, the lipid nanoparticle formulation comprises: (i) less than 5%, 4%, 3%, 2%, 1%, 0.9%, 0.8%, 0.7%, 0.6%, 0.5%, 0.4%, 0.3%, 0.2%, or 0.1% total reactive impurity (e.g., aldehyde) content; and (ii) less than 5%, 4%, 3%, 2%, 1%, 0.9%, 0.8%, 0.7%, 0.6%, 0.5%, 0.4%, 0.3%, 0.2%, or 0.1% of any single reactive impurity (e.g., aldehyde) species.

In some embodiments, one or more, or optionally all, of the lipid reagents used for a lipid nanoparticle as described herein or a formulation thereof comprise less than 5%, 4%, 3%, 2%, 1%, 0.9%, 0.8%, 0.7%, 0.6%, 0.5%, 0.4%, 0.3%, 0.2%, or 0.1% total reactive impurity (e.g., aldehyde) content. In some embodiments, one or more, or optionally all, of the lipid reagents used for a lipid nanoparticle as described herein or a formulation thereof comprise less than 5%,

4%, 3%, 2%, 1%, 0.9%, 0.8%, 0.7%, 0.6%, 0.5%, 0.4%, 0.3%, 0.2%, or 0.1% of any single reactive impurity (e.g., aldehyde) species. In some embodiments, one or more, or optionally all, of the lipid reagents used for a lipid nanoparticle as described herein or a formulation thereof comprise: (i) less than 5%, 4%, 3%, 2%, 1%, 0.9%, 0.8%, 0.7%, 0.6%, 0.5%, 0.4%, 0.3%, 0.2%, or 0.1% total reactive impurity (e.g., aldehyde) content; and (ii) less than 5%, 4%, 3%, 2%, 1%, 0.9%, 0.8%, 0.7%, 0.6%, 0.5%, 0.4%, 0.3%, 0.2%, or 0.1% of any single reactive impurity (e.g., aldehyde) species.

In some embodiments, total aldehyde content and/or quantity of any single reactive impurity (e.g., aldehyde) species is determined by liquid chromatography (LC), e.g., coupled with tandem mass spectrometry (MS/MS), e.g., according to the method described in Example 40 of PCT/US21/20948. In some embodiments, reactive impurity (e.g., aldehyde) content and/or quantity of reactive impurity (e.g., aldehyde) species is determined by detecting one or more chemical modifications of a nucleic acid molecule (e.g., an RNA molecule, e.g., as described herein) associated with the presence of reactive impurities (e.g., aldehydes), e.g., in the lipid reagents. In some embodiments, reactive impurity (e.g., aldehyde) content and/or quantity of reactive impurity (e.g., aldehyde) species is determined by detecting one or more chemical modifications of a nucleotide or nucleoside (e.g., a ribonucleotide or ribonucleoside, e.g., comprised in or isolated from a template nucleic acid, e.g., as described herein) associated with the presence of reactive impurities (e.g., aldehydes), e.g., in the lipid reagents, e.g., according to the method described in Example 41 of PCT/US21/20948. In embodiments, chemical modifications of a nucleic acid molecule, nucleotide, or nucleoside are detected by determining the presence of one or more modified nucleotides or nucleosides, e.g., using LC-MS/MS analysis, e.g., according to the method described in Example 41 of PCT/US21/20948.

In some embodiments, a nucleic acid (e.g., RNA) described herein (e.g., a template nucleic acid or a nucleic acid encoding a gene modifying polypeptide) does not comprise an aldehyde modification, or comprises less than a preselected amount of aldehyde modifications. In some embodiments, on average, a nucleic acid has less than 50, 20, 10, 5, 2, or 1 aldehyde modifications per 1000 nucleotides, e.g., wherein a single cross-linking of two nucleotides is a single aldehyde modification. In some embodiments, the aldehyde modification is an RNA adduct (e.g., a lipid-RNA adduct). In some embodiments, the aldehyde-modified nucleotide is

cross-linking between bases . In some embodiments, a nucleic acid (e.g., RNA) described herein comprises less than 50, 20, 10, 5, 2, or 1 cross-links between nucleotide.

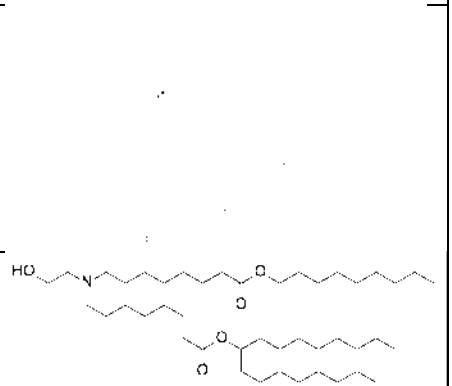
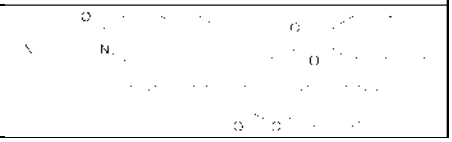
In some embodiments, LNPs are directed to specific tissues by the addition of targeting domains. For example, biological ligands may be displayed on the surface of LNPs to enhance interaction with cells displaying cognate receptors, thus driving association with and cargo delivery to tissues wherein cells express the receptor. In some embodiments, the biological ligand may be a ligand that drives delivery to the liver, e.g., LNPs that display GalNAc result in delivery of nucleic acid cargo to hepatocytes that display asialoglycoprotein receptor (ASGPR). The work of Akinc et al. *Mol Ther* 18(7):1357-1364 (2010) teaches the conjugation of a trivalent GalNAc ligand to a PEG-lipid (GalNAc-PEG-DSG) to yield LNPs dependent on ASGPR for observable LNP cargo effect (see, e.g., Figure 6 therein). Other ligand-displaying LNP formulations, e.g., incorporating folate, transferrin, or antibodies, are discussed in WO2017223135, which is incorporated herein by reference in its entirety, in addition to the references used therein, namely Kolhatkar et al., Curr Drug Discov Technol. 2011 8:197-206; Musacchio and Torchilin, Front Biosci. 2011 16:1388-1412; Yu et al., Mol Membr Biol. 2010 27:286-298; Patil et al., Crit Rev Ther Drug Carrier Syst. 2008 25:1-61 ; Benoit et al., Biomacromolecules. 2011 12:2708-2714; Zhao et al., Expert Opin Drug Deliv. 2008 5:309-319; Akinc et al., Mol Ther. 2010 18:1357-1364; Srinivasan et al., Methods Mol Biol. 2012 820:105-116; Ben-Arie et al., Methods Mol Biol. 2012 757:497-507; Peer 2010 J Control Release. 20:63-68; Peer et al., Proc Natl Acad Sci U S A. 2007 104:4095-4100; Kim et al., Methods Mol Biol. 2011 721:339-353; Subramanya et al., Mol Ther. 2010 18:2028-2037; Song et al., Nat Biotechnol. 2005 23:709-717; Peer et al., Science. 2008 319:627-630; and Peer and Lieberman, Gene Ther. 2011 18:1127-1133.

In some embodiments, LNPs are selected for tissue-specific activity by the addition of a Selective ORgan Targeting (SORT) molecule to a formulation comprising traditional components, such as ionizable cationic lipids, amphipathic phospholipids, cholesterol and poly(ethylene glycol) (PEG) lipids. The teachings of Cheng et al. Nat Nanotechnol 15(4):313-320 (2020) demonstrate that the addition of a supplemental “SORT” component precisely alters the *in vivo* RNA delivery profile and mediates tissue-specific (e.g., lungs, liver, spleen) gene delivery and editing as a function of the percentage and biophysical property of the SORT molecule.

In some embodiments, the LNPs comprise biodegradable, ionizable lipids. In some embodiments, the LNPs comprise (9Z,l2Z)-3-((4,4-bis(octyloxy)butanoyl)oxy)-2-((((3-(diethylamino)propoxy)carbonyl)oxy)methyl)propyl octadeca-9,l2-dienoate, also called 3- ((4,4-bis(octyloxy)butanoyl)oxy)-2-((((3-(diethylamino)propoxy)carbonyl)oxy)methyl)propyl (9Z,l2Z)-octadeca-9,l2-dienoate) or another ionizable lipid. See, e.g, lipids of WO2019/067992, WO/2017/173054, WO2015/095340, and WO2014/136086, as well as references provided therein. In some embodiments, the term cationic and ionizable in the context of LNP lipids is interchangeable, e.g., wherein ionizable lipids are cationic depending on the pH.

In some embodiments, an LNP described herein comprises a lipid described in Table 19.

Table 19: Exemplary Lipids

LIPID ID	Chemical Name	Molecular Weight	Structure
LIPIDV003	(9Z,12Z)-3-((4,4-bis(octyloxy)butanoyl)oxy)-2-((((3-(diethylamino)propoxy)carbonyl)oxy)methyl)propyl octadeca-9,12-dienoate	852.29	
LIPIDV004	Heptadecan-9-yl 8-((2-hydroxyethyl)(8-(nonyloxy)-8-oxooctyl)amino)octanoate	710.18	
LIPIDV005		919.56	

In some embodiments, multiple components of a gene modifying system may be prepared as a single LNP formulation, e.g., an LNP formulation comprises mRNA encoding for the gene modifying polypeptide and an RNA template. Ratios of nucleic acid components may be varied in order to maximize the properties of a therapeutic. In some embodiments, the ratio of RNA template to mRNA encoding a gene modifying polypeptide is about 1:1 to 100:1, e.g., about 1:1 to 20:1, about 20:1 to 40:1, about 40:1 to 60:1, about 60:1 to 80:1, or about 80:1 to 100:1, by molar ratio. In other embodiments, a system of multiple nucleic acids may be prepared by separate formulations, e.g., one LNP formulation comprising a template RNA and a second

LNP formulation comprising an mRNA encoding a gene modifying polypeptide. In some embodiments, the system may comprise more than two nucleic acid components formulated into LNPs. In some embodiments, the system may comprise a protein, e.g., a gene modifying polypeptide, and a template RNA formulated into at least one LNP formulation.

In some embodiments, the average LNP diameter of the LNP formulation may be between 10s of nm and 100s of nm, e.g., measured by dynamic light scattering (DLS). In some embodiments, the average LNP diameter of the LNP formulation may be from about 40 nm to about 150 nm, such as about 40 nm, 45 nm, 50 nm, 55 nm, 60 nm, 65 nm, 70 nm, 75 nm, 80 nm, 85 nm, 90 nm, 95 nm, 100 nm, 105 nm, 110 nm, 115 nm, 120 nm, 125 nm, 130 nm, 135 nm, 140 nm, 145 nm, or 150 nm. In some embodiments, the average LNP diameter of the LNP formulation may be from about 50 nm to about 100 nm, from about 50 nm to about 90 nm, from about 50 nm to about 80 nm, from about 50 nm to about 70 nm, from about 50 nm to about 60 nm, from about 60 nm to about 100 nm, from about 60 nm to about 90 nm, from about 60 nm to about 80 nm, from about 60 nm to about 70 nm, from about 70 nm to about 100 nm, from about 70 nm to about 90 nm, from about 70 nm to about 80 nm, from about 80 nm to about 100 nm, from about 80 nm to about 90 nm, or from about 90 nm to about 100 nm. In some embodiments, the average LNP diameter of the LNP formulation may be from about 70 nm to about 100 nm. In a particular embodiment, the average LNP diameter of the LNP formulation may be about 80 nm. In some embodiments, the average LNP diameter of the LNP formulation may be about 100 nm. In some embodiments, the average LNP diameter of the LNP formulation ranges from about l mm to about 500 mm, from about 5 mm to about 200 mm, from about 10 mm to about 100 mm, from about 20 mm to about 80 mm, from about 25 mm to about 60 mm, from about 30 mm to about 55 mm, from about 35 mm to about 50 mm, or from about 38 mm to about 42 mm.

An LNP may, in some instances, be relatively homogenous. A polydispersity index may be used to indicate the homogeneity of an LNP, e.g., the particle size distribution of the lipid nanoparticles. A small (e.g., less than 0.3) polydispersity index generally indicates a narrow particle size distribution. An LNP may have a polydispersity index from about 0 to about 0.25, such as 0.01, 0.02, 0.03, 0.04, 0.05, 0.06, 0.07, 0.08, 0.09, 0.10, 0.11, 0.12, 0.13, 0.14, 0.15, 0.16, 0.17, 0.18, 0.19, 0.20, 0.21, 0.22, 0.23, 0.24, or 0.25. In some embodiments, the polydispersity index of an LNP may be from about 0.10 to about 0.20.

The zeta potential of an LNP may be used to indicate the electrokinetic potential of the composition. In some embodiments, the zeta potential may describe the surface charge of an LNP. Lipid nanoparticles with relatively low charges, positive or negative, are generally desirable, as more highly charged species may interact undesirably with cells, tissues, and other elements in the body. In some embodiments, the zeta potential of an LNP may be from about -10 mV to about +20 mV, from about -10 mV to about +15 mV, from about -10 mV to about +10 mV, from about -10 mV to about +5 mV, from about -10 mV to about 0 mV, from about -10 mV to about -5 mV, from about -5 mV to about +20 mV, from about -5 mV to about +15 mV, from about -5 mV to about +10 mV, from about -5 mV to about +5 mV, from about -5 mV to about 0 mV, from about 0 mV to about +20 mV, from about 0 mV to about +15 mV, from about 0 mV to about +10 mV, from about 0 mV to about +5 mV, from about +5 mV to about +20 mV, from about +5 mV to about +15 mV, or from about +5 mV to about +10 mV.

The efficiency of encapsulation of a protein and/or nucleic acid, e.g., gene modifying polypeptide or mRNA encoding the polypeptide, describes the amount of protein and/or nucleic acid that is encapsulated or otherwise associated with an LNP after preparation, relative to the initial amount provided. The encapsulation efficiency is desirably high (e.g., close to 100%). The encapsulation efficiency may be measured, for example, by comparing the amount of protein or nucleic acid in a solution containing the lipid nanoparticle before and after breaking up the lipid nanoparticle with one or more organic solvents or detergents. An anion exchange resin may be used to measure the amount of free protein or nucleic acid (e.g., RNA) in a solution. Fluorescence may be used to measure the amount of free protein and/or nucleic acid (e.g., RNA) in a solution. For the lipid nanoparticles described herein, the encapsulation efficiency of a protein and/or nucleic acid may be at least 50%, for example 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100%. In some embodiments, the encapsulation efficiency may be at least 80%. In some embodiments, the encapsulation efficiency may be at least 90%. In some embodiments, the encapsulation efficiency may be at least 95%.

An LNP may optionally comprise one or more coatings. In some embodiments, an LNP may be formulated in a capsule, film, or table having a coating. A capsule, film, or tablet including a composition described herein may have any useful size, tensile strength, hardness or density.

Additional exemplary lipids, formulations, methods, and characterization of LNPs are taught by WO2020061457, which is incorporated herein by reference in its entirety.

In some embodiments, *in vitro* or *ex vivo* cell lipofections are performed using Lipofectamine MessengerMax (Thermo Fisher) or TransIT-mRNA Transfection Reagent (Mirus Bio). In certain embodiments, LNPs are formulated using the GenVoy_ILM ionizable lipid mix (Precision NanoSystems). In certain embodiments, LNPs are formulated using 2,2-dilinoleyl-4-dimethylaminoethyl-[1,3]-dioxolane (DLin-KC2-DMA) or dilinoleylmethyl-4-dimethylaminobutyrate (DLin-MC3-DMA or MC3), the formulation and *in vivo* use of which are taught in Jayaraman et al. Angew Chem Int Ed Engl 51(34):8529-8533 (2012), incorporated herein by reference in its entirety.

LNP formulations optimized for the delivery of CRISPR-Cas systems, e.g., Cas9-gRNA RNP, gRNA, Cas9 mRNA, are described in WO2019067992 and WO2019067910, both incorporated by reference.

Additional specific LNP formulations useful for delivery of nucleic acids are described in US8158601 and US8168775, both incorporated by reference, which include formulations used in patisiran, sold under the name ONPATTRO.

Exemplary dosing of gene modifying LNP may include about 0.1, 0.25, 0.3, 0.5, 1, 2, 3, 4, 5, 6, 8, 10, or 100 mg/kg (RNA). Exemplary dosing of AAV comprising a nucleic acid encoding one or more components of the system may include an MOI of about 10^{11}, 10^{12}, 10^{13}, and 10^{14} vg/kg.

Kits, Articles of Manufacture, and Pharmaceutical Compositions

In an aspect the disclosure provides a kit comprising a gene modifying polypeptide or a gene modifying system, e.g., as described herein. In some embodiments, the kit comprises a gene modifying polypeptide (or a nucleic acid encoding the polypeptide) and a template RNA (or DNA encoding the template RNA). In some embodiments, the kit further comprises a reagent for introducing the system into a cell, e.g., transfection reagent, LNP, and the like. In some embodiments, the kit is suitable for any of the methods described herein. In some embodiments, the kit comprises one or more elements, compositions (e.g., pharmaceutical compositions), gene modifying polypeptides, and/or gene modifying systems, or a functional fragment or component

thereof, e.g., disposed in an article of manufacture. In some embodiments, the kit comprises instructions for use thereof.

In an aspect, the disclosure provides an article of manufacture, e.g., in which a kit as described herein, or a component thereof, is disposed.

In an aspect, the disclosure provides a pharmaceutical composition comprising a gene modifying polypeptide or a gene modifying system, e.g., as described herein. In some embodiments, the pharmaceutical composition further comprises a pharmaceutically acceptable carrier or excipient. In some embodiments, the pharmaceutical composition comprises a template RNA and/or an RNA encoding the polypeptide. In embodiments, the pharmaceutical composition has one or more (e.g., 1, 2, 3, or 4) of the following characteristics:

(a) less than 1% (e.g., less than 0.5%, 0.4%, 0.3%, 0.2%, or 0.1%) DNA template relative to the template RNA and/or the RNA encoding the polypeptide, e.g., on a molar basis;

(b) less than 1% (e.g., less than 0.5%, 0.4%, 0.3%, 0.2%, or 0.1%) uncapped RNA relative to the template RNA and/or the RNA encoding the polypeptide, e.g., on a molar basis;

(c) less than 1% (e.g., less than 0.5%, 0.4%, 0.3%, 0.2%, or 0.1%) partial length RNAs relative to the template RNA and/or the RNA encoding the polypeptide, e.g., on a molar basis;

(d) substantially lacks unreacted cap dinucleotides.

Chemistry, Manufacturing, and Controls (CMC)

Purification of protein therapeutics is described, for example, in Franks, Protein Biotechnology: *Isolation, Characterization, and Stabilization*, Humana Press (2013); and in Cutler, *Protein Purification Protocols (Methods in Molecular Biology)*, Humana Press (2010).

In some embodiments, a gene modifying system, polypeptide, and/or template nucleic acid (e.g., template RNA) conforms to certain quality standards. In some embodiments, a gene modifying system, polypeptide, and/or template nucleic acid (e.g., template RNA) produced by a method described herein conforms to certain quality standards. Accordingly, the disclosure is directed, in some aspects, to methods of manufacturing a gene modifying system, polypeptide, and/or template nucleic acid (e.g., template RNA) that conforms to certain quality standards, e.g., in which said quality standards are assayed. The disclosure is also directed, in some aspects, to methods of assaying said quality standards in a gene modifying system, polypeptide, and/or

template nucleic acid (e.g., template RNA). In some embodiments, quality standards include, but are not limited to, one or more (e.g., 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, or 12) of the following:

(i) the length of the template RNA, e.g., whether the template RNA has a length that is above a reference length or within a reference length range, e.g., whether at least 80%, 85%, 90%, 95%, 96%, 97%, 98%, or 99% of the template RNA present is greater than 100, 125, 150, 175, or 200 nucleotides long;

(ii) the presence, absence, and/or length of a polyA tail on the template RNA, e.g., whether at least 80%, 85%, 90%, 95%, 96%, 97%, 98%, or 99% of the template RNA present contains a polyA tail (e.g., a polyA tail that is at least 5, 10, 20, 30, 50, 70, 100 nucleotides in length (SEQ ID NO: 37640));

(iii) the presence, absence, and/or type of a 5´ cap on the template RNA, e.g., whether at least 80%, 85%, 90%, 95%, 96%, 97%, 98%, or 99% of the template RNA present contains a 5´ cap, e.g., whether that cap is a 7-methylguanosine cap, e.g., a O-Me-m7G cap;

(iv) the presence, absence, and/or type of one or more modified nucleotides (e.g., selected from pseudouridine, dihydrouridine, inosine, 7-methylguanosine, 1-N-methylpseudouridine (1-Me-Ψ), 5-methoxyuridine (5-MO-U), 5-methylcytidine (5mC), or a locked nucleotide) in the template RNA, e.g., whether at least 80%, 85%, 90%, 95%, 96%, 97%, 98%, or 99% of the template RNA present contains one or more modified nucleotides;

(v) the stability of the template RNA (e.g., over time and/or under a pre-selected condition), e.g., whether at least 80%, 85%, 90%, 95%, 96%, 97%, 98%, or 99% of the template RNA remains intact (e.g., greater than 100, 125, 150, 175, or 200 nucleotides long) after a stability test;

(vi) the potency of the template RNA in a system for modifying DNA, e.g., whether at least 1% of target sites are modified after a system comprising the template RNA is assayed for potency;

(vii) the length of the polypeptide, first polypeptide, or second polypeptide, e.g., whether the polypeptide, first polypeptide, or second polypeptide has a length that is above a reference length or within a reference length range, e.g., whether at least 80%, 85%, 90%, 95%, 96%, 97%, 98%, or 99% of the polypeptide, first polypeptide, or second polypeptide present is greater than 600, 650, 700, 750, 800, 850, 900, 950, 1000, 1050, 1100, 1150, 1200, 1250, 1300, 1350, 1400,

1450, 1500, 1600, 1700, 1800, 1900, or 2000 amino acids long (and optionally, no larger than 2500, 2000, 1500, 1400, 1300, 1200, 1100, 1000, 900, 800, 700, or 600 amino acids long);

(viii) the presence, absence, and/or type of post-translational modification on the polypeptide, first polypeptide, or second polypeptide, e.g., whether at least 80, 85, 90, 95, 96, 97, 98, or 99% of the polypeptide, first polypeptide, or second polypeptide contains phosphorylation, methylation, acetylation, myristoylation, palmitoylation, isoprenylation, glipyatyon, or lipoylation, or any combination thereof;

(ix) the presence, absence, and/or type of one or more artificial, synthetic, or non-canonical amino acids (e.g., selected from ornithine, β-alanine, GABA, δ-Aminolevulinic acid, PABA, a D-amino acid (e.g., D-alanine or D-glutamate), aminoisobutyric acid, dehydroalanine, cystathionine, lanthionine, Djenkolic acid, Diaminopimelic acid, Homoalanine, Norvaline, Norleucine, Homonorleucine, homoserine, O-methyl-homoserine and O-ethyl-homoserine, ethionine, selenocysteine, selenohomocysteine, selenomethionine, selenoethionine, tellurocysteine, or telluromethionine) in the polypeptide, first polypeptide, or second polypeptide, e.g., whether at least 80%, 85%, 90%, 95%, 96%, 97%, 98%, or 99% of the polypeptide, first polypeptide, or second polypeptide present contains one or more artificial, synthetic, or non-canonical amino acids;

(x) the stability of the polypeptide, first polypeptide, or second polypeptide (e.g., over time and/or under a pre-selected condition), e.g., whether at least 80%, 85%, 90%, 95%, 96%, 97%, 98%, or 99% of the polypeptide, first polypeptide, or second polypeptide remains intact (e.g., greater than 600, 650, 700, 750, 800, 850, 900, 950, 1000, 1050, 1100, 1150, 1200, 1250, 1300, 1350, 1400, 1450, 1500, 1600, 1700, 1800, 1900, or 2000 amino acids long (and optionally, no larger than 2500, 2000, 1500, 1400, 1300, 1200, 1100, 1000, 900, 800, 700, or 600 amino acids long)) after a stability test;

(xi) the potency of the polypeptide, first polypeptide, or second polypeptide in a system for modifying DNA, e.g., whether at least 1% of target sites are modified after a system comprising the polypeptide, first polypeptide, or second polypeptide is assayed for potency; or

(xii) the presence, absence, and/or level of one or more of a pyrogen, virus, fungus, bacterial pathogen, or host cell protein, e.g., whether the system is free or substantially free of pyrogen, virus, fungus, bacterial pathogen, or host cell protein contamination.

In some embodiments, a system or pharmaceutical composition described herein is endotoxin free.

In some embodiments, the presence, absence, and/or level of one or more of a pyrogen, virus, fungus, bacterial pathogen, and/or host cell protein is determined. In embodiments, whether the system is free or substantially free of pyrogen, virus, fungus, bacterial pathogen, and/or host cell protein contamination is determined.

In some embodiments, a pharmaceutical composition or system as described herein has one or more (e.g., 1, 2, 3, or 4) of the following characteristics:

(a) less than 1% (e.g., less than 0.5%, 0.4%, 0.3%, 0.2%, or 0.1%) DNA template relative to the template RNA and/or the RNA encoding the polypeptide, e.g., on a molar basis;

(b) less than 1% (e.g., less than 0.5%, 0.4%, 0.3%, 0.2%, or 0.1%) uncapped RNA relative to the template RNA and/or the RNA encoding the polypeptide, e.g., on a molar basis;

(c) less than 1% (e.g., less than 0.5%, 0.4%, 0.3%, 0.2%, or 0.1%) partial length RNAs relative to the template RNA and/or the RNA encoding the polypeptide, e.g., on a molar basis;

(d) substantially lacks unreacted cap dinucleotides.

EXAMPLES

Example 1: Screening configurations of template RNAs that correct the R408W mutation in a genomic landing pad in human cells

This example describes the use of gene modifying system containing a gene modifying polypeptide and template RNAs comprising varied lengths of heterologous object sequences and PBS sequences to quantify the activity of template RNAs for correction of the R408W mutation. In this example, a template RNA contains:

(1) a gRNA spacer;
(2) a gRNA scaffold;
(3) a heterologous object sequence; and
(4) a primer binding site (PBS) sequence.

One or more template RNAs described in Tables 1A-4D can be tested as described in this example. The heterologous object sequences and PBS sequences were designed to correct the

PAH mutation in a landing pad by replacing a “T” nucleotide with a “C” nucleotide at the mutation site via gene editing, to reverse a R408W mutation in the corresponding protein.

A cell line is created to have a “landing pad” or a stable integration that mimics a region of the PAH gene that contains the R408W mutation site and flanking sequences. The DNA for the landing pad is chemically synthesized and cloned into the pLenti-N-tGFP vector. The cloned landing pad sequence in the lentiviral expression vector is confirmed and the sequence is verified by Sanger sequencing of the landing pad. The sequence verified plasmids (9µg) along with the lentiviral packaging mix (9µg, Biosettia) are transfected using Lipofectamine2000™ according to the manufacturer instructions into a packaging cell line, LentiX-293T (Takara Bio). The transfected cells are incubated at 37˚C, 5% CO_2 for 48 hours (including one medium change at 24hrs) and the viral particle containing medium is collected from the cell culture dish. The collected medium is filtered through a 0.2 µm filter to remove cell debris and is prepared for transduction of HEK293T cells. The virus-containing medium is diluted in DMEM and mixed with polybrene to prepare a dilution series for transduction of HEK293T cells where the final concentration of polybrene is 8 µg/ml. The HEK293T cells are grown in virus containing medium for 48 hours and then split with fresh medium. The split cells are grown to confluence and transduction efficiency of the different dilutions of virus is measured by GFP expression via flow cytometry and ddPCR detection of the genomic integrated lentivirus that contained GFP and the PAH landing pads.

A gene modifying system comprising a (i) compatible gene modifying polypeptide described herein, e.g., having: an NLS of Table 11, a compatible Cas9 domain having a sequence of Table 8 (e.g., SpyCas9-SpRY), a linker of Table 10, an RT sequence of Table 6 (e.g., MLVMS_P03355_PLV919), and a second NLS of Table 11 and (ii) a template RNA of any of Tables 1A-4D (e.g., a template RNA of ID #1) is transfected into the HEK293T landing pad cell line. The gene modifying polypeptide and the template RNAs are delivered by nucleofection in RNA format. Specifically, 1µg of gene modifying polypeptide mRNA is combined with 10µM template RNAs. The mRNA and template RNAs are added to 25µL SF buffer containing 250,000 HEK293T landing pad cells and cells are nucleofected using program DS-150. After nucleofection, are were grown at 37˚C, 5% CO_2 for 3 days prior to cell lysis and genomic DNA extraction. To analyze gene editing activity, primers flanking the PAH mutation site are used to amplify across the locus. Amplicons are analyzed via short read sequencing using an Illumina

MiSeq. In some embodiments, the assay will indicate that at least 5%, 10%, 20%, 30%, 40%, or 50% of copies of the PAH gene in the sample are converted to the desired wild-type sequence.

Example 2: Gene modifying polypeptide selection by pooled screening in HEK293T & U2OS cells

This example describes the use of an RNA gene modifying system for the targeted editing of a coding sequence in the human genome. More specifically, this example describes the infection of HEK293T and U2OS cells with a library of gene modifying candidates, followed by transfection of a template guide RNA (tgRNA) for *in vitro* gene modifying in the cells, e.g., as a means of evaluating a new gene modifying polypeptide for editing activity in human cells by a pooled screening approach.

The gene modifying polypeptide library candidates assayed herein each comprise: 1) a *S. pyogenes* (Spy) Cas9 nickase containing an N863A mutation that inactivates one endonuclease active site; 2) one of the 122 peptide linkers depicted at **Table 10**; and 3) a reverse transcriptase (RT) domain from **Table 6** of retroviral origin. The particular retroviral RT domains utilized were selected if they were expected to function as a monomer. For each selected RT domain, the wild-type sequences were tested, as well as versions with point mutations installed in the primary wild-type sequence. In particular, 143 RT domains were tested, either wild type or containing various mutations. In total, 17,446 Cas-linker-RT gene modifying polypeptides were tested.

The system described here is a two-component system comprising: 1) an expression plasmid encoding a human codon-optimized gene modifying polypeptide library candidate within a lentiviral cassette, and 2) a tgRNA expression plasmid expressing a non-coding tgRNA sequence that is recognized by Cas and localizes it to the genomic locus of interest, and that also templates reverse transcription of the desired edit into the genome by the RT domain, driven by a U6 promoter. The lentiviral cassette comprises: (i) a CMV promoter for expression in mammalian cells; (ii) a gene modifying polypeptide library candidate as shown; (iii) a self-cleaving T2A polypeptide; (iv) a puromycin resistance gene enabling selection in mammalian cells; and (v) a polyA tail termination signal.

To prepare a pool of cells expressing gene modifying polypeptide library candidates, HEK293T or U2OS cells were transduced with pooled lentiviral preparations of the gene modifying candidate plasmid library. HEK293 Lenti-X cells were seeded in 15 cm plates ($12x10^6$ cells) prior to lentiviral plasmid transfection. Lentiviral plasmid transfection using the Lentiviral

Packaging Mix (Biosettia, 27 ug) and the plasmid DNA for the gene modifying candidate library (27 ug) was performed the following day using Lipofectamine 2000 and Opti-MEM media according to the manufacturer's protocol. Extracellular DNA was removed by a full media change the next day and virus-containing media was harvested 48 hours after. Lentiviral media was concentrated using Lenti-X Concentrator (TaKaRa Biosciences) and 5 mL lentiviral aliquots were made and stored at -80°C. Lentiviral titering was performed by enumerating colony forming units post Puromycin selection. HEK293T or U2OS cells carrying a BFP-expressing genomic landing pad were seeded at $6x10^7$ cells in culture plates and transduced at a 0.3 multiplicity of infection (MOI) to minimize multiple infections per cell. Puromycin (2.5 ug/mL) was added 48 hours post infection to allow for selection of infected cells. Cells were kept under puromycin selection for at least 7 days and then scaled up for tgRNA electroporation.

To determine the genome-editing capacity of the gene modifying library candidates in the assay, infected BFP-expressing HEK293T or U2OS cells were then transfected by electroporation of 250,000 cells/well with 200 ng of a tgRNA (either g4 or g10) plasmid, designed to convert BFP to GFP, at sufficient cell count for >1000x coverage per library candidate.

The g4 tgRNA (5′ to 3′) is as follows: 20 nucleotide spacer region (GCCGAAGCACTGCACGCCGT; SEQ ID NO: 11,011), a scaffold region (GTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGC; SEQ ID NO: 11,012), the template region encoding the single base pair substitution to change BFP to GFP (**bold**) and a PAM inactivation that introduces a synonymous point mutation in the SpyCas9 PAM (NGG to NCG) that prevents re-engagement of the gene modifying polypeptide upon completion of a functional gene modifying reaction (underline) (ACCCTGAC<u>G</u>**T**ACG; SEQ ID NO: 11,013), and the 13 nucleotide PBS (GCGTGCAGTGCTT; SEQ ID NO: 11,014).

Similarly, the g10 tgRNA (5′ to 3′) is as follows: 20 nucleotide spacer region (AGAAGTCGTGCTGCTTCATG; SEQ ID NO: 11,015), a scaffold region (GTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGC; SEQ ID NO: 11,016), the template region encoding the single base pair substitution to change BFP to GFP (**bold**) and a PAM inactivation that introduces a synonymous point mutation in the SpyCas9 PAM (NGG to NGA) that prevents re-engagement of the gene modifying polypeptide upon completion of a functional gene modifying

reaction (underline)
(ACCCTGACCTACGGCGTGCAGTGCTTCGGCCGCTACCCCGATCACAT; SEQ ID NO: 11,017), and 13 nucleotide PBS (GAAGCAGCACGAC; SEQ ID NO: 11,018).

To assess the genome-editing capacity of the various constructs in the assay, cells were sorted by Fluorescence-Activated Cell Sorting (FACS) for GFP expression 6-7 days post-electroporation. Cells were sorted and harvested as distinct populations of unedited (BFP+) cells, edited (GFP+) cells and imperfect edit (BFP-, GFP-) cells. A sample of unsorted cells was also harvested as the input population to determine enrichment during analysis.

To determine which gene modifying library candidates have genome-editing capacity in this assay, genomic DNA (gDNA) was harvested from sorted and unsorted cell populations, and analyzed by sequencing the gene modifying library candidates in each population. Briefly, gene modifying sequences were amplified from the genome using primers specific to the lentiviral cassette, amplified in a second round of PCR to dilute genomic DNA, and then sequenced using Oxford Nanopore Sequencing Technology according to the manufacturer's protocol.

After quality control of sequencing reads, reads of at least 1500 and no more than 3200 nucleotides were mapped to the gene modifying polypeptide library sequences and those containing a minimum of an 80% match to a library sequence were considered to be successfully aligned to a given candidate. To identify gene modifying candidates capable of performing gene editing in the assay, the read count of each library candidate in the edited population was compared to its read count in the initial, unsorted population. For purposes of this pooled screen, gene modifying candidates with genome-editing capacity were selected as those candidates that were enriched in the converted (GFP+) population relative to unsorted (input) cells and wherein the enrichment was determined to be at or above the enrichment level of a reference (Element ID No: 17380).

A large number of gene modifying polypeptide candidates were determined to be enriched in the GFP+ cell populations. For example, of the 17,446 candidates tested, over 3,300 exhibited enrichment in GFP+ sorted populations (relative to unsorted) that was at least equivalent to that of the reference under similar experimental conditions (HEK293T using g4 tgRNA; HEK293T cells using g10 tgRNA; or U2OS cells using g4 tgRNA), shown in Table D. Although the 17,446 candidates were also tested in U2OS cells using g10 tgRNA, the pooled screen did not yield

candidates that were enriched in the converted (GFP+) population relative to unsorted (input) cells under that experimental condition; further investigation is required to explain these results.

Table D. Combinations of linker and RT sequences screened. The amino acid sequence of each RT in this table is provided in Table 6.

Linker amino acid sequence	SEQ ID NO:	RT domain name
EAAAKGSS	12,001	PERV_Q4VFZ2_3mutA_WS
EAAAKEAAAKEAAAKEAAAK	12,002	MLVMS_P03355_PLV919
PAPEAAAK	12,003	MLVFF_P26809_3mutA
EAAAKPAPGGG	12,004	MLVFF_P26809_3mutA
GSSGSSGSSGSSGSSGSS	12,005	PERV_Q4VFZ2_3mut
PAPGGGEAAAK	12,006	MLVAV_P03356_3mutA
AEAAAKEAAAKEAAAKEAAAKALEAEAAAKEAAAKEAAAKEAAAKA	12,007	MLVMS_P03355_PLV919
GSSEAAAK	12,008	MLVFF_P26809_3mutA
EAAAKPAPGGS	12,009	MLVFF_P26809_3mutA
GGSGGSGGSGGSGGSGGS	12,010	MLVFF_P26809_3mutA
AEAAAKEAAAKEAAAKEAAAKALEAEAAAKEAAAKEAAAKEAAAKA	12,011	XMRV6_A1Z651_3mutA
AEAAAKEAAAKEAAAKEAAAKALEAEAAAKEAAAKEAAAKEAAAKA	12,012	PERV_Q4VFZ2_3mutA_WS
EAAAKEAAAKEAAAK	12,013	MLVFF_P26809_3mutA
PAPEAAAKGSS	12,014	MLVFF_P26809_3mutA
AEAAAKEAAAKEAAAKEAAAKALEAEAAAKEAAAKEAAAKEAAAKA	12,015	PERV_Q4VFZ2_3mutA_WS
EAAAKEAAAKEAAAK	12,016	PERV_Q4VFZ2_3mutA_WS
AEAAAKEAAAKEAAAKEAAAKALEAEAAAKEAAAKEAAAKEAAAKA	12,017	AVIRE_P03360_3mutA
PAPAPAPAPAP	12,018	MLVCB_P08361_3mutA
PAPAPAPAPAP	12,019	MLVFF_P26809_3mutA
EAAAKGGSPAP	12,020	PERV_Q4VFZ2_3mutA_WS
PAP		MLVMS_P03355_PLV919
PAPGGGGSS	12,022	WMSV_P03359_3mutA
SGSETPGTSESATPES	12,023	MLVFF_P26809_3mutA
PAPEAAAKGSS	12,024	XMRV6_A1Z651_3mutA
EAAAKGGSGGG	12,025	MLVMS_P03355_PLV919
GGGGSGGGGS	12,026	MLVFF_P26809_3mutA
GGGPAPGSS	12,027	MLVAV_P03356_3mutA
GGSGGSGGSGGSGGSGGS	12,028	XMRV6_A1Z651_3mut
GGGGSGGGGSGGGGSGGGGSGGGGSGGGGS	12,029	MLVCB_P08361_3mutA

Linker amino acid sequence	SEQ ID NO:	RT domain name
GSSPAP	12,030	AVIRE_P03360_3mutA
EAAAKGSSPAP	12,031	MLVFF_P26809_3mutA
GSSGGGEAAAK	12,032	MLVFF_P26809_3mutA
GGSGGSGGSGGSGGSGGS	12,033	MLVMS_P03355_3mutA_WS
PAPAPAPAP	12,034	MLVFF_P26809_3mutA
EAAAKEAAAKEAAAKEAAAK	12,035	XMRV6_A1Z651_3mutA
EAAAKGGSPAP	12,036	MLVMS_P03355_3mutA_WS
PAPGGSEAAAK	12,037	AVIRE_P03360_3mutA
GGGGSGGGGSGGGGSGGGGSGGGGSGGGGS	12,038	AVIRE_P03360_3mutA
EAAAKGGGGSEAAAK	12,039	MLVCB_P08361_3mutA
AEAAAKEAAAKEAAAKEAAAKALEAEAAAKEAAAKEAAAKEAAAKA	12,040	WMSV_P03359_3mutA
GSS		MLVMS_P03355_PLV919
GSSGSSGSSGSS	12,042	MLVMS_P03355_PLV919
GSSPAPEAAAK	12,043	XMRV6_A1Z651_3mutA
GGSPAPEAAAK	12,044	MLVFF_P26809_3mutA
GGGEAAAKGGS	12,045	MLVFF_P26809_3mutA
EAAAKEAAAKEAAAKEAAAKEAAAK	12,046	PERV_Q4VFZ2_3mutA_WS
GGGGGGGG	12,047	PERV_Q4VFZ2_3mut
GGGPAP	12,048	MLVCB_P08361_3mutA
PAPAPAPAPAPAP	12,049	MLVCB_P08361_3mutA
GGSGGSGGSGGSGGSGGS	12,050	MLVCB_P08361_3mutA
PAP		MLVMS_P03355_3mutA_WS
GGSGGSGGSGGSGGSGGS	12,052	PERV_Q4VFZ2_3mutA_WS
PAPAPAPAPAPAP	12,053	MLVMS_P03355_PLV919
EAAAKPAPGSS	12,054	MLVMS_P03355_3mutA_WS
EAAAKEAAAKEAAAKEAAAK	12,055	MLVMS_P03355_3mutA_WS
EAAAKGGS	12,056	MLVMS_P03355_3mutA_WS
GGGGSEAAAKGGGGS	12,057	MLVFF_P26809_3mutA
EAAAKPAPGSS	12,058	MLVFF_P26809_3mutA
GGGGSGGGGSGGGGSGGGGS	12,059	MLVMS_P03355_PLV919
EAAAKGGGGGS	12,060	MLVMS_P03355_PLV919
GGSPAP	12,061	XMRV6_A1Z651_3mutA
EAAAKGGGPAP	12,062	MLVMS_P03355_PLV919
EAAAKEAAAKEAAAKEAAAKEAAAK	12,063	MLVFF_P26809_3mutA
PAP		MLVCB_P08361_3mutA
EAAAK	12,065	XMRV6_A1Z651_3mutA
GGSGSSPAP	12,066	PERV_Q4VFZ2_3mutA_WS
GSSGSSGSSGSSGSSGSS	12,067	MLVMS_P03355_PLV919
GSSEAAAKGGG	12,068	MLVAV_P03356_3mutA
GGGEAAAKGGS	12,069	XMRV6_A1Z651_3mutA

Linker amino acid sequence	SEQ ID NO:	RT domain name
EAAAKGGGGSEAAAK	12,070	MLVAV_P03356_3mutA
GGGGSGGGGSGGGGS	12,071	MLVFF_P26809_3mutA
GGGGSGGGGSGGGGSGGGGS	12,072	AVIRE_P03360_3mutA
SGSETPGTSESATPES	12,073	AVIRE_P03360_3mutA
GGGEAAAKPAP	12,074	MLVFF_P26809_3mutA
EAAAKGSSGGG	12,075	MLVMS_P03355_3mutA_WS
EAAAKEAAAKEAAAKEAAAKEAAAK	12,076	WMSV_P03359_3mut
GGSGGSGGSGGS	12,077	XMRV6_A1Z651_3mutA
GGSEAAAKPAP	12,078	MLVFF_P26809_3mutA
EAAAKGSSGGG	12,079	XMRV6_A1Z651_3mutA
GGGGS	12,080	MLVFF_P26809_3mutA
GGGEAAAKGSS	12,081	MLVMS_P03355_PLV919
PAPAPAPAPAPAP	12,082	MLVAV_P03356_3mutA
GGGGSGGGGSGGGGSGGGGS	12,083	MLVCB_P08361_3mutA
GGGEAAAKGSS	12,084	MLVCB_P08361_3mutA
PAPGGSGSS	12,085	MLVFF_P26809_3mutA
GSAGSAAGSGEF	12,086	MLVCB_P08361_3mutA
PAPGGSEAAAK	12,087	MLVMS_P03355_3mutA_WS
GGSGSS	12,088	XMRV6_A1Z651_3mutA
PAPGGGGSS	12,089	MLVMS_P03355_PLV919
GSSGSSGSS	12,090	XMRV6_A1Z651_3mut
AEAAAKEAAAKEAAAKEAAAKALEAEAAAKEAAAKEAAAKEAAAKA	12,091	MLVMS_P03355_3mutA_WS
EAAAK	12,092	MLVMS_P03355_PLV919
GSSGSSGSSGSS	12,093	MLVFF_P26809_3mutA
PAPGGGGSS	12,094	MLVCB_P08361_3mutA
GGGEAAAKGGS	12,095	MLVCB_P08361_3mutA
PAPGGGEAAAK	12,096	MLVMS_P03355_PLV919
GGGGGSPAP	12,097	XMRV6_A1Z651_3mutA
EAAAKGGS	12,098	XMRV6_A1Z651_3mutA
EAAAKGSSPAP	12,099	XMRV6_A1Z651_3mut
PAPEAAAK	12,100	MLVAV_P03356_3mutA
GGSGGSGGSGGS	12,101	MLVMS_P03355_3mutA_WS
GGGPAPGGS	12,102	MLVMS_P03355_PLV919
GSSGSSGSSGSS	12,103	PERV_Q4VFZ2_3mutA_WS
EAAAKPAPGGS	12,104	MLVCB_P08361_3mutA
GSSGSS	12,105	MLVFF_P26809_3mutA
EAAAKEAAAKEAAAKEAAAK	12,106	MLVCB_P08361_3mutA
EAAAKEAAAKEAAAKEAAAK	12,107	FLV_P10273_3mutA
GSS		MLVFF_P26809_3mutA
EAAAKEAAAK	12,109	MLVMS_P03355_3mutA_WS

Linker amino acid sequence	SEQ ID NO:	RT domain name
PAPEAAAKGGG	12,110	MLVAV_P03356_3mutA
GGSGSSEAAAK	12,111	MLVFF_P26809_3mutA
EAAAKEAAAKEAAAKEAAAKEAAAK	12,112	PERV_Q4VFZ2
GSSEAAAKPAP	12,113	AVIRE_P03360_3mutA
EAAAKEAAAKEAAAKEAAAKEAAAK	12,114	MLVCB_P08361_3mutA
EAAAKGGG	12,115	MLVFF_P26809_3mutA
GSSPAPGGG	12,116	MLVCB_P08361_3mutA
GGGPAPGSS	12,117	MLVMS_P03355_PLV919
GGGGGS	12,118	MLVMS_P03355_3mutA_WS
EAAAKEAAAKEAAAKEAAAKEAAAKEAAAK	12,119	PERV_Q4VFZ2_3mut
GGGGSGGGGSGGGGSGGGGSGGGGS	12,120	WMSV_P03359_3mutA
EAAAKEAAAKEAAAK	12,121	PERV_Q4VFZ2_3mut
PAPAPAPAP	12,122	MLVCB_P08361_3mutA
GSSGSSGSSGSSGSS	12,123	PERV_Q4VFZ2_3mut
GGGGSSEAAAK	12,124	MLVMS_P03355_3mutA_WS
GGSGGSGGSGGS	12,125	MLVCB_P08361_3mutA
PAPEAAAKGGS	12,126	MLVCB_P08361_3mutA
EAAAKEAAAKEAAAKEAAAKEAAAKEAAAK	12,127	MLVCB_P08361_3mutA
EAAAKGGGGSEAAAK	12,128	MLVMS_P03355_PLV919
EAAAKGGGGSEAAAK	12,129	MLVMS_P03355_3mutA_WS
EAAAKGGGPAP	12,130	XMRV6_A1Z651_3mut
EAAAKEAAAKEAAAKEAAAKEAAAK	12,131	MLVMS_P03355_3mutA_WS
AEAAAKEAAAKEAAAKEAAAKALEAEAAAKEAAAKEAAAKEAAAKA	12,132	FLV_P10273_3mutA
GGSEAAAKGGG	12,133	MLVMS_P03355_3mutA_WS
GGGGSGGGGSGGGGSGGGGSGGGGSGGGGS	12,134	KORV_Q9TTC1-Pro_3mutA
GGGPAPGGS	12,135	MLVCB_P08361_3mutA
PAPAPAPAPAPAP	12,136	XMRV6_A1Z651_3mutA
GGSGSSGGG	12,137	XMRV6_A1Z651_3mutA
GGSGSSGGG	12,138	MLVCB_P08361_3mutA
GGGEAAAKGGS	12,139	MLVMS_P03355_3mutA_WS
EAAAK	12,140	MLVCB_P08361_3mutA
GGSPAPGSS	12,141	MLVMS_P03355_3mutA_WS
GGGGSSEAAAK	12,142	PERV_Q4VFZ2_3mut
PAPAPAPAPAP	12,143	MLVBM_Q7SVK7_3mut
EAAAKEAAAKEAAAKEAAAK	12,144	MLVAV_P03356_3mutA
GGGGGSGSS	12,145	MLVCB_P08361_3mutA
EAAAKGSSPAP	12,146	MLVMS_P03355_3mutA_WS
PAPAPAPAPAPAP	12,147	MLVMS_P03355_3mutA_WS
GSSGGGGGS	12,148	MLVMS_P03355_3mutA_WS
PAPGSSGGG	12,149	MLVMS_P03355_PLV919

Linker amino acid sequence	SEQ ID NO:	RT domain name
GGSGGGPAP	12,150	MLVCB_P08361_3mutA
GGGGGGG	12,151	MLVCB_P08361_3mutA
GSSGSSGSSGSSGSSGSS	12,152	MLVCB_P08361_3mutA
GGGPAPGGS	12,153	MLVFF_P26809_3mutA
EAAAKGGSGGG	12,154	PERV_Q4VFZ2_3mut
EAAAKGGGGSS	12,155	MLVMS_P03355_3mutA_WS
GSSGSSGSSGSSGSSGSS	12,156	MLVMS_P03355_3mut
GGGGSGGGGSGGGGSGGGGS	12,157	MLVBM_Q7SVK7_3mutA_WS
PAPAPAPAPAP	12,158	MLVMS_P03355_PLV919
GGGEAAAKGGS	12,159	MLVMS_P03355_PLV919
AEAAAKEAAAKEAAAKEAAAKALEAEAAAKEAAAKEAAAKEAAAKA	12,160	MLVMS_P03355_3mut
GSAGSAAGSGEF	12,161	MLVMS_P03355_3mutA_WS
GSSGSSGSSGSSGSS	12,162	MLVFF_P26809_3mutA
EAAAKGGSGSS	12,163	MLVFF_P26809_3mutA
PAPGGG	12,164	MLVFF_P26809_3mutA
GGGPAPGSS	12,165	XMRV6_A1Z651_3mutA
PAPEAAAKGGS	12,166	AVIRE_P03360_3mutA
PAPGGGEAAAK	12,167	MLVFF_P26809_3mut
GGGGSSEAAAK	12,168	MLVCB_P08361_3mutA
EAAAK	12,169	MLVMS_P03355_PLV919
GGGGSGGGGSGGGGSGGGGSGGGGSGGGGS	12,170	BAEVM_P10272_3mutA
GGSGGGEAAAK	12,171	MLVMS_P03355_PLV919
AEAAAKEAAAKEAAAKEAAAKALEAEAAAKEAAAKEAAAKEAAAKA	12,172	MLVFF_P26809_3mutA
GSSPAPGGS	12,173	XMRV6_A1Z651_3mutA
GGSGGGPAP	12,174	MLVMS_P03355_PLV919
EAAAK	12,175	AVIRE_P03360_3mutA
GSS		XMRV6_A1Z651_3mutA
GGSGGSGGS	12,177	MLVFF_P26809_3mutA
EAAAKEAAAKEAAAKEAAAK	12,178	AVIRE_P03360_3mut
PAPEAAAKGGG	12,179	PERV_Q4VFZ2_3mutA_WS
GGGGGSEAAAK	12,180	BAEVM_P10272_3mutA
GGSGSSGGG	12,181	MLVMS_P03355_3mutA_WS
GGGGGGG	12,182	MLVMS_P03355_3mutA_WS
GSSEAAAKPAP	12,183	PERV_Q4VFZ2_3mut
GGGGGSEAAAK	12,184	WMSV_P03359_3mut
GGGGSGGGGSGGGGSGGGGSGGGGS	12,185	MLVFF_P26809_3mut
GGGEAAAKGGS	12,186	AVIRE_P03360_3mutA
GGSPAPGGG	12,187	AVIRE_P03360_3mutA
GSAGSAAGSGEF	12,188	MLVAV_P03356_3mutA
EAAAK	12,189	MLVAV_P03356_3mutA

Linker amino acid sequence	SEQ ID NO:	RT domain name
EAAAKPAPGSS	12,190	WMSV_P03359_3mutA
EAAAKEAAAKEAAAKEAAAKEAAAKEAAAK	12,191	PERV_Q4VFZ2_3mutA_WS
GGSEAAAKPAP	12,192	MLVCB_P08361_3mutA
PAPAPAPAPAPAP	12,193	MLVBM_Q7SVK7_3mutA_WS
GGSPAPGGG	12,194	MLVMS_P03355_3mutA_WS
GGSEAAAKGGG	12,195	MLVMS_P03355_3mut
GGSGGSGGSGGS	12,196	MLVFF_P26809_3mutA
EAAAKEAAAKEAAAKEAAAKEAAAKEAAAK	12,197	MLVFF_P26809_3mutA
GGG		AVIRE_P03360_3mutA
AEAAAKEAAAKEAAAKEAAAKALEAEAAAKEAAAKEAAAKEAAAKA	12,199	PERV_Q4VFZ2_3mut
GGSGGSGGSGGS	12,200	MLVMS_P03355_3mutA_WS
GGGEAAAK	12,201	MLVCB_P08361_3mutA
GSSGSSGSSGSSGSSGSS	12,202	MLVMS_P03355_3mutA_WS
GSSGGGPAP	12,203	MLVMS_P03355_3mutA_WS
GSSEAAAKPAP	12,204	MLVFF_P26809_3mutA
EAAAKEAAAK	12,205	MLVMS_P03355_PLV919
GGGGSGGGGSGGGGSGGGGSGGGGSGGGGS	12,206	MLVCB_P08361_3mut
GGGGGG	12,207	MLVMS_P03355_3mutA_WS
GGSGSSGGG	12,208	MLVFF_P26809_3mutA
GSSGGGEAAAK	12,209	PERV_Q4VFZ2_3mutA_WS
PAPAPAPAPAP	12,210	PERV_Q4VFZ2_3mut
EAAAKEAAAKEAAAKEAAAKEAAAKEAAAK	12,211	SFV3L_P27401_2mut
EAAAKGGSGGG	12,212	BAEVM_P10272_3mutA
GGGGSSPAP	12,213	PERV_Q4VFZ2_3mutA_WS
GGGEAAAKPAP	12,214	MLVMS_P03355_PLV919
GGSGGGPAP	12,215	BAEVM_P10272_3mutA
PAPGSSGGS	12,216	MLVMS_P03355_PLV919
GGSGGGPAP	12,217	MLVMS_P03355_3mutA_WS
EAAAKGGSPAP	12,218	PERV_Q4VFZ2_3mutA_WS
EAAAKGGSGGG	12,219	MLVMS_P03355_3mutA_WS
PAPGSSGGG	12,220	MLVFF_P26809_3mutA
GSSEAAAKGGS	12,221	MLVFF_P26809_3mutA
PAPGSSEAAAK	12,222	MLVFF_P26809_3mutA
EAAAKGSSPAP	12,223	KORV_Q9TTC1-Pro_3mutA
EAAAKEAAAKEAAAKEAAAKEAAAK	12,224	MLVBM_Q7SVK7_3mutA_WS
PAPGSSEAAAK	12,225	MLVMS_P03355_PLV919
EAAAKGSSGGG	12,226	MLVMS_P03355_3mutA_WS
EAAAKGGGGGS	12,227	AVIRE_P03360_3mutA
EAAAKEAAAKEAAAK	12,228	MLVMS_P03355_PLV919
PAPAPAPAPAPAP	12,229	MLVFF_P26809_3mutA

Linker amino acid sequence	SEQ ID NO:	RT domain name
GGGGSGGGGSGGGGS	12,230	MLVCB_P08361_3mutA
PAPGGSEAAAK	12,231	MLVCB_P08361_3mutA
PAPGSSEAAAK	12,232	MLVBM_Q7SVK7_3mutA_WS
PAPEAAAKGSS	12,233	AVIRE_P03360_3mutA
GGSPAPGSS	12,234	WMSV_P03359_3mutA
PAPGGSGGG	12,235	MLVMS_P03355_PLV919
EAAAKGGSGSS	12,236	MLVMS_P03355_3mutA_WS
GGSGGG	12,237	MLVFF_P26809_3mutA
GGSEAAAKGSS	12,238	KORV_Q9TTC1_3mutA
AEAAAKEAAAKEAAAKEAAAKALEAEAAAKEAAAKEAAAKEAAAKA	12,239	MLVCB_P08361_3mutA
PAPAPAPAPAPAP	12,240	PERV_Q4VFZ2_3mutA_WS
PAPEAAAK	12,241	MLVMS_P03355_3mutA_WS
GGSEAAAKGGG	12,242	MLVMS_P03355_PLV919
GSSPAP	12,243	MLVMS_P03355_3mutA_WS
GGGGSS	12,244	MLVMS_P03355_PLV919
GGGEAAAKPAP	12,245	AVIRE_P03360_3mutA
EAAAKPAPGGS	12,246	MLVAV_P03356_3mutA
EAAAKGGGPAP	12,247	MLVAV_P03356_3mutA
PAPGGSEAAAK	12,248	BAEVM_P10272_3mutA
PAPGGSGSS	12,249	MLVMS_P03355_3mutA_WS
PAPGGSGSS	12,250	AVIRE_P03360_3mutA
GGSGGGPAP	12,251	MLVMS_P03355_3mutA_WS
EAAAKEAAAKEAAAKEAAAK	12,252	BAEVM_P10272_3mutA
GGGGSGGGGSGGGGSGGGGSGGGGS	12,253	MLVMS_P03355_PLV919
GGGGSSPAP	12,254	MLVCB_P08361_3mutA
GSSGGGPAP	12,255	MLVFF_P26809_3mutA
GGGGSSGGS	12,256	MLVMS_P03355_PLV919
GGSGGG	12,257	MLVCB_P08361_3mutA
GSSGGGGGS	12,258	MLVMS_P03355_PLV919
SGGSSGGSSGSETPGTSESATPESSGGSSGGSS	12,259	XMRV6_A1Z651_3mutA
GGGGGSGSS	12,260	KORV_Q9TTC1_3mut
GGGEAAAKGGS	12,261	BAEVM_P10272_3mutA
GGSGGG	12,262	BAEVM_P10272_3mutA
PAPAPAP	12,263	KORV_Q9TTC1-Pro_3mut
AEAAAKEAAAKEAAAKEAAAKALEAEAAAKEAAAKEAAAKEAAAKA	12,264	SFV3L_P27401_2mutA
AEAAAKEAAAKEAAAKEAAAKALEAEAAAKEAAAKEAAAKEAAAKA	12,265	MLVBM_Q7SVK7_3mutA_WS
GSSGSSGSSGSSGSS	12,266	MLVMS_P03355_3mutA_WS
GSSGGGEAAAK	12,267	MLVMS_P03355_3mutA_WS
GSSGGSEAAAK	12,268	MLVFF_P26809_3mutA
PAP		MLVMS_P03355_PLV919

Linker amino acid sequence	SEQ ID NO:	RT domain name
EAAAKGGGGSEAAAK	12,270	MLVBM_Q7SVK7_3mutA_WS
PAPAP	12,271	AVIRE_P03360_3mutA
PAP		MLVFF_P26809_3mutA
GSSGGG	12,273	MLVMS_P03355_3mut
GSSPAPGGS	12,274	MLVFF_P26809_3mutA
PAPAPAPAP	12,275	XMRV6_A1Z651_3mutA
EAAAKGSSGGS	12,276	PERV_Q4VFZ2_3mut
PAPEAAAKGGG	12,277	KORV_Q9TTC1-Pro_3mutA
PAPGGS	12,278	MLVCB_P08361_3mutA
EAAAKGGG	12,279	MLVCB_P08361_3mutA
GSSEAAAKPAP	12,280	MLVMS_P03355_PLV919
PAPGGS	12,281	MLVFF_P26809_3mutA
EAAAKGGS	12,282	MLVCB_P08361_3mutA
EAAAKEAAAKEAAAKEAAAKEAAAKEAAAK	12,283	FLV_P10273_3mutA
PAPGGSEAAAK	12,284	MLVAV_P03356_3mutA
GSS		MLVCB_P08361_3mutA
GSSGSSGSSGSS	12,286	AVIRE_P03360_3mutA
GSSGSSGSS	12,287	MLVFF_P26809_3mutA
GSSGGG	12,288	MLVMS_P03355_PLV919
EAAAK	12,289	MLVFF_P26809_3mutA
GGSPAPEAAAK	12,290	MLVCB_P08361_3mutA
GGSGSS	12,291	MLVCB_P08361_3mutA
GSSPAPGGG	12,292	MLVMS_P03355_PLV919
EAAAKEAAAKEAAAKEAAAKEAAAK	12,293	MLVAV_P03356_3mutA
EAAAKGSSPAP	12,294	FLV_P10273_3mutA
GGGGSS	12,295	XMRV6_A1Z651_3mutA
GGSPAPGSS	12,296	MLVMS_P03355_PLV919
EAAAKEAAAKEAAAKEAAAKEAAAK	12,297	MLVMS_P03355_3mutA_WS
PAPEAAAKGGG	12,298	FLV_P10273_3mutA
EAAAKPAPGGS	12,299	XMRV6_A1Z651_3mut
PAPAP	12,300	BAEVM_P10272_3mutA
EAAAKEAAAKEAAAKEAAAK	12,301	MLVMS_P03355_PLV919
GSSPAPGGG	12,302	MLVMS_P03355_PLV919
EAAAKGGGPAP	12,303	KORV_Q9TTC1_3mutA
PAPEAAAK	12,304	MLVMS_P03355_PLV919
PAPGGGEAAAK	12,305	PERV_Q4VFZ2_3mutA_WS
EAAAKGSSGGS	12,306	MLVMS_P03355_3mutA_WS
EAAAKEAAAKEAAAK	12,307	MLVMS_P03355_PLV919
GSSEAAAK	12,308	MLVMS_P03355_3mutA_WS
GSSGSSGSSGSS	12,309	MLVMS_P03355_3mutA_WS

Linker amino acid sequence	SEQ ID NO:	RT domain name
GGGGSGGGGSGGGGSGGGGS	12,310	MLVMS_P03355_3mutA_WS
EAAAKGGGGSEAAAK	12,311	MLVMS_P03355_3mut
GGS		MLVCB_P08361_3mutA
GGGGSGGGGSGGGGSGGGGSGGGGSGGGGS	12,313	XMRV6_A1Z651_3mutA
GGSGSSPAP	12,314	MLVCB_P08361_3mutA
GGGGSGGGGSGGGGS	12,315	XMRV6_A1Z651_3mutA
PAPAPAPAPAP	12,316	BAEVM_P10272_3mutA
PAPAPAPAPAP	12,317	MLVMS_P03355_3mutA_WS
EAAAKEAAAKEAAAKEAAAK	12,318	MLVBM_Q7SVK7_3mut
GGGGSGGGGSGGGGSGGGGSGGGGS	12,319	BAEVM_P10272_3mutA
GGSGGSGGS	12,320	MLVMS_P03355_3mutA_WS
EAAAKPAPGSS	12,321	MLVMS_P03355_PLV919
GSS		MLVMS_P03355_3mutA_WS
PAPEAAAKGGS	12,323	MLVMS_P03355_3mutA_WS
GGGPAPGGS	12,324	MLVMS_P03355_3mutA_WS
EAAAKGGGGSS	12,325	MLVAV_P03356_3mutA
GSSGSSGSSGSSGSS	12,326	MLVFF_P26809_3mut
SGSETPGTSESATPES	12,327	PERV_Q4VFZ2_3mut
GGSEAAAKGGG	12,328	MLVMS_P03355_3mut
GSSGSSGSSGSSGSSGSS	12,329	AVIRE_P03360_3mutA
PAPAPAPAPAPAP	12,330	AVIRE_P03360_3mut
GGSGGS	12,331	XMRV6_A1Z651_3mutA
PAPGSSEAAAK	12,332	MLVCB_P08361_3mut
GGSPAPEAAAK	12,333	PERV_Q4VFZ2_3mut
EAAAKGGGGGS	12,334	MLVCB_P08361_3mutA
GGSGGSGGSGGS	12,335	MLVMS_P03355_PLV919
GGGGSSEAAAK	12,336	MLVMS_P03355_PLV919
GSSEAAAKGGG	12,337	MLVFF_P26809_3mutA
PAPGGS	12,338	MLVMS_P03355_3mutA_WS
EAAAKGGSGGG	12,339	MLVCB_P08361_3mutA
EAAAKGGG	12,340	PERV_Q4VFZ2_3mut
PAPGGS	12,341	XMRV6_A1Z651_3mutA
GSSPAPGGG	12,342	XMRV6_A1Z651_3mutA
PAPEAAAKGGG	12,343	MLVMS_P03355_3mutA_WS
GSSEAAAKGGG	12,344	PERV_Q4VFZ2_3mutA_WS
PAPGGSEAAAK	12,345	XMRV6_A1Z651_3mutA
GGGGGS	12,346	MLVMS_P03355_3mutA_WS
GGSPAPEAAAK	12,347	MLVMS_P03355_3mutA_WS
GGGPAP	12,348	MLVFF_P26809_3mutA
PAPGSSGGG	12,349	XMRV6_A1Z651_3mutA

Linker amino acid sequence	SEQ ID NO:	RT domain name
PAPGSSGGG	12,350	MLVBM_Q7SVK7_3mutA_WS
GGGEAAAKGSS	12,351	MLVMS_P03355_3mutA_WS
GSSEAAAKGGS	12,352	MLVCB_P08361_3mutA
PAPGGSGSS	12,353	MLVCB_P08361_3mutA
EAAAKGGGGSEAAAK	12,354	BAEVM_P10272_3mutA
PAPAPAP	12,355	PERV_Q4VFZ2_3mutA_WS
GGGGGG	12,356	MLVAV_P03356_3mutA
GSSPAPEAAAK	12,357	MLVCB_P08361_3mutA
GGSGGSGGS	12,358	MLVMS_P03355_3mutA_WS
GSSGSSGSSGSSGSS	12,359	XMRV6_A1Z651_3mut
GGGPAPGGS	12,360	XMRV6_A1Z651_3mutA
GGGPAPEAAAK	12,361	BAEVM_P10272_3mutA
GGSGGG	12,362	AVIRE_P03360_3mutA
SGSETPGTSESATPES	12,363	PERV_Q4VFZ2_3mutA_WS
EAAAKGSSPAP	12,364	MLVMS_P03355_PLV919
GSSEAAAK	12,365	XMRV6_A1Z651_3mut
GSSGGSGGG	12,366	MLVFF_P26809_3mutA
EAAAKEAAAKEAAAKEAAAKEAAAK	12,367	WMSV_P03359_3mutA
GGGGSEAAAKGGGGS	12,368	MLVMS_P03355_PLV919
PAPGGGGSS	12,369	MLVMS_P03355_3mutA_WS
SGSETPGTSESATPES	12,370	MLVMS_P03355_3mutA_WS
GGSPAPEAAAK	12,371	KORV_Q9TTC1-Pro_3mutA
GSSEAAAKGGG	12,372	MLVMS_P03355_3mutA_WS
GSSEAAAK	12,373	WMSV_P03359_3mutA
GGGGSEAAAKGGGGS	12,374	AVIRE_P03360_3mutA
GSS		WMSV_P03359_3mutA
PAPGGSEAAAK	12,376	MLVFF_P26809_3mutA
GGGGS	12,377	MLVMS_P03355_3mutA_WS
GGGPAP	12,378	MLVMS_P03355_3mutA_WS
EAAAKEAAAKEAAAKEAAAKEAAAKEAAAK	12,379	MLVMS_P03355_3mutA_WS
EAAAKPAPGSS	12,380	PERV_Q4VFZ2_3mut
EAAAKPAPGSS	12,381	MLVCB_P08361_3mutA
GGGGGG	12,382	WMSV_P03359_3mutA
EAAAKPAPGGS	12,383	MLVMS_P03355_PLV919
PAPGGGEAAAK	12,384	PERV_Q4VFZ2_3mut
EAAAKEAAAKEAAAKEAAAKEAAAK	12,385	AVIRE_P03360_3mutA
GSSEAAAKPAP	12,386	XMRV6_A1Z651_3mutA
PAPGGSEAAAK	12,387	MLVBM_Q7SVK7_3mutA_WS
PAPGSS	12,388	MLVCB_P08361_3mutA
EAAAKGGG	12,389	MLVMS_P03355_3mutA_WS

Linker amino acid sequence	SEQ ID NO:	RT domain name
EAAAKPAP	12,390	MLVCB_P08361_3mutA
PAPEAAAKGGS	12,391	MLVBM_Q7SVK7_3mutA_WS
GGSPAPGGG	12,392	MLVCB_P08361_3mutA
PAPGGSGSS	12,393	WMSV_P03359_3mutA
EAAAKEAAAKEAAAKEAAAKEAAAKEAAAK	12,394	MLVMS_P03355_PLV919
GGSGGGPAP	12,395	MLVMS_P03355_PLV919
AEAAAKEAAAKEAAAKEAAAKALEAEAAAKEAAAKEAAAKEAAAKA	12,396	MLVMS_P03355
PAPEAAAKGSS	12,397	MLVCB_P08361_3mutA
EAAAKGSS	12,398	MLVMS_P03355_3mutA_WS
GGSGGS	12,399	MLVMS_P03355_3mutA_WS
EAAAKEAAAKEAAAKEAAAKEAAAK	12,400	BAEVM_P10272_3mutA
GGGGSEAAAKGGGGS	12,401	FLV_P10273_3mutA
GGSEAAAKGGG	12,402	MLVCB_P08361_3mutA
GSSGSSGSSGSSGSS	12,403	BAEVM_P10272_3mutA
GGGGSGGGGSGGGGSGGGGSGGGGSGGGGS	12,404	MLVFF_P26809_3mutA
EAAAKGGG	12,405	PERV_Q4VFZ2_3mut
GGGGGSEAAAK	12,406	MLVCB_P08361_3mutA
EAAAKPAPGGS	12,407	MLVMS_P03355_3mutA_WS
GGGGGSGSS	12,408	XMRV6_A1Z651_3mutA
PAPGSSEAAAK	12,409	MLVMS_P03355_3mutA_WS
GSSEAAAKPAP	12,410	MLVCB_P08361_3mutA
EAAAKGSSPAP	12,411	MLVAV_P03356_3mutA
GGGPAPGGS	12,412	WMSV_P03359_3mutA
GGSPAP	12,413	MLVMS_P03355_3mutA_WS
GGSEAAAKGGG	12,414	MLVMS_P03355_3mutA_WS
GGGGGGGG	12,415	MLVFF_P26809_3mutA
GGGGSGGGGSGGGGSGGGGSGGGGSGGGGS	12,416	MLVMS_P03355_3mutA_WS
GGGGSGGGGSGGGGSGGGGSGGGGSGGGGS	12,417	MLVBM_Q7SVK7_3mutA_WS
GSSPAPGGG	12,418	MLVAV_P03356_3mutA
GGGGGG	12,419	AVIRE_P03360_3mutA
GSSGGS	12,420	MLVMS_P03355_3mutA_WS
GGSPAPGSS	12,421	MLVFF_P26809_3mutA
PAPEAAAKGGG	12,422	PERV_Q4VFZ2_3mut
EAAAKGGGPAP	12,423	MLVFF_P26809_3mutA
GGGEAAAKGGS	12,424	MLVMS_P03355_PLV919
GGSGSSPAP	12,425	MLVFF_P26809_3mutA
SGSETPGTSESATPES	12,426	WMSV_P03359_3mutA
PAPGGSEAAAK	12,427	MLVBM_Q7SVK7_3mutA_WS
GGSGGG	12,428	MLVMS_P03355_PLV919
GGGGSSPAP	12,429	PERV_Q4VFZ2_3mut

Linker amino acid sequence	SEQ ID NO:	RT domain name
GGGEAAAKGSS	12,430	MLVAV_P03356_3mutA
PAPAPAPAPAPAP	12,431	MLVMS_P03355_3mutA_WS
EAAAKGGGGSEAAAK	12,432	PERV_Q4VFZ2
EAAAKEAAAKEAAAKEAAAKEAAAK	12,433	MLVMS_P03355_PLV919
GGGGGSEAAAK	12,434	PERV_Q4VFZ2_3mut
PAPGSSEAAAK	12,435	MLVCB_P08361_3mutA
GSAGSAAGSGEF	12,436	PERV_Q4VFZ2_3mutA_WS
EAAAKGGGGSEAAAK	12,437	MLVFF_P26809_3mutA
GGSPAPGGG	12,438	PERV_Q4VFZ2_3mutA_WS
GSSEAAAKGGG	12,439	AVIRE_P03360_3mutA
GGGEAAAKPAP	12,440	MLVMS_P03355_3mutA_WS
GGGPAP	12,441	AVIRE_P03360_3mutA
GGSEAAAK	12,442	MLVCB_P08361_3mutA
SGGSSGGSSGSETPGTSESATPESSGGSSGGSS	12,443	PERV_Q4VFZ2_3mut
EAAAKPAPGGS	12,444	MLVBM_Q7SVK7_3mutA_WS
AEAAAKEAAAKEAAAKEAAAKALEAEAAAKEAAAKEAAAKEAAAKA	12,445	XMRV6_A1Z651_3mut
GGGGGGGG	12,446	MLVCB_P08361_3mutA
PAPGSS	12,447	PERV_Q4VFZ2_3mut
EAAAK	12,448	PERV_Q4VFZ2_3mut
GSAGSAAGSGEF	12,449	MLVMS_P03355_3mutA_WS
PAPGGGEAAAK	12,450	PERV_Q4VFZ2_3mut
EAAAKGSSGGS	12,451	MLVFF_P26809_3mut
GGGGSEAAAKGGGGS	12,452	BAEVM_P10272_3mutA
GGGGSGGGGSGGGGS	12,453	MLVMS_P03355_PLV919
EAAAKGGGGSEAAAK	12,454	BAEVM_P10272_3mut
PAPGGGEAAAK	12,455	MLVMS_P03355_3mutA_WS
GGSEAAAKPAP	12,456	MLVMS_P03355_3mutA_WS
PAPAP	12,457	MLVCB_P08361_3mutA
PAPAP	12,458	MLVFF_P26809_3mutA
GGSPAP	12,459	AVIRE_P03360_3mutA
EAAAKGSSGGS	12,460	MLVCB_P08361_3mutA
PAPGSSGGS	12,461	AVIRE_P03360_3mutA
EAAAKGGGGSEAAAK	12,462	XMRV6_A1Z651_3mutA
PAPAPAP	12,463	BAEVM_P10272_3mutA
GGSGGSGGSGGSGGSGGS	12,464	MLVMS_P03355_PLV919
GGGGGSGSS	12,465	MLVMS_P03355_PLV919
PAPGSSEAAAK	12,466	XMRV6_A1Z651_3mut
GGSEAAAKPAP	12,467	XMRV6_A1Z651_3mutA
EAAAKEAAAKEAAAKEAAAK	12,468	XMRV6_A1Z651_3mut
AEAAAKEAAAKEAAAKEAAAKALEAEAAAKEAAAKEAAAKEAAAKA	12,469	WMSV_P03359_3mut

Linker amino acid sequence	SEQ ID NO:	RT domain name
GGSGGGEAAAK	12,470	XMRV6_A1Z651_3mutA
GGGEAAAK	12,471	XMRV6_A1Z651_3mutA
GGGGSGGGGSGGGGS	12,472	MLVMS_P03355_3mutA_WS
GGSGGSGGSGGSGGS	12,473	MLVFF_P26809_3mutA
GSSGGGGGS	12,474	MLVMS_P03355_3mut
PAPGGSEAAAK	12,475	MLVMS_P03355_3mutA_WS
GSSGGSPAP	12,476	MLVMS_P03355_3mutA_WS
SGSETPGTSESATPES	12,477	XMRV6_A1Z651_3mutA
GGGGSGGGGS	12,478	MLVMS_P03355_PLV919
PAPAPAPAPAP	12,479	MLVMS_P03355_3mut
GSSGSS	12,480	XMRV6_A1Z651_3mutA
GSSEAAAKPAP	12,481	PERV_Q4VFZ2_3mut
GGSGSSGGG	12,482	MLVMS_P03355_3mutA_WS
EAAAKEAAAK	12,483	MLVCB_P08361_3mutA
GSSGSSGSSGSS	12,484	MLVMS_P03355_3mutA_WS
GSSPAPGGG	12,485	PERV_Q4VFZ2_3mutA_WS
EAAAKEAAAKEAAAK	12,486	MLVMS_P03355_3mutA_WS
AEAAAKEAAAKEAAAKEAAAKALEAEAAAKEAAAKEAAAKEAAAKA	12,487	SFV1_P23074_2mutA
GGGGSGGGGSGGGGSGGGGSGGGGSGGGGS	12,488	MLVMS_P03355_PLV919
GSAGSAAGSGEF	12,489	MLVMS_P03355_PLV919
PAPGSSEAAAK	12,490	MLVMS_P03355_3mutA_WS
GGSEAAAK	12,491	MLVMS_P03355_3mutA_WS
GSSGSSGSSGSSGSS	12,492	PERV_Q4VFZ2_3mutA_WS
GGSEAAAKPAP	12,493	PERV_Q4VFZ2_3mutA_WS
GGSGGSGGS	12,494	MLVCB_P08361_3mutA
EAAAKGGSGSS	12,495	MLVCB_P08361_3mutA
GGGGSGGGGSGGGGSGGGGSGGGGS	12,496	FLV_P10273_3mutA
EAAAKEAAAKEAAAKEAAAK	12,497	MLVBM_Q7SVK7_3mutA_WS
GGSGSSPAP	12,498	BAEVM_P10272_3mutA
EAAAKEAAAKEAAAKEAAAKEAAAK	12,499	XMRV6_A1Z651_3mutA
GGGGSGGGGSGGGGSGGGGSGGGGS	12,500	MLVBM_Q7SVK7_3mutA_WS
GGSGSS	12,501	WMSV_P03359_3mutA
PAPEAAAK	12,502	MLVCB_P08361_3mutA
EAAAKPAP	12,503	BAEVM_P10272_3mutA
GSSPAP	12,504	PERV_Q4VFZ2_3mutA_WS
GGGPAP	12,505	PERV_Q4VFZ2_3mutA_WS
EAAAKGGSGSS	12,506	MLVMS_P03355_3mutA_WS
EAAAKGGGGSEAAAK	12,507	AVIRE_P03360_3mutA
GGSGGG	12,508	KORV_Q9TTC1-Pro_3mutA
GSSPAP	12,509	MLVFF_P26809_3mutA

Linker amino acid sequence	SEQ ID NO:	RT domain name
GGSGSSEAAAK	12,510	BAEVM_P10272_3mutA
PAPGSSGGS	12,511	BAEVM_P10272_3mutA
GGGGGG	12,512	MLVFF_P26809_3mutA
PAPGGSEAAAK	12,513	MLVMS_P03355_PLV919
PAPGGS	12,514	MLVMS_P03355_PLV919
GGSGGSGGSGGS	12,515	BAEVM_P10272_3mutA
GSSPAP	12,516	MLVCB_P08361_3mutA
PAPAPAPAP	12,517	MLVMS_P03355_3mutA_WS
GGGGGG	12,518	MLVCB_P08361_3mutA
GSSGSSGSSGSSGSSGSS	12,519	KORV_Q9TTC1-Pro_3mutA
GSSEAAAKGGS	12,520	BAEVM_P10272_3mutA
GGSEAAAK	12,521	FLV_P10273_3mutA
GGSGGSGGSGGSGGS	12,522	KORV_Q9TTC1-Pro_3mutA
GSSPAPEAAAK	12,523	PERV_Q4VFZ2_3mut
GSSGSSGSSGSSGSS	12,524	XMRV6_A1Z651_3mutA
EAAAKPAPGGS	12,525	MLVMS_P03355_3mut
SGGSSGGSSGSETPGTSESATPESSGGSSGGSS	12,526	FLV_P10273_3mut
GGSPAPEAAAK	12,527	XMRV6_A1Z651_3mut
EAAAKGGSGGG	12,528	MLVFF_P26809_3mutA
EAAAKEAAAKEAAAKEAAAK	12,529	MLVFF_P26809_3mutA
GSSPAP	12,530	WMSV_P03359_3mutA
PAPAPAPAP	12,531	MLVAV_P03356_3mutA
PAPGGSEAAAK	12,532	KORV_Q9TTC1_3mut
GGSGSSEAAAK	12,533	MLVBM_Q7SVK7_3mutA_WS
GSSGGG	12,534	MLVCB_P08361_3mutA
GGGEAAAKGSS	12,535	PERV_Q4VFZ2_3mut
PAPGGSGGG	12,536	MLVFF_P26809_3mutA
AEAAAKEAAAKEAAAKEAAAKALEAEAAAKEAAAKEAAAKEAAAKA	12,537	FFV_O93209
PAPGGGGSS	12,538	MLVMS_P03355_3mutA_WS
EAAAKGGS	12,539	MLVAV_P03356_3mutA
EAAAKEAAAKEAAAKEAAAKEAAAKEAAAK	12,540	MLVBM_Q7SVK7_3mutA_WS
GGSGGSGGS	12,541	WMSV_P03359_3mutA
PAPAP	12,542	MLVMS_P03355_3mutA_WS
GSSGGGEAAAK	12,543	MLVAV_P03356_3mutA
GGGGSSEAAAK	12,544	MLVFF_P26809_3mutA
EAAAKGSSGGS	12,545	MLVMS_P03355_PLV919
EAAAKGGGGSEAAAK	12,546	MLVMS_P03355_3mutA_WS
GGGGGGGG	12,547	MLVMS_P03355_PLV919
GSSGSSGSS	12,548	MLVMS_P03355_PLV919
GGGEAAAKPAP	12,549	PERV_Q4VFZ2_3mutA_WS

Linker amino acid sequence	SEQ ID NO:	RT domain name
GGGGGSGSS	12,550	MLVMS_P03355_3mutA_WS
GGGGGGG	12,551	MLVMS_P03355_PLV919
GGS		MLVMS_P03355_PLV919
GSSGGG	12,553	MLVMS_P03355_3mutA_WS
EAAAKGGSGSS	12,554	PERV_Q4VFZ2_3mutA_WS
PAPGSSEAAAK	12,555	MLVMS_P03355_PLV919
GSSEAAAKPAP	12,556	MLVMS_P03355_PLV919
GGSPAPGSS	12,557	BAEVM_P10272_3mutA
GSAGSAAGSGEF	12,558	MLVCB_P08361_3mut
GGSPAPGGG	12,559	PERV_Q4VFZ2_3mut
GGGGSGGGGSGGGGSGGGGS	12,560	MLVMS_P03355_3mut
GSSGSSGSS	12,561	PERV_Q4VFZ2_3mutA_WS
EAAAKEAAAKEAAAKEAAAKEAAAKEAAAK	12,562	PERV_Q4VFZ2_3mut
GGGGSEAAAKGGGGS	12,563	MLVCB_P08361_3mutA
GGSEAAAKGSS	12,564	MLVAV_P03356_3mutA
EAAAKGGGGSEAAAK	12,565	MLVCB_P08361_3mut
EAAAKEAAAKEAAAKEAAAKEAAAKEAAAK	12,566	XMRV6_A1Z651_3mutA
PAPGGGEAAAK	12,567	MLVMS_P03355_3mutA_WS
GSSGGGEAAAK	12,568	PERV_Q4VFZ2_3mutA_WS
GSSGSS	12,569	MLVCB_P08361_3mut
PAPAPAPAPAPAP	12,570	PERV_Q4VFZ2_3mut
GGSPAPGGG	12,571	MLVFF_P26809_3mutA
GGSGGSGGSGGSGGS	12,572	MLVCB_P08361_3mutA
EAAAKEAAAK	12,573	MLVFF_P26809_3mutA
AEAAAKEAAAKEAAAKEAAAKALEAEAAAKEAAAKEAAAKEAAAKA	12,574	GALV_P21414_3mut
PAPAPAPAPAPAP	12,575	WMSV_P03359_3mutA
GGGEAAAKGGS	12,576	KORV_Q9TTC1_3mutA
EAAAKGGGPAP	12,577	KORV_Q9TTC1_3mut
PAPEAAAKGSS	12,578	MLVBM_Q7SVK7_3mutA_WS
PAPEAAAKGSS	12,579	FLV_P10273_3mutA
PAPGGSEAAAK	12,580	MLVMS_P03355_3mut
GSSPAPGGG	12,581	BAEVM_P10272_3mutA
GGGEAAAKPAP	12,582	KORV_Q9TTC1-Pro_3mutA
GGGGSGGGGS	12,583	MLVMS_P03355_PLV919
GGGEAAAKGSS	12,584	MLVFF_P26809_3mutA
PAPGGGGSS	12,585	MLVBM_Q7SVK7_3mutA_WS
GSSEAAAK	12,586	BAEVM_P10272_3mutA
GGGGGGGG	12,587	MLVMS_P03355_PLV919
PAPGSSGGS	12,588	MLVAV_P03356_3mutA
GGGGSGGGGSGGGGSGGGGS	12,589	BAEVM_P10272_3mutA

Linker amino acid sequence	SEQ ID NO:	RT domain name
PAP		MLVMS_P03355_3mut
EAAAKGSSPAP	12,591	XMRV6_A1Z651_3mutA
PAPEAAAKGGS	12,592	MLVFF_P26809_3mutA
GSSGGGEAAAK	12,593	BAEVM_P10272_3mutA
PAPAPAP	12,594	MLVMS_P03355_3mutA_WS
GGSEAAAKGGG	12,595	MLVMS_P03355_PLV919
GSSEAAAK	12,596	PERV_Q4VFZ2_3mut
GGGG	12,597	MLVMS_P03355_3mutA_WS
GGGGGS	12,598	MLVMS_P03355_3mut
GGGGSSEAAAK	12,599	PERV_Q4VFZ2_3mut
EAAAKEAAAKEAAAKEAAAKEAAAKEAAAK	12,600	SFV3L_P27401-Pro_2mutA
GGSEAAAKGSS	12,601	MLVMS_P03355_3mutA_WS
PAPGSSGGS	12,602	XMRV6_A1Z651_3mutA
GGSPAP	12,603	MLVMS_P03355_3mutA_WS
GGGGSSEAAAK	12,604	BAEVM_P10272_3mut
GGSGGSGGSGGS	12,605	AVIRE_P03360_3mutA
PAPGSSGGS	12,606	MLVFF_P26809_3mutA
GSSPAPGGG	12,607	MLVMS_P03355_3mutA_WS
GGGGGGG	12,608	MLVMS_P03355_3mutA_WS
EAAAKGGGGS	12,609	MLVMS_P03355_3mutA_WS
EAAAKGGSGGG	12,610	MLVMS_P03355_PLV919
GGGGSSEAAAK	12,611	XMRV6_A1Z651_3mutA
GGGGSEAAAKGGGGS	12,612	MLVBM_Q7SVK7_3mutA_WS
GSSGSS	12,613	MLVMS_P03355_PLV919
GGSGGG	12,614	MLVMS_P03355_PLV919
PAPEAAAKGGG	12,615	AVIRE_P03360_3mutA
AEAAAKEAAAKEAAAKEAAAKALEAEAAAKEAAAKEAAAKEAAAKA	12,616	FOAMV_P14350-Pro_2mutA
GGGGGSGSS	12,617	PERV_Q4VFZ2_3mut
GSSGSSGSSGSSGSS	12,618	KORV_Q9TTC1-Pro_3mut
GGGGSEAAAKGGGGS	12,619	MLVMS_P03355_3mutA_WS
GGGGGSPAP	12,620	FLV_P10273_3mut
GGGEAAAK	12,621	MLVMS_P03355_3mutA_WS
GGSGGSGGSGGS	12,622	FLV_P10273_3mutA
GGG		MLVMS_P03355_PLV919
GGSPAPEAAAK	12,624	BAEVM_P10272_3mutA
EAAAKEAAAK	12,625	FLV_P10273_3mutA
GGGEAAAKPAP	12,626	BAEVM_P10272_3mutA
GGGEAAAKGGS	12,627	PERV_Q4VFZ2_3mut
GGSGGSGGS	12,628	PERV_Q4VFZ2_3mut
EAAAKGGGPAP	12,629	XMRV6_A1Z651_3mutA

Linker amino acid sequence	SEQ ID NO:	RT domain name
EAAAK	12,630	MLVBM_Q7SVK7_3mutA_WS
PAPEAAAKGGG	12,631	PERV_Q4VFZ2_3mut
EAAAKGSS	12,632	MLVCB_P08361_3mutA
GGSEAAAKGGG	12,633	MLVBM_Q7SVK7_3mutA_WS
GGGGSGGGGSGGGGSGGGGS	12,634	XMRV6_A1Z651_3mutA
GGGGSGGGGSGGGGSGGGGSGGGGS	12,635	BAEVM_P10272_3mut
GGGGSSPAP	12,636	PERV_Q4VFZ2_3mutA_WS
GGSGGSGGSGGSGGSGGS	12,637	PERV_Q4VFZ2_3mut
GGGEAAAKPAP	12,638	PERV_Q4VFZ2_3mut
EAAAKEAAAK	12,639	BAEVM_P10272_3mutA
GGSGSSEAAAK	12,640	XMRV6_A1Z651_3mutA
PAPEAAAKGSS	12,641	WMSV_P03359_3mutA
PAPAPAPAPAP	12,642	XMRV6_A1Z651_3mutA
GSSGGGEAAAK	12,643	MLVMS_P03355_PLV919
GSSPAPGGG	12,644	MLVFF_P26809_3mutA
GGSPAPEAAAK	12,645	MLVFF_P26809_3mut
PAPGGSEAAAK	12,646	PERV_Q4VFZ2_3mut
GGGGSS	12,647	MLVFF_P26809_3mutA
GGSGSSGGG	12,648	BAEVM_P10272_3mutA
GSSGGGEAAAK	12,649	MLVMS_P03355_3mutA_WS
EAAAKGGS	12,650	MLVBM_Q7SVK7_3mutA_WS
GGGPAPGGS	12,651	MLVMS_P03355_PLV919
EAAAKEAAAK	12,652	MLVMS_P03355_PLV919
GSSGSSGSS	12,653	MLVMS_P03355_PLV919
GGGEAAAKPAP	12,654	MLVAV_P03356_3mutA
SGSETPGTSESATPES	12,655	FLV_P10273_3mutA
PAPAPAPAPAP	12,656	KORV_Q9TTC1-Pro_3mut
AEAAAKEAAAKEAAAKEAAAKALEAEAAAKEAAAKEAAAKEAAAKA	12,657	BAEVM_P10272_3mutA
PAPGSSGGG	12,658	MLVMS_P03355_3mutA_WS
GSSGGGEAAAK	12,659	XMRV6_A1Z651_3mutA
GGGGSGGGGSGGGGSGGGGSGGGGS	12,660	XMRV6_A1Z651_3mutA
GGGGSSPAP	12,661	MLVFF_P26809_3mutA
GGSGGGPAP	12,662	PERV_Q4VFZ2_3mutA_WS
GSS		PERV_Q4VFZ2_3mut
EAAAKGSSPAP	12,664	MLVMS_P03355_3mut
EAAAKGGG	12,665	XMRV6_A1Z651_3mutA
GSSGSSGSSGSS	12,666	WMSV_P03359_3mutA
PAPEAAAKGSS	12,667	MLVMS_P03355_PLV919
GSSEAAAK	12,668	AVIRE_P03360_3mutA
EAAAKGGSGSS	12,669	AVIRE_P03360_3mutA

Linker amino acid sequence	SEQ ID NO:	RT domain name
GSSEAAAK	12,670	MLVMS_P03355_3mut
GGSGSSEAAAK	12,671	MLVMS_P03355_PLV919
GGSEAAAKGGG	12,672	MLVFF_P26809_3mutA
GGGGSGGGGSGGGGSGGGGS	12,673	MLVAV_P03356_3mutA
PAPAPAPAPAPAP	12,674	MLVFF_P26809_3mut
EAAAKPAPGSS	12,675	KORV_Q9TTC1-Pro_3mut
PAPGSSEAAAK	12,676	MLVAV_P03356_3mutA
GGGGSSPAP	12,677	WMSV_P03359_3mutA
EAAAKGGGGGS	12,678	MLVMS_P03355_3mutA_WS
GGGEAAAKGGS	12,679	MLVMS_P03355_3mut
GGSGSSGGG	12,680	MLVMS_P03355_3mut
GGGPAPGGS	12,681	MLVAV_P03356_3mutA
PAPGGGGGS	12,682	MLVMS_P03355_PLV919
GGGPAPGSS	12,683	PERV_Q4VFZ2_3mut
GGGGGGG	12,684	MLVFF_P26809_3mutA
GGSGGGGSS	12,685	MLVCB_P08361_3mutA
GGGGGG	12,686	FLV_P10273_3mutA
GGSEAAAKGSS	12,687	PERV_Q4VFZ2_3mut
GGSPAPGGG	12,688	BAEVM_P10272_3mutA
GGSPAPGSS	12,689	AVIRE_P03360_3mutA
GGSGGSGGSGGS	12,690	KORV_Q9TTC1_3mut
EAAAKEAAAKEAAAKEAAAKEAAAK	12,691	MLVBM_Q7SVK7_3mut
PAPGSSGGS	12,692	XMRV6_A1Z651_3mut
EAAAKGGGGSS	12,693	PERV_Q4VFZ2_3mutA_WS
GGSGGSGGSGGSGGS	12,694	PERV_Q4VFZ2_3mutA_WS
PAPGGSGGG	12,695	MLVMS_P03355_PLV919
PAPGSSGGG	12,696	PERV_Q4VFZ2_3mutA_WS
GSSGSS	12,697	BAEVM_P10272_3mutA
EAAAKGSS	12,698	MLVFF_P26809_3mutA
GGGPAP	12,699	MLVMS_P03355_PLV919
EAAAKGGGGGS	12,700	MLVFF_P26809_3mutA
EAAAKGGSPAP	12,701	MLVBM_Q7SVK7_3mutA_WS
EAAAKEAAAKEAAAKEAAAKEAAAKEAAAK	12,702	WMSV_P03359_3mutA
GSSPAPGGG	12,703	MLVBM_Q7SVK7_3mutA_WS
GGGEAAAKGSS	12,704	AVIRE_P03360_3mutA
GGGGSSEAAAK	12,705	AVIRE_P03360_3mutA
GGGGGGGG	12,706	PERV_Q4VFZ2_3mutA_WS
PAPGSSEAAAK	12,707	BAEVM_P10272_3mutA
EAAAKGSS	12,708	MLVFF_P26809_3mut
GSSEAAAKGGG	12,709	MLVCB_P08361_3mutA

Linker amino acid sequence	SEQ ID NO:	RT domain name
GGSEAAAK	12,710	MLVBM_Q7SVK7_3mutA_WS
GSSEAAAKGGG	12,711	PERV_Q4VFZ2_3mutA_WS
PAPGGSGGG	12,712	WMSV_P03359_3mutA
GSSGGSGGG	12,713	MLVCB_P08361_3mutA
EAAAKGSSGGG	12,714	FLV_P10273_3mutA
GSSEAAAK	12,715	MLVCB_P08361_3mutA
GSSGGGEAAAK	12,716	MLVMS_P03355_3mut
GGGGSGGGGS	12,717	MLVCB_P08361_3mutA
EAAAKGGGGSEAAAK	12,718	MLVBM_Q7SVK7_3mutA_WS
EAAAKGGG	12,719	PERV_Q4VFZ2_3mutA_WS
EAAAKGGSPAP	12,720	MLVMS_P03355_PLV919
GGGPAPGGS	12,721	AVIRE_P03360_3mutA
GSSEAAAK	12,722	MLVBM_Q7SVK7_3mutA_WS
GSSGGGEAAAK	12,723	PERV_Q4VFZ2_3mut
SGSETPGTSESATPES	12,724	MLVMS_P03355_PLV919
GGSGSSPAP	12,725	MLVMS_P03355_3mut
GGGGGG	12,726	MLVBM_Q7SVK7_3mutA_WS
GGSPAPGGG	12,727	XMRV6_A1Z651_3mutA
GGSGSS	12,728	PERV_Q4VFZ2_3mutA_WS
PAP		MLVBM_Q7SVK7_3mutA_WS
EAAAKPAPGSS	12,730	MLVMS_P03355_PLV919
EAAAKGGG	12,731	MLVMS_P03355_3mut
GSSEAAAKPAP	12,732	PERV_Q4VFZ2_3mutA_WS
GGGGSS	12,733	MLVMS_P03355_3mutA_WS
GGSGSSEAAAK	12,734	PERV_Q4VFZ2_3mut
GGGGSS	12,735	BAEVM_P10272_3mutA
PAPAP	12,736	MLVFF_P26809_3mut
PAPEAAAKGGG	12,737	BAEVM_P10272_3mutA
EAAAKGGS	12,738	MLVMS_P03355_PLV919
PAPAPAPAPAPAP	12,739	PERV_Q4VFZ2_3mutA_WS
GGGGGSEAAAK	12,740	MLVMS_P03355_3mut
PAPGGS	12,741	PERV_Q4VFZ2_3mut
GGGGSS	12,742	MLVCB_P08361_3mutA
GGGGS	12,743	MLVAV_P03356_3mutA
GSSPAPEAAAK	12,744	MLVMS_P03355_PLV919
GGGGSSGGS	12,745	MLVFF_P26809_3mutA
PAPEAAAKGSS	12,746	MLVMS_P03355_PLV919
GGSGSSEAAAK	12,747	MLVMS_P03355_3mutA_WS
EAAAKGGG	12,748	MLVAV_P03356_3mutA
PAPGSSEAAAK	12,749	FLV_P10273_3mutA

Linker amino acid sequence	SEQ ID NO:	RT domain name
EAAAKGSSGGG	12,750	MLVCB_P08361_3mutA
PAPEAAAK	12,751	KORV_Q9TTC1-Pro_3mutA
GGSPAPEAAAK	12,752	KORV_Q9TTC1-Pro_3mut
GGSGGSGGSGGSGGSGGS	12,753	MLVAV_P03356_3mutA
GSSEAAAKPAP	12,754	MLVBM_Q7SVK7_3mutA_WS
AEAAAKEAAAKEAAAKEAAAKALEAEAAAKEAAAKEAAAKEAAAKA	12,755	KORV_Q9TTC1-Pro_3mutA
GSSGGGEAAAK	12,756	XMRV6_A1Z651_3mut
PAPGGSGGG	12,757	AVIRE_P03360_3mutA
PAPGGSEAAAK	12,758	PERV_Q4VFZ2_3mutA_WS
GGGGS	12,759	MLVMS_P03355_3mutA_WS
GGGGSGGGGSGGGGS	12,760	MLVBM_Q7SVK7_3mutA_WS
PAPAPAPAPAP	12,761	PERV_Q4VFZ2_3mutA_WS
EAAAKEAAAKEAAAKEAAAKEAAAK	12,762	MLVMS_P03355_3mut
GSSGGSEAAAK	12,763	MLVMS_P03355_3mutA_WS
GGSGGSGGSGGS	12,764	WMSV_P03359_3mutA
EAAAKGSSGGG	12,765	WMSV_P03359_3mutA
EAAAKGGG	12,766	PERV_Q4VFZ2_3mutA_WS
SGSETPGTSESATPES	12,767	PERV_Q4VFZ2_3mut
PAPGSSGGS	12,768	MLVMS_P03355_3mutA_WS
PAPEAAAKGSS	12,769	PERV_Q4VFZ2_3mut
PAPEAAAK	12,770	AVIRE_P03360_3mutA
GSSEAAAKGGG	12,771	BAEVM_P10272_3mutA
GSSPAP	12,772	MLVAV_P03356_3mutA
EAAAKEAAAKEAAAKEAAAK	12,773	MLVFF_P26809_3mut
PAPGGSGSS	12,774	MLVAV_P03356_3mutA
GGGGSGGGGSGGGGS	12,775	PERV_Q4VFZ2_3mutA_WS
GSSGGSEAAAK	12,776	MLVCB_P08361_3mutA
EAAAKGGS	12,777	KORV_Q9TTC1-Pro_3mutA
EAAAKGGS	12,778	MLVFF_P26809_3mutA
GGSPAP	12,779	MLVMS_P03355_PLV919
GGSGSS	12,780	MLVMS_P03355_PLV919
SGSETPGTSESATPES	12,781	WMSV_P03359_3mut
GGGGGGG	12,782	WMSV_P03359_3mut
GGSPAPGSS	12,783	MLVCB_P08361_3mutA
GGGGSSGGS	12,784	WMSV_P03359_3mut
PAPGGS	12,785	MLVMS_P03355_PLV919
PAPGSSGGS	12,786	MLVCB_P08361_3mutA
EAAAKEAAAKEAAAKEAAAKEAAAK	12,787	MLVFF_P26809_3mut
SGGSSGGSSGSETPGTSESATPESSGGSSGGSS	12,788	PERV_Q4VFZ2_3mut
GGSGGSGGSGGSGGS	12,789	BAEVM_P10272_3mutA

Linker amino acid sequence	SEQ ID NO:	RT domain name
GSSEAAAK	12,790	PERV_Q4VFZ2_3mut
EAAAKEAAAKEAAAKEAAAK	12,791	KORV_Q9TTC1-Pro_3mutA
GGSGGSGGSGGSGGS	12,792	MLVMS_P03355_3mut
PAPAPAPAPAPAP	12,793	MLVMS_P03355_3mut
GGSPAPEAAAK	12,794	MLVMS_P03355_PLV919
EAAAK	12,795	WMSV_P03359_3mutA
EAAAKGSSGGS	12,796	MLVBM_Q7SVK7_3mutA_WS
GGSGGGGSS	12,797	MLVMS_P03355_3mutA_WS
GGGEAAAKPAP	12,798	MLVMS_P03355_3mut
EAAAKGGSGGG	12,799	XMRV6_A1Z651_3mutA
GGGGGSEAAAK	12,800	KORV_Q9TTC1-Pro_3mutA
GGGGGG	12,801	BAEVM_P10272_3mutA
GGGGGG	12,802	MLVMS_P03355_3mut
GGGGGGG	12,803	MLVBM_Q7SVK7_3mutA_WS
AEAAAKEAAAKEAAAKEAAAKALEAEAAAKEAAAKEAAAKEAAAKA	12,804	AVIRE_P03360
PAPGSSGGS	12,805	PERV_Q4VFZ2_3mut
GGGGGS	12,806	XMRV6_A1Z651_3mut
EAAAKPAP	12,807	XMRV6_A1Z651_3mutA
GGG		MLVMS_P03355_3mutA_WS
AEAAAKEAAAKEAAAKEAAAKALEAEAAAKEAAAKEAAAKEAAAKA	12,809	FLV_P10273_3mut
EAAAKGSSPAP	12,810	MLVMS_P03355_3mut
SGSETPGTSESATPES	12,811	BAEVM_P10272_3mutA
GGSPAPEAAAK	12,812	MLVMS_P03355_3mut
GSSGSSGSSGSS	12,813	MLVAV_P03356_3mutA
AEAAAKEAAAKEAAAKEAAAKALEAEAAAKEAAAKEAAAKEAAAKA	12,814	MLVMS_P03355_3mut
GGSPAP	12,815	MLVCB_P08361_3mutA
GGGGGSEAAAK	12,816	MLVMS_P03355_3mutA_WS
GGGGG	12,817	MLVFF_P26809_3mutA
GSSEAAAK	12,818	MLVAV_P03356_3mutA
GGS		BAEVM_P10272_3mut
EAAAKGGSPAP	12,820	MLVCB_P08361_3mutA
PAPAPAPAP	12,821	FLV_P10273_3mutA
PAPGGGEAAAK	12,822	MLVCB_P08361_3mutA
GGGGSSEAAAK	12,823	MLVMS_P03355_3mutA_WS
GGGGG	12,824	PERV_Q4VFZ2_3mutA_WS
GGSGGSGGSGGSGGSGGS	12,825	PERV_Q4VFZ2_3mut
GGGGG	12,826	MLVMS_P03355_3mut
PAPEAAAKGGG	12,827	MLVBM_Q7SVK7_3mutA_WS
GSSGGGPAP	12,828	XMRV6_A1Z651_3mutA
GSSGSSGSSGSSGSSGSS	12,829	PERV_Q4VFZ2_3mutA_WS

Linker amino acid sequence	SEQ ID NO:	RT domain name
EAAAKGGSPAP	12,830	PERV_Q4VFZ2_3mut
GSSGGSEAAAK	12,831	MLVMS_P03355_PLV919
GSS		PERV_Q4VFZ2_3mut
EAAAKGGS	12,833	WMSV_P03359_3mutA
GGGGGSPAP	12,834	PERV_Q4VFZ2_3mutA_WS
EAAAKGSS	12,835	MLVMS_P03355_PLV919
EAAAKGGGGSS	12,836	KORV_Q9TTC1-Pro_3mutA
PAPGSSGGG	12,837	PERV_Q4VFZ2_3mut
GGGGSSEAAAK	12,838	MLVFF_P26809_3mut
PAPAPAP	12,839	MLVMS_P03355_3mut
GSSGGSEAAAK	12,840	XMRV6_A1Z651_3mut
PAPEAAAKGSS	12,841	MLVMS_P03355_3mutA_WS
GGSGGSGGSGGSGGS	12,842	MLVMS_P03355_3mutA_WS
GGSGSSPAP	12,843	XMRV6_A1Z651_3mutA
GGGGSSPAP	12,844	MLVMS_P03355_PLV919
GGGGS	12,845	MLVCB_P08361_3mutA
EAAAKEAAAKEAAAKEAAAK	12,846	PERV_Q4VFZ2_3mutA_WS
EAAAKEAAAK	12,847	KORV_Q9TTC1_3mutA
PAPGGGEAAAK	12,848	BAEVM_P10272_3mutA
GSSGGSEAAAK	12,849	XMRV6_A1Z651_3mutA
EAAAKEAAAKEAAAKEAAAKEAAAKEAAAK	12,850	FLV_P10273_3mut
GSSEAAAKPAP	12,851	MLVMS_P03355_3mutA_WS
EAAAKPAPGSS	12,852	PERV_Q4VFZ2_3mutA_WS
GSSGGSPAP	12,853	XMRV6_A1Z651_3mutA
GSSEAAAKGGG	12,854	PERV_Q4VFZ2_3mut
GGGEAAAKGGS	12,855	WMSV_P03359_3mutA
GSSEAAAKGGG	12,856	MLVFF_P26809_3mut
PAPAPAP	12,857	KORV_Q9TTC1-Pro_3mutA
EAAAKGGSPAP	12,858	MLVMS_P03355_3mutA_WS
PAPGGSEAAAK	12,859	PERV_Q4VFZ2_3mut
GGGGS	12,860	MLVBM_Q7SVK7_3mutA_WS
EAAAKGSSGGG	12,861	KORV_Q9TTC1_3mut
EAAAKGGGPAP	12,862	MLVCB_P08361_3mutA
EAAAKGSS	12,863	BAEVM_P10272_3mutA
GGSPAPGGG	12,864	MLVBM_Q7SVK7_3mutA_WS
GGGGSEAAAKGGGGS	12,865	MLVMS_P03355_3mutA_WS
GGGEAAAKGGS	12,866	PERV_Q4VFZ2_3mutA_WS
EAAAKGGGGSS	12,867	MLVMS_P03355_3mutA_WS
EAAAKGGGPAP	12,868	MLVFF_P26809_3mut
GSSPAP	12,869	PERV_Q4VFZ2_3mutA_WS

Linker amino acid sequence	SEQ ID NO:	RT domain name
EAAAKGGS	12,870	MLVMS_P03355_3mut
GGGGSS	12,871	KORV_Q9TTC1-Pro_3mutA
EAAAKGSSPAP	12,872	MLVMS_P03355_3mutA_WS
GGGPAP	12,873	PERV_Q4VFZ2_3mut
EAAAKGSSGGS	12,874	XMRV6_A1Z651_3mutA
PAPGGG	12,875	MLVAV_P03356_3mutA
GSSPAPEAAAK	12,876	BAEVM_P10272_3mutA
GGGPAP	12,877	MLVBM_Q7SVK7_3mutA_WS
GSSGGGGGS	12,878	AVIRE_P03360_3mutA
SGSETPGTSESATPES	12,879	MLVMS_P03355_PLV919
GGGPAP	12,880	MLVFF_P26809_3mut
EAAAKGGGGSS	12,881	XMRV6_A1Z651_3mutA
GGGGSSPAP	12,882	XMRV6_A1Z651_3mut
GGGGSEAAAKGGGGS	12,883	MLVMS_P03355_3mut
GSSPAP	12,884	MLVBM_Q7SVK7_3mutA_WS
GGSGSSEAAAK	12,885	FLV_P10273_3mutA
SGSETPGTSESATPES	12,886	MLVBM_Q7SVK7_3mutA_WS
PAPGGG	12,887	AVIRE_P03360_3mutA
GGGEAAAKPAP	12,888	MLVMS_P03355_3mutA_WS
EAAAKGGSGSS	12,889	PERV_Q4VFZ2_3mut
GGSPAPGGG	12,890	MLVAV_P03356_3mutA
PAPGGSGSS	12,891	BAEVM_P10272_3mutA
GSSGGSPAP	12,892	MLVFF_P26809_3mutA
EAAAKGSSGGG	12,893	PERV_Q4VFZ2_3mut
GGGGSGGGGS	12,894	PERV_Q4VFZ2_3mutA_WS
GSSGGGGGS	12,895	BAEVM_P10272_3mutA
GGGGSSGGS	12,896	MLVBM_Q7SVK7_3mutA_WS
EAAAKGGS	12,897	PERV_Q4VFZ2_3mutA_WS
GSSGSSGSSGSS	12,898	MLVMS_P03355_3mut
GGS		MLVMS_P03355_3mutA_WS
GSSGGSEAAAK	12,900	MLVBM_Q7SVK7_3mutA_WS
SGGSSGGSSGSETPGTSESATPESSGGSSGGSS	12,901	XMRV6_A1Z651
GGGGG	12,902	FLV_P10273_3mutA
PAPEAAAKGSS	12,903	PERV_Q4VFZ2_3mut
GGGGGG	12,904	WMSV_P03359_3mut
EAAAKGGG	12,905	BAEVM_P10272_3mutA
GGGGSS	12,906	MLVMS_P03355_3mutA_WS
GSSGGGEAAAK	12,907	KORV_Q9TTC1_3mut
GGSGSS	12,908	AVIRE_P03360_3mutA
EAAAKPAP	12,909	MLVMS_P03355_3mut

Linker amino acid sequence	SEQ ID NO:	RT domain name
EAAAKEAAAKEAAAK	12,910	FLV_P10273_3mutA
GGGG	12,911	XMRV6_A1Z651_3mutA
GSSPAPGGS	12,912	BAEVM_P10272_3mutA
GSSGGGGGS	12,913	MLVFF_P26809_3mutA
GGGGSSGGS	12,914	MLVAV_P03356_3mutA
GGS		PERV_Q4VFZ2_3mut
GGGGG	12,916	WMSV_P03359_3mutA
GSSGSSGSSGSSGSSGSS	12,917	FLV_P10273_3mutA
PAPGGGGSS	12,918	MLVAV_P03356_3mutA
GGGGGGGG	12,919	BAEVM_P10272_3mutA
SGSETPGTSESATPES	12,920	MLVCB_P08361_3mutA
PAPGGG	12,921	BAEVM_P10272_3mutA
GSSGSSGSS	12,922	MLVCB_P08361_3mutA
GGSGSS	12,923	MLVMS_P03355_3mutA_WS
EAAAKGGGGSEAAAK	12,924	WMSV_P03359_3mutA
GGGGGGGG	12,925	FLV_P10273_3mutA
GSSGSS	12,926	MLVMS_P03355_3mutA_WS
PAPEAAAKGGS	12,927	XMRV6_A1Z651_3mutA
EAAAKEAAAK	12,928	MLVMS_P03355_3mut
GGGGSGGGGSGGGGS	12,929	BAEVM_P10272_3mutA
EAAAKGSSPAP	12,930	MLVMS_P03355_PLV919
GGGGSSEAAAK	12,931	MLVMS_P03355_3mut
GGGGSSEAAAK	12,932	BAEVM_P10272_3mutA
PAPGGSGSS	12,933	PERV_Q4VFZ2_3mut
GGSGGGEAAAK	12,934	MLVFF_P26809_3mut
PAPEAAAKGGS	12,935	PERV_Q4VFZ2_3mut
GGGPAPGSS	12,936	AVIRE_P03360_3mut
PAPGGSGGG	12,937	PERV_Q4VFZ2_3mutA_WS
GGGGGGGG	12,938	PERV_Q4VFZ2_3mutA_WS
GSSEAAAK	12,939	MLVMS_P03355_3mutA_WS
GGGGSGGGGSGGGGS	12,940	PERV_Q4VFZ2_3mutA_WS
EAAAKGGS	12,941	MLVMS_P03355_3mut
GGGGGSGSS	12,942	MLVCB_P08361_3mut
GGGPAP	12,943	KORV_Q9TTC1-Pro_3mutA
EAAAKPAPGGG	12,944	MLVCB_P08361_3mut
GSSGGSPAP	12,945	MLVCB_P08361_3mutA
SGGSSGGSSGSETPGTSESATPESSGGSSGGSS	12,946	MLVMS_P03355_3mut
PAPAPAPAP	12,947	MLVMS_P03355_3mut
GSSGGS	12,948	XMRV6_A1Z651_3mutA
GSSEAAAKGGG	12,949	MLVMS_P03355_3mut

Linker amino acid sequence	SEQ ID NO:	RT domain name
GGSGSSPAP	12,950	MLVMS_P03355_3mutA_WS
GSSEAAAKGGS	12,951	MLVMS_P03355_PLV919
EAAAKEAAAKEAAAKEAAAKEAAAK	12,952	BAEVM_P10272_3mut
PAPGGGGSS	12,953	KORV_Q9TTC1_3mutA
EAAAKGSS	12,954	MLVMS_P03355_3mutA_WS
AEAAAKEAAAKEAAAKEAAAKALEAEAAAKEAAAKEAAAKEAAAKA	12,955	FFV_O93209_2mut
GGSGGSGGSGGSGGSGGS	12,956	BAEVM_P10272_3mutA
GGGGGG	12,957	MLVMS_P03355_PLV919
PAPEAAAK	12,958	BAEVM_P10272_3mutA
GGSGSSEAAAK	12,959	MLVAV_P03356_3mutA
GGG		MLVCB_P08361_3mutA
GGGGG	12,961	MLVCB_P08361_3mutA
GGSGGSGGSGGS	12,962	KORV_Q9TTC1-Pro_3mutA
GSSGSSGSSGSSGSSGSS	12,963	XMRV6_A1Z651_3mutA
GSSEAAAKPAP	12,964	FLV_P10273_3mutA
GGGEAAAKPAP	12,965	MLVCB_P08361_3mutA
GSSGSSGSS	12,966	MLVMS_P03355_3mutA_WS
PAPAPAPAP	12,967	MLVMS_P03355_PLV919
EAAAKGGG	12,968	MLVMS_P03355_PLV919
PAPAPAPAPAPAP	12,969	FLV_P10273_3mutA
EAAAKGGSGSS	12,970	MLVMS_P03355_3mut
GGGGGG	12,971	PERV_Q4VFZ2_3mutA_WS
PAPGGG	12,972	MLVCB_P08361_3mutA
GGGGGSGSS	12,973	KORV_Q9TTC1_3mutA
GGGGSGGGGSGGGGSGGGGS	12,974	XMRV6_A1Z651_3mut
GGSGGSGGS	12,975	KORV_Q9TTC1-Pro_3mutA
EAAAKPAPGGG	12,976	MLVMS_P03355_3mutA_WS
AEAAAKEAAAKEAAAKEAAAKALEAEAAAKEAAAKEAAAKEAAAKA	12,977	XMRV6_A1Z651
GGGGSGGGGSGGGGSGGGGSGGGGSGGGGS	12,978	FLV_P10273_3mutA
EAAAKGGGGSEAAAK	12,979	PERV_Q4VFZ2_3mutA_WS
GGGPAPGSS	12,980	AVIRE_P03360_3mutA
GGGGG	12,981	MLVMS_P03355_3mutA_WS
GGGGSGGGGSGGGGSGGGGSGGGGSGGGGS	12,982	MLVMS_P03355_3mut
GGGGSGGGGS	12,983	MLVMS_P03355_3mutA_WS
EAAAKGGSPAP	12,984	XMRV6_A1Z651_3mutA
EAAAKGSSPAP	12,985	AVIRE_P03360_3mutA
PAPGGSGSS	12,986	KORV_Q9TTC1-Pro_3mutA
GSS		MLVBM_Q7SVK7_3mutA_WS
GSS		WMSV_P03359_3mut
GGGPAPGSS	12,989	MLVFF_P26809_3mutA

Linker amino acid sequence	SEQ ID NO:	RT domain name
EAAAKPAP	12,990	MLVMS_P03355_3mut
GSSPAPEAAAK	12,991	FLV_P10273_3mutA
GGSPAPGSS	12,992	MLVBM_Q7SVK7_3mutA_WS
GGGGGSEAAAK	12,993	XMRV6_A1Z651_3mut
PAPEAAAKGGG	12,994	WMSV_P03359_3mutA
PAPGGG	12,995	PERV_Q4VFZ2_3mut
GGSPAPEAAAK	12,996	WMSV_P03359_3mutA
GGSGGGGSS	12,997	PERV_Q4VFZ2_3mut
EAAAKGGGGSS	12,998	PERV_Q4VFZ2_3mut
EAAAKGGSPAP	12,999	AVIRE_P03360_3mut
GGSGGGGSS	13,000	WMSV_P03359_3mutA
PAPGSSEAAAK	13,001	MLVFF_P26809_3mut
GSSEAAAK	13,002	MLVMS_P03355_PLV919
GSAGSAAGSGEF	13,003	AVIRE_P03360_3mutA
EAAAKGGSGSS	13,004	MLVMS_P03355_3mut
GGSEAAAKPAP	13,005	MLVMS_P03355_PLV919
GGGGSGGGGSGGGGSGGGGSGGGGS	13,006	MLVFF_P26809_3mutA
PAPGSSEAAAK	13,007	PERV_Q4VFZ2_3mutA_WS
GGGGSSPAP	13,008	MLVMS_P03355_3mutA_WS
PAPAPAP	13,009	MLVCB_P08361_3mutA
EAAAKPAPGGG	13,010	MLVBM_Q7SVK7_3mutA_WS
GGGPAPGSS	13,011	BAEVM_P10272_3mutA
PAP		MLVMS_P03355_3mutA_WS
PAPGGSGGG	13,013	MLVMS_P03355_3mutA_WS
GGSGGSGGSGGSGGS	13,014	MLVBM_Q7SVK7_3mutA_WS
PAPAPAPAP	13,015	XMRV6_A1Z651_3mut
GSSPAPGGG	13,016	MLVMS_P03355_3mutA_WS
GSSPAPGGG	13,017	MLVMS_P03355_3mut
PAPGGG	13,018	MLVMS_P03355_PLV919
GGGEAAAKGSS	13,019	WMSV_P03359_3mut
EAAAKGSS	13,020	KORV_Q9TTC1-Pro_3mutA
EAAAKGGS	13,021	PERV_Q4VFZ2_3mut
EAAAKEAAAKEAAAKEAAAKEAAAK	13,022	PERV_Q4VFZ2_3mut
PAPEAAAKGGG	13,023	MLVMS_P03355_PLV919
EAAAKGSSGGG	13,024	MLVFF_P26809_3mut
AEAAAKEAAAKEAAAKEAAAKALEAEAAAKEAAAKEAAAKEAAAKA	13,025	PERV_Q4VFZ2
EAAAKEAAAKEAAAKEAAAKEAAAKEAAAK	13,026	MLVAV_P03356_3mutA
GSSGGSGGG	13,027	MLVFF_P26809_3mut
GSSGSSGSSGSS	13,028	PERV_Q4VFZ2_3mutA_WS
GGSPAPGGG	13,029	MLVMS_P03355_PLV919

Linker amino acid sequence	SEQ ID NO:	RT domain name
GSS		BAEVM_P10272_3mut
GGGPAPGSS	13,031	MLVMS_P03355_3mutA_WS
GGGGSS	13,032	KORV_Q9TTC1_3mutA
GSSGGSGGG	13,033	BAEVM_P10272_3mutA
EAAAKEAAAKEAAAK	13,034	MLVCB_P08361_3mutA
SGGSSGGSSGSETPGTSESATPESSGGSSGGSS	13,035	FLV_P10273_3mutA
PAPGGGGGS	13,036	PERV_Q4VFZ2_3mut
PAPAPAPAPAP	13,037	KORV_Q9TTC1-Pro_3mutA
EAAAK	13,038	MLVMS_P03355_3mutA_WS
GGG		MLVCB_P08361_3mut
GGSEAAAKGGG	13,040	BAEVM_P10272_3mutA
GGGGGSGSS	13,041	MLVAV_P03356_3mutA
EAAAKGSSPAP	13,042	MLVBM_Q7SVK7_3mutA_WS
GGSGGSGGS	13,043	XMRV6_A1Z651_3mut
EAAAKPAPGGG	13,044	KORV_Q9TTC1-Pro_3mutA
GGGPAPEAAAK	13,045	FLV_P10273_3mutA
GGSPAPEAAAK	13,046	MLVMS_P03355_3mutA_WS
GGSGGSGGSGGSGGS	13,047	MLVFF_P26809_3mut
EAAAKGGSGSS	13,048	MLVMS_P03355_PLV919
GGGEAAAKGGS	13,049	MLVBM_Q7SVK7_3mutA_WS
PAPAPAPAP	13,050	BAEVM_P10272_3mutA
EAAAKEAAAKEAAAKEAAAK	13,051	MLVMS_P03355_3mut
EAAAKPAP	13,052	XMRV6_A1Z651_3mut
EAAAKEAAAK	13,053	MLVBM_Q7SVK7_3mutA_WS
EAAAKGGG	13,054	BAEVM_P10272_3mut
EAAAKGSS	13,055	MLVAV_P03356_3mutA
EAAAKEAAAKEAAAKEAAAKEAAAKEAAAK	13,056	MLVFF_P26809_3mut
GGGPAPGSS	13,057	PERV_Q4VFZ2_3mutA_WS
GGGG	13,058	PERV_Q4VFZ2_3mut
EAAAKGGSGSS	13,059	MLVMS_P03355_PLV919
GGGGSGGGGSGGGGS	13,060	MLVMS_P03355_3mutA_WS
EAAAK	13,061	MLVMS_P03355_3mutA_WS
GGGGSS	13,062	PERV_Q4VFZ2
PAPEAAAKGGS	13,063	MLVCB_P08361_3mut
GSS		MLVMS_P03355_3mut
GSAGSAAGSGEF	13,065	MLVFF_P26809_3mutA
EAAAKEAAAKEAAAKEAAAKEAAAKEAAAK	13,066	KORV_Q9TTC1-Pro_3mut
GGGGSGGGGS	13,067	AVIRE_P03360_3mutA
EAAAK	13,068	MLVMS_P03355_3mut
GGGPAPGGS	13,069	PERV_Q4VFZ2_3mut

Linker amino acid sequence	SEQ ID NO:	RT domain name
GGGGSGGGGSGGGGS	13,070	MLVMS_P03355_PLV919
PAPGGG	13,071	MLVMS_P03355_3mutA_WS
GGGEAAAKPAP	13,072	PERV_Q4VFZ2_3mutA_WS
EAAAKPAPGSS	13,073	KORV_Q9TTC1-Pro_3mutA
PAPGSS	13,074	KORV_Q9TTC1_3mutA
GSAGSAAGSGEF	13,075	PERV_Q4VFZ2_3mut
PAPGGGGSS	13,076	KORV_Q9TTC1-Pro_3mutA
GSSGGGEAAAK	13,077	MLVCB_P08361_3mutA
GSS		AVIRE_P03360_3mutA
GSSGSSGSSGSS	13,079	XMRV6_A1Z651_3mutA
PAPEAAAKGGG	13,080	MLVMS_P03355_PLV919
GGGPAPEAAAK	13,081	MLVCB_P08361_3mutA
PAPGGGGGS	13,082	MLVCB_P08361_3mutA
EAAAKEAAAKEAAAKEAAAK	13,083	PERV_Q4VFZ2_3mutA_WS
GGGGGSPAP	13,084	MLVFF_P26809_3mutA
GSSGSSGSSGSSGSS	13,085	PERV_Q4VFZ2
GSSPAPEAAAK	13,086	MLVMS_P03355_PLV919
GSSGSSGSSGSSGSSGSS	13,087	MLVBM_Q7SVK7_3mutA_WS
GSSGSSGSSGSSGSSGSS	13,088	MLVMS_P03355_3mutA_WS
GGSPAPEAAAK	13,089	MLVAV_P03356_3mutA
GSSGGG	13,090	BAEVM_P10272_3mut
EAAAKGSSGGS	13,091	KORV_Q9TTC1-Pro_3mutA
GGSGSSEAAAK	13,092	MLVMS_P03355_3mutA_WS
GGGPAPEAAAK	13,093	MLVFF_P26809_3mutA
GGGPAPGGS	13,094	MLVMS_P03355_3mutA_WS
GGGGG	13,095	MLVMS_P03355_PLV919
GGGEAAAKPAP	13,096	MLVBM_Q7SVK7_3mutA_WS
GGGGSGGGGS	13,097	WMSV_P03359_3mut
GGGPAPEAAAK	13,098	PERV_Q4VFZ2_3mut
GGSGSSEAAAK	13,099	MLVMS_P03355_PLV919
EAAAKGGGPAP	13,100	MLVMS_P03355_3mutA_WS
GSSGSSGSSGSSGSS	13,101	KORV_Q9TTC1-Pro_3mutA
PAPAP	13,102	WMSV_P03359_3mutA
GGSPAPGSS	13,103	MLVAV_P03356_3mutA
GGSGGGPAP	13,104	MLVMS_P03355_3mut
GGSPAP	13,105	MLVMS_P03355_PLV919
EAAAKGGSPAP	13,106	PERV_Q4VFZ2_3mut
GSSPAPGGG	13,107	KORV_Q9TTC1-Pro_3mutA
GSAGSAAGSGEF	13,108	MLVMS_P03355_3mut
GGSPAP	13,109	PERV_Q4VFZ2_3mut

Linker amino acid sequence	SEQ ID NO:	RT domain name
GSSGSS	13,110	KORV_Q9TTC1-Pro_3mut
GGGPAPGSS	13,111	MLVMS_P03355_3mutA_WS
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PAPGSSGGG	13,113	MLVMS_P03355_PLV919
GGSEAAAKPAP	13,114	BAEVM_P10272_3mutA
GGGGGS	13,115	MLVCB_P08361_3mutA
PAPEAAAKGGS	13,116	MLVMS_P03355_3mutA_WS
EAAAKEAAAKEAAAKEAAAKEAAAKEAAAK	13,117	BAEVM_P10272_3mutA
GGSEAAAK	13,118	BAEVM_P10272_3mutA
GSSPAPEAAAK	13,119	MLVMS_P03355_3mutA_WS
PAPGGG	13,120	WMSV_P03359_3mut
EAAAKPAP	13,121	PERV_Q4VFZ2_3mut
GSSGSSGSSGSSGSS	13,122	WMSV_P03359_3mut
PAPGGG	13,123	MLVBM_Q7SVK7_3mutA_WS
GGSGGGEAAAK	13,124	BAEVM_P10272_3mutA
PAPGGS	13,125	MLVMS_P03355_3mut
GGSGGSGGSGGS	13,126	MLVBM_Q7SVK7_3mutA_WS
EAAAKEAAAKEAAAKEAAAK	13,127	PERV_Q4VFZ2_3mut
GGSEAAAKGGG	13,128	WMSV_P03359_3mutA
GGGPAP	13,129	BAEVM_P10272_3mutA
GGGGSGGGGSGGGGSGGGGSGGGGSGGGGS	13,130	XMRV6_A1Z651_3mut
GGSPAPGSS	13,131	KORV_Q9TTC1_3mut
GGGPAPGSS	13,132	MLVMS_P03355_3mut
GGGGSSGGS	13,133	BAEVM_P10272_3mutA
GGGEAAAKGSS	13,134	KORV_Q9TTC1-Pro_3mutA
PAPAP	13,135	MLVBM_Q7SVK7_3mutA_WS
GGSPAPGGG	13,136	PERV_Q4VFZ2_3mut
PAPGSS	13,137	PERV_Q4VFZ2_3mutA_WS
GSSGGSPAP	13,138	MLVBM_Q7SVK7_3mutA_WS
EAAAKGGGGSEAAAK	13,139	PERV_Q4VFZ2_3mut
GSSEAAAKGGS	13,140	KORV_Q9TTC1-Pro_3mut
PAPAPAPAP	13,141	KORV_Q9TTC1-Pro_3mutA
GGSEAAAKPAP	13,142	WMSV_P03359_3mutA
PAPGGS	13,143	FLV_P10273_3mutA
EAAAKGGGPAP	13,144	PERV_Q4VFZ2_3mut
GGSGSSGGG	13,145	AVIRE_P03360_3mutA
EAAAKGGSGSS	13,146	BAEVM_P10272_3mutA
SGGSSGGSSGSETPGTSESATPESSGGSSGGSS	13,147	MLVCB_P08361_3mutA
GSSEAAAKGGS	13,148	XMRV6_A1Z651_3mutA
GGGGG	13,149	BAEVM_P10272_3mutA

Linker amino acid sequence	SEQ ID NO:	RT domain name
GGGGSGGGGSGGGGSGGGGSGGGGSGGGGS	13,150	SFV3L_P27401_2mutA
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EAAAKGGGGSEAAAK	13,152	KORV_Q9TTC1_3mutA
EAAAKGGG	13,153	AVIRE_P03360_3mut
GGSGGG	13,154	MLVMS_P03355_3mutA_WS
GGSGSSGGG	13,155	MLVMS_P03355_PLV919
GGGGSGGGGSGGGGSGGGGSGGGGSGGGGS	13,156	KORV_Q9TTC1_3mut
GGGGSEAAAKGGGGS	13,157	KORV_Q9TTC1_3mutA
PAPAPAPAPAP	13,158	FLV_P10273_3mutA
GGS		MLVBM_Q7SVK7_3mutA_WS
GGGGGSEAAAK	13,160	MLVBM_Q7SVK7_3mutA_WS
GSSGSSGSSGSSGSS	13,161	MLVMS_P03355_3mutA_WS
EAAAKEAAAKEAAAKEAAAKEAAAK	13,162	MLVMS_P03355_3mut
GGSGSSGGG	13,163	PERV_Q4VFZ2_3mut
PAP		MLVFF_P26809_3mut
GSSPAPEAAAK	13,165	MLVAV_P03356_3mutA
EAAAKGGGGSS	13,166	MLVMS_P03355_3mut
GGGEAAAKGGS	13,167	XMRV6_A1Z651_3mut
GGSGGGPAP	13,168	MLVBM_Q7SVK7_3mutA_WS
GSAGSAAGSGEF	13,169	BAEVM_P10272_3mutA
GSSEAAAK	13,170	MLVCB_P08361_3mut
PAPGSS	13,171	MLVMS_P03355_3mut
EAAAKEAAAKEAAAK	13,172	MLVAV_P03356_3mutA
GSAGSAAGSGEF	13,173	XMRV6_A1Z651_3mutA
GSSGSSGSSGSS	13,174	BAEVM_P10272_3mutA
AEAAAKEAAAKEAAAKEAAAKALEAEAAAKEAAAKEAAAKEAAAKA	13,175	KORV_Q9TTC1-Pro_3mut
GGGGSSEAAAK	13,176	WMSV_P03359_3mut
GSSGGGEAAAK	13,177	MLVBM_Q7SVK7_3mutA_WS
EAAAKPAP	13,178	MLVFF_P26809_3mutA
GGSPAPGGG	13,179	KORV_Q9TTC1_3mutA
PAPEAAAK	13,180	FLV_P10273_3mutA
GSSGSSGSS	13,181	MLVBM_Q7SVK7_3mutA_WS
GSSGGGEAAAK	13,182	FLV_P10273_3mutA
GGSPAP	13,183	MLVBM_Q7SVK7_3mutA_WS
GSAGSAAGSGEF	13,184	KORV_Q9TTC1-Pro_3mutA
PAPGGSEAAAK	13,185	MLVMS_P03355_PLV919
GGSPAPEAAAK	13,186	MLVBM_Q7SVK7_3mutA_WS
GGGGGSPAP	13,187	MLVBM_Q7SVK7_3mutA_WS
EAAAKGSSPAP	13,188	WMSV_P03359_3mut
EAAAKGGGPAP	13,189	MLVBM_Q7SVK7_3mutA_WS

Linker amino acid sequence	SEQ ID NO:	RT domain name
PAPGSS	13,190	KORV_Q9TTC1-Pro_3mutA
GGSGSSGGG	13,191	BAEVM_P10272_3mut
SGGSSGGSSGSETPGTSESATPESSGGSSGGSS	13,192	FFV_O93209-Pro_2mut
GGSGGSGGSGGSGGSGGS	13,193	WMSV_P03359_3mutA
GGSGGSGGS	13,194	PERV_Q4VFZ2_3mutA_WS
GGGGG	13,195	PERV_Q4VFZ2_3mutA_WS
GGGPAP	13,196	FLV_P10273_3mutA
PAPGGSGGG	13,197	XMRV6_A1Z651_3mutA
GGGGSEAAAKGGGGS	13,198	XMRV6_A1Z651_3mut
EAAAKGSSGGG	13,199	KORV_Q9TTC1-Pro_3mutA
GSSGGSEAAAK	13,200	WMSV_P03359_3mut
EAAAKGGSGSS	13,201	PERV_Q4VFZ2_3mut
PAPAPAPAPAP	13,202	PERV_Q4VFZ2_3mut
GGGGSGGGGSGGGGSGGGGSGGGGSGGGGS	13,203	MLVMS_P03355_3mutA_WS
GGGGGGG	13,204	KORV_Q9TTC1_3mutA
EAAAK	13,205	KORV_Q9TTC1-Pro_3mutA
GGGEAAAKGGS	13,206	KORV_Q9TTC1-Pro_3mutA
GGGEAAAKGGS	13,207	PERV_Q4VFZ2_3mutA_WS
GGGGGSPAP	13,208	XMRV6_A1Z651_3mut
GGGGSGGGGSGGGGSGGGGS	13,209	MLVFF_P26809_3mut
GGGGGGG	13,210	MLVFF_P26809_3mut
PAPAPAPAPAPAP	13,211	AVIRE_P03360_3mutA
GSSPAPGGG	13,212	FLV_P10273_3mutA
GGGGGSPAP	13,213	MLVMS_P03355_3mutA_WS
GGGGSGGGGSGGGGS	13,214	MLVMS_P03355_3mut
GGGGSGGGGSGGGGS	13,215	KORV_Q9TTC1_3mut
GSSEAAAKGGS	13,216	MLVAV_P03356_3mutA
GSSGSSGSSGSSGSS	13,217	MLVMS_P03355_3mut
EAAAKGGGGGS	13,218	PERV_Q4VFZ2_3mutA_WS
GSSGGGGGS	13,219	PERV_Q4VFZ2_3mut
GGGEAAAKPAP	13,220	MLVMS_P03355_3mut
GSSGGSPAP	13,221	PERV_Q4VFZ2_3mutA_WS
GSSGGGPAP	13,222	BAEVM_P10272_3mutA
GGGGGSGSS	13,223	MLVMS_P03355_PLV919
AEAAAKEAAAKEAAAKEAAAKALEAEAAAKEAAAKEAAAKEAAAKA	13,224	BAEVM_P10272_3mut
PAPEAAAK	13,225	MLVMS_P03355_3mut
GGGGSGGGGSGGGGS	13,226	FLV_P10273_3mutA
GGSGSSGGG	13,227	WMSV_P03359_3mutA
EAAAKGGS	13,228	PERV_Q4VFZ2_3mut
EAAAKGSSPAP	13,229	MLVCB_P08361_3mut

Linker amino acid sequence	SEQ ID NO:	RT domain name
EAAAKGGSGSS	13,230	WMSV_P03359_3mutA
GSSGSS	13,231	PERV_Q4VFZ2_3mutA_WS
PAPAPAPAP	13,232	MLVMS_P03355_PLV919
GGSGGG	13,233	PERV_Q4VFZ2_3mutA_WS
GSS		MLVBM_Q7SVK7_3mutA_WS
PAP		KORV_Q9TTC1-Pro_3mutA
GGSGSSEAAAK	13,236	MLVFF_P26809_3mut
PAPEAAAKGSS	13,237	KORV_Q9TTC1-Pro_3mutA
GGSGGS	13,238	MLVCB_P08361_3mutA
GGGGGGG	13,239	PERV_Q4VFZ2_3mutA_WS
GGSPAPEAAAK	13,240	MLVBM_Q7SVK7_3mut
EAAAKEAAAKEAAAKEAAAKEAAAKEAAAK	13,241	KORV_Q9TTC1_3mutA
GGSPAP	13,242	MLVMS_P03355_3mut
GGSEAAAKGGG	13,243	PERV_Q4VFZ2_3mut
GGGGSGGGGS	13,244	FLV_P10273_3mutA
GGGEAAAK	13,245	BAEVM_P10272_3mutA
GGGGSGGGGSGGGGSGGGGSGGGGSGGGGS	13,246	SFV3L_P27401_2mut
GGSEAAAKPAP	13,247	KORV_Q9TTC1-Pro_3mutA
GSSGGGEAAAK	13,248	MLVMS_P03355_PLV919
GGGGGSEAAAK	13,249	MLVMS_P03355_PLV919
EAAAKGGSGGG	13,250	MLVMS_P03355_3mutA_WS
GGGGSSPAP	13,251	MLVAV_P03356_3mutA
EAAAKEAAAK	13,252	MLVMS_P03355_3mutA_WS
AEAAAKEAAAKEAAAKEAAAKALEAEAAAKEAAAKEAAAKEAAAKA	13,253	SFV3L_P27401_2mut
GSSGSSGSSGSSGSS	13,254	MLVMS_P03355_PLV919
GSSGGG	13,255	KORV_Q9TTC1-Pro_3mutA
GSSGGS	13,256	MLVFF_P26809_3mutA
GGGGSGGGGS	13,257	XMRV6_A1Z651_3mutA
PAPGSS	13,258	MLVBM_Q7SVK7_3mutA_WS
GGGPAPEAAAK	13,259	XMRV6_A1Z651_3mutA
EAAAKGGS	13,260	MLVFF_P26809_3mut
GSS		KORV_Q9TTC1_3mutA
GGGG	13,262	PERV_Q4VFZ2_3mut
GGGGGSEAAAK	13,263	AVIRE_P03360_3mutA
GSSGSSGSSGSSGSS	13,264	MLVMS_P03355_PLV919
PAPGGSGGG	13,265	PERV_Q4VFZ2_3mut
GGGPAP	13,266	PERV_Q4VFZ2_3mut
GGGPAPEAAAK	13,267	AVIRE_P03360_3mutA
GGGEAAAK	13,268	MLVCB_P08361_3mut
GGG		MLVFF_P26809_3mutA

Linker amino acid sequence	SEQ ID NO:	RT domain name
EAAAKPAPGSS	13,270	XMRV6_A1Z651_3mutA
GGSGSSEAAAK	13,271	PERV_Q4VFZ2_3mutA_WS
EAAAKGSS	13,272	MLVMS_P03355_3mut
GGSGSSEAAAK	13,273	BAEVM_P10272_3mut
GGSGGG	13,274	MLVBM_Q7SVK7_3mutA_WS
GGGPAP	13,275	MLVMS_P03355_PLV919
GGSPAPGGG	13,276	PERV_Q4VFZ2_3mutA_WS
GGGGGSEAAAK	13,277	MLVFF_P26809_3mutA
EAAAKGSSGGS	13,278	MLVBM_Q7SVK7_3mut
PAPAP	13,279	XMRV6_A1Z651_3mut
GSSPAPGGS	13,280	MLVBM_Q7SVK7_3mutA_WS
GSSEAAAKGGG	13,281	WMSV_P03359_3mutA
EAAAKGGGGGS	13,282	PERV_Q4VFZ2_3mut
GSSGSSGSSGSSGSS	13,283	MLVCB_P08361_3mutA
EAAAKGGGGSS	13,284	PERV_Q4VFZ2_3mut
EAAAKGSS	13,285	PERV_Q4VFZ2_3mut
EAAAKEAAAKEAAAKEAAAKEAAAKEAAAK	13,286	AVIRE_P03360_3mutA
EAAAKGGS	13,287	MLVCB_P08361_3mut
GSSGGSEAAAK	13,288	MLVAV_P03356_3mutA
EAAAKPAPGGS	13,289	PERV_Q4VFZ2_3mut
GGSGGS	13,290	MLVAV_P03356_3mutA
EAAAKGSSGGG	13,291	AVIRE_P03360_3mutA
GGSGGSGGSGGS	13,292	PERV_Q4VFZ2_3mut
GGGGGGGG	13,293	KORV_Q9TTC1_3mutA
GGSGSSEAAAK	13,294	MLVCB_P08361_3mutA
EAAAKGGG	13,295	MLVBM_Q7SVK7_3mutA_WS
GGGGSGGGGSGGGGS	13,296	MLVCB_P08361_3mut
GGSGGSGGSGGS	13,297	PERV_Q4VFZ2_3mutA_WS
PAPAPAPAPAP	13,298	WMSV_P03359_3mut
EAAAKEAAAKEAAAKEAAAK	13,299	PERV_Q4VFZ2_3mut
GGSGGSGGS	13,300	XMRV6_A1Z651_3mutA
PAPGGGGSS	13,301	BAEVM_P10272_3mutA
GSSEAAAKGGS	13,302	MLVCB_P08361_3mut
GSSGGGPAP	13,303	MLVCB_P08361_3mutA
GGSGSS	13,304	MLVBM_Q7SVK7_3mutA_WS
GGGGGSEAAAK	13,305	MLVAV_P03356_3mutA
GSSEAAAK	13,306	PERV_Q4VFZ2_3mutA_WS
GGGGGSGSS	13,307	MLVBM_Q7SVK7_3mutA_WS
EAAAKGGSGSS	13,308	MLVFF_P26809_3mut
PAP		FLV_P10273_3mutA

Linker amino acid sequence	SEQ ID NO:	RT domain name
GGGGG	13,310	MLVMS_P03355_3mutA_WS
EAAAK	13,311	PERV_Q4VFZ2_3mut
GSS		FLV_P10273_3mutA
PAPAPAPAPAPAP	13,313	KORV_Q9TTC1-Pro_3mutA
EAAAKEAAAKEAAAKEAAAK	13,314	MLVCB_P08361_3mut
EAAAKGGGGSEAAAK	13,315	XMRV6_A1Z651_3mut
PAPGGSGGG	13,316	MLVBM_Q7SVK7_3mutA_WS
GGSGGGPAP	13,317	WMSV_P03359_3mutA
GGGGSSEAAAK	13,318	MLVBM_Q7SVK7_3mutA_WS
PAPGGGGSS	13,319	MLVCB_P08361_3mut
GGSGGSGGSGGS	13,320	PERV_Q4VFZ2_3mutA_WS
PAPGGSGGG	13,321	MLVMS_P03355_3mutA_WS
GSSPAPGGS	13,322	MLVCB_P08361_3mutA
GSSGSSGSS	13,323	MLVFF_P26809_3mut
PAPGGGGGS	13,324	MLVBM_Q7SVK7_3mutA_WS
GSSPAP	13,325	PERV_Q4VFZ2_3mut
GGSGGG	13,326	KORV_Q9TTC1-Pro_3mut
EAAAKGGGGSEAAAK	13,327	PERV_Q4VFZ2_3mutA_WS
GGSPAPEAAAK	13,328	PERV_Q4VFZ2_3mutA_WS
EAAAKPAP	13,329	BAEVM_P10272_3mut
GGGGSGGGGSGGGGSGGGGSGGGGSGGGGS	13,330	MLVMS_P03355_3mut
EAAAKGGGGSS	13,331	MLVFF_P26809_3mut
EAAAKEAAAK	13,332	MLVCB_P08361_3mut
GSSEAAAKGGS	13,333	PERV_Q4VFZ2_3mut
GGSPAP	13,334	KORV_Q9TTC1-Pro_3mutA
EAAAKEAAAKEAAAKEAAAK	13,335	MLVMS_P03355_3mutA_WS
GSSGSSGSSGSSGSS	13,336	BAEVM_P10272_3mut
PAPEAAAK	13,337	MLVMS_P03355_3mut
GSSGGSPAP	13,338	PERV_Q4VFZ2
GGGPAPGGS	13,339	BAEVM_P10272_3mutA
EAAAKPAPGGS	13,340	MLVMS_P03355_PLV919
GGGGSGGGGS	13,341	PERV_Q4VFZ2
GGGEAAAK	13,342	KORV_Q9TTC1-Pro_3mut
EAAAKGGGGGS	13,343	FLV_P10273_3mutA
GGSPAPGSS	13,344	MLVMS_P03355_3mut
GSSPAPEAAAK	13,345	MLVMS_P03355_3mutA_WS
GSAGSAAGSGEF	13,346	MLVBM_Q7SVK7_3mutA_WS
EAAAK	13,347	BAEVM_P10272_3mutA
EAAAKGGGGSS	13,348	BAEVM_P10272_3mutA
GGG		WMSV_P03359_3mut

Linker amino acid sequence	SEQ ID NO:	RT domain name
GGSGSSPAP	13,350	BAEVM_P10272_3mut
GGSEAAAKPAP	13,351	MLVBM_Q7SVK7_3mutA_WS
EAAAKGGSGSS	13,352	MLVCB_P08361_3mut
PAPGSS	13,353	MLVAV_P03356_3mutA
PAPEAAAKGGG	13,354	MLVCB_P08361_3mutA
AEAAAKEAAAKEAAAKEAAAKALEAEAAAKEAAAKEAAAKEAAAKA	13,355	FOAMV_P14350-Pro_2mut
GSSGSSGSS	13,356	PERV_Q4VFZ2_3mut
PAPGGG	13,357	MLVMS_P03355_3mut
PAPGGS	13,358	PERV_Q4VFZ2_3mut
GSSGGG	13,359	MLVMS_P03355_PLV919
GSSGSSGSSGSSGSSGSS	13,360	WMSV_P03359_3mut
PAP		AVIRE_P03360_3mutA
EAAAKGSSPAP	13,362	MLVBM_Q7SVK7_3mutA_WS
GSSGSSGSSGSS	13,363	MLVMS_P03355_PLV919
GGGGSGGGGSGGGGSGGGGSGGGGS	13,364	AVIRE_P03360
GGGGS	13,365	PERV_Q4VFZ2_3mut
EAAAKGSSGGG	13,366	MLVBM_Q7SVK7_3mutA_WS
GGGGGG	13,367	KORV_Q9TTC1-Pro_3mut
GGSGSSEAAAK	13,368	PERV_Q4VFZ2_3mut
GSSPAPEAAAK	13,369	MLVBM_Q7SVK7_3mutA_WS
GGGGSGGGGS	13,370	MLVBM_Q7SVK7_3mutA_WS
GSSGGGGGS	13,371	MLVAV_P03356_3mutA
GSAGSAAGSGEF	13,372	WMSV_P03359_3mutA
GGGEAAAKGSS	13,373	BAEVM_P10272_3mutA
AEAAAKEAAAKEAAAKEAAAKALEAEAAAKEAAAKEAAAKEAAAKA	13,374	FFV_O93209-Pro_2mut
PAPGGSGGG	13,375	MLVCB_P08361_3mutA
EAAAKEAAAKEAAAKEAAAKEAAAK	13,376	SFV3L_P27401_2mut
GGSGSSPAP	13,377	MLVMS_P03355_PLV919
GGGGGG	13,378	PERV_Q4VFZ2_3mut
EAAAKEAAAKEAAAKEAAAKEAAAK	13,379	PERV_Q4VFZ2_3mut
EAAAKGSSPAP	13,380	MLVFF_P26809_3mut
GGGPAPGGS	13,381	MLVBM_Q7SVK7_3mutA_WS
AEAAAKEAAAKEAAAKEAAAKALEAEAAAKEAAAKEAAAKEAAAKA	13,382	SFV3L_P27401
PAP		PERV_Q4VFZ2_3mut
EAAAKGGS	13,384	MLVMS_P03355_PLV919
GSSGGSEAAAK	13,385	WMSV_P03359_3mutA
GGSGSSEAAAK	13,386	KORV_Q9TTC1-Pro_3mutA
EAAAKEAAAKEAAAK	13,387	PERV_Q4VFZ2
GGSGGGEAAAK	13,388	MLVMS_P03355_3mutA_WS
GGGGSGGGGSGGGGSGGGGS	13,389	BAEVM_P10272_3mut

Linker amino acid sequence	SEQ ID NO:	RT domain name
EAAAKGSS	13,390	XMRV6_A1Z651_3mutA
GSSGGGGGS	13,391	WMSV_P03359_3mutA
GSSGSSGSSGSSGSSGSS	13,392	MLVFF_P26809_3mutA
GGSGSS	13,393	MLVAV_P03356_3mutA
EAAAKGGGGSEAAAK	13,394	MLVMS_P03355_PLV919
EAAAKGGGPAP	13,395	PERV_Q4VFZ2
GGSEAAAKGGG	13,396	MLVAV_P03356_3mutA
EAAAKEAAAKEAAAKEAAAKEAAAKEAAAK	13,397	MLVBM_Q7SVK7_3mut
EAAAKEAAAKEAAAKEAAAKEAAAKEAAAK	13,398	KORV_Q9TTC1-Pro_3mutA
GSSPAPEAAAK	13,399	MLVFF_P26809_3mutA
GGGGSEAAAKGGGGS	13,400	PERV_Q4VFZ2_3mut
GSSGSSGSSGSS	13,401	PERV_Q4VFZ2_3mut
GGSEAAAK	13,402	MLVFF_P26809_3mutA
GGGGGGGG	13,403	MLVMS_P03355_3mut
GSSGGG	13,404	XMRV6_A1Z651_3mutA
EAAAKGGS	13,405	BAEVM_P10272_3mutA
GGGGS	13,406	BAEVM_P10272_3mutA
GGSEAAAKGGG	13,407	KORV_Q9TTC1-Pro_3mutA
GGSGSSGGG	13,408	KORV_Q9TTC1_3mutA
GGSGSSEAAAK	13,409	WMSV_P03359_3mut
EAAAKGGSGSS	13,410	MLVBM_Q7SVK7_3mutA_WS
GGS		BAEVM_P10272_3mutA
GGGPAPGSS	13,412	WMSV_P03359_3mutA
GSSGSSGSSGSSGSS	13,413	AVIRE_P03360_3mut
GGGEAAAKPAP	13,414	XMRV6_A1Z651_3mut
GSSGGG	13,415	MLVFF_P26809_3mutA
GGSPAPGSS	13,416	PERV_Q4VFZ2_3mut
PAPGGS	13,417	MLVCB_P08361_3mut
PAPAPAPAPAP	13,418	KORV_Q9TTC1_3mutA
GSSGGS	13,419	MLVCB_P08361_3mutA
GSSGGSEAAAK	13,420	PERV_Q4VFZ2_3mut
EAAAKGSSGGS	13,421	MLVMS_P03355_PLV919
EAAAKGGG	13,422	WMSV_P03359_3mut
PAPGGGGGS	13,423	BAEVM_P10272_3mutA
GGGGSEAAAKGGGGS	13,424	WMSV_P03359_3mutA
EAAAKEAAAKEAAAKEAAAKEAAAKEAAAK	13,425	MLVMS_P03355_3mutA_WS
GGS		KORV_Q9TTC1-Pro_3mutA
GSSGGSPAP	13,427	BAEVM_P10272_3mutA
GGG		MLVMS_P03355_PLV919
PAPGSS	13,429	KORV_Q9TTC1-Pro_3mut

Linker amino acid sequence	SEQ ID NO:	RT domain name
GGSEAAAKGGG	13,430	FLV_P10273_3mutA
GGSEAAAKPAP	13,431	PERV_Q4VFZ2_3mutA_WS
GGGGSSPAP	13,432	XMRV6_A1Z651_3mutA
EAAAKEAAAKEAAAKEAAAKEAAAK	13,433	PERV_Q4VFZ2_3mutA_WS
GGGG	13,434	PERV_Q4VFZ2_3mutA_WS
GGSEAAAKPAP	13,435	MLVMS_P03355_3mut
PAPGSSGGG	13,436	MLVMS_P03355_3mutA_WS
PAPEAAAKGGS	13,437	AVIRE_P03360_3mut
GGGGSSPAP	13,438	MLVMS_P03355_3mutA_WS
GGGGSGGGGSGGGGSGGGGS	13,439	PERV_Q4VFZ2_3mut
GGGEAAAK	13,440	MLVMS_P03355_3mut
GGGGSS	13,441	MLVFF_P26809_3mut
GGSPAPGSS	13,442	XMRV6_A1Z651_3mut
GGGGS	13,443	KORV_Q9TTC1-Pro_3mutA
EAAAKGSSGGS	13,444	FLV_P10273_3mutA
GSS		MLVMS_P03355_PLV919
GGGG	13,446	MLVMS_P03355_PLV919
GSSGGS	13,447	MLVMS_P03355_PLV919
GGSGGSGGSGGS	13,448	MLVMS_P03355_3mut
PAPEAAAKGGS	13,449	MLVMS_P03355_3mut
EAAAKGSSGGG	13,450	BAEVM_P10272_3mutA
GSSEAAAK	13,451	KORV_Q9TTC1-Pro_3mutA
GSAGSAAGSGEF	13,452	KORV_Q9TTC1_3mutA
GGGGGSEAAAK	13,453	MLVCB_P08361_3mut
GGGG	13,454	WMSV_P03359_3mut
GGGGSSEAAAK	13,455	MLVMS_P03355_PLV919
PAPGGG	13,456	WMSV_P03359_3mutA
EAAAKGGSGGG	13,457	MLVAV_P03356_3mutA
GGGPAPGGS	13,458	MLVMS_P03355_3mut
EAAAKPAP	13,459	PERV_Q4VFZ2_3mutA_WS
GSSGSSGSS	13,460	KORV_Q9TTC1-Pro_3mutA
GSSPAPGGS	13,461	XMRV6_A1Z651_3mut
GGGGGSPAP	13,462	BAEVM_P10272_3mutA
GGSGSSGGG	13,463	PERV_Q4VFZ2_3mutA_WS
GGGEAAAKGSS	13,464	AVIRE_P03360_3mut
GSSEAAAK	13,465	FLV_P10273_3mutA
EAAAK	13,466	MLVMS_P03355_3mut
EAAAKGGSGSS	13,467	WMSV_P03359_3mut
GSSEAAAKGGG	13,468	PERV_Q4VFZ2_3mut
PAPGSSGGG	13,469	BAEVM_P10272_3mutA

Linker amino acid sequence	SEQ ID NO:	RT domain name
EAAAKGGGGGS	13,470	MLVMS_P03355_3mut
GGSEAAAKPAP	13,471	AVIRE_P03360_3mut
GGGPAPGGS	13,472	XMRV6_A1Z651_3mut
GGGGS	13,473	KORV_Q9TTC1_3mutA
GGSGGSGGSGGSGGS	13,474	XMRV6_A1Z651_3mut
GGGPAP	13,475	KORV_Q9TTC1-Pro_3mut
EAAAKPAP	13,476	MLVBM_Q7SVK7_3mutA_WS
GGSEAAAK	13,477	MLVMS_P03355_PLV919
GSSEAAAKPAP	13,478	KORV_Q9TTC1-Pro_3mutA
GGSGSS	13,479	MLVMS_P03355_3mut
EAAAKPAPGGG	13,480	PERV_Q4VFZ2_3mut
GGSPAPEAAAK	13,481	KORV_Q9TTC1_3mutA
GGSEAAAKGGG	13,482	AVIRE_P03360_3mutA
GGGGSEAAAKGGGGS	13,483	MLVMS_P03355_PLV919
GSSGGGEAAAK	13,484	KORV_Q9TTC1-Pro_3mutA
EAAAKGGGPAP	13,485	WMSV_P03359_3mut
GSSPAP	13,486	XMRV6_A1Z651_3mutA
AEAAAKEAAAKEAAAKEAAAKALEAEAAAKEAAAKEAAAKEAAAKA	13,487	SFV3L_P27401-Pro
GGSEAAAKGSS	13,488	MLVMS_P03355_PLV919
GSSGGSEAAAK	13,489	KORV_Q9TTC1-Pro_3mutA
GGSEAAAKGSS	13,490	KORV_Q9TTC1-Pro_3mutA
EAAAKGGG	13,491	AVIRE_P03360_3mutA
GSSGGSEAAAK	13,492	BAEVM_P10272_3mutA
GGGGSEAAAKGGGGS	13,493	KORV_Q9TTC1-Pro_3mut
PAPGSSEAAAK	13,494	MLVMS_P03355_3mut
PAPEAAAK	13,495	WMSV_P03359_3mut
PAPGGSGSS	13,496	PERV_Q4VFZ2_3mutA_WS
PAPGSS	13,497	BAEVM_P10272_3mut
PAPGGGGGS	13,498	MLVMS_P03355_3mut
EAAAKPAPGSS	13,499	MLVBM_Q7SVK7_3mutA_WS
GSSPAPGGS	13,500	MLVMS_P03355_PLV919
GGSGSSEAAAK	13,501	MLVMS_P03355_3mut
GGGGGG	13,502	KORV_Q9TTC1-Pro_3mutA
EAAAKEAAAKEAAAKEAAAK	13,503	MLVBM_Q7SVK7_3mut
GGSPAPGSS	13,504	MLVMS_P03355_PLV919
PAPAPAPAPAP	13,505	MLVCB_P08361_3mut
GGSGSSPAP	13,506	WMSV_P03359_3mutA
EAAAKGGSGGG	13,507	PERV_Q4VFZ2_3mutA_WS
GSSGSSGSSGSSGSS	13,508	PERV_Q4VFZ2_3mut
AEAAAKEAAAKEAAAKEAAAKALEAEAAAKEAAAKEAAAKEAAAKA	13,509	KORV_Q9TTC1_3mutA

Linker amino acid sequence	SEQ ID NO:	RT domain name
GSSGGGEAAAK	13,510	WMSV_P03359_3mutA
GSSGGSEAAAK	13,511	FLV_P10273_3mutA
GGGGGGGG	13,512	PERV_Q4VFZ2_3mut
PAPGGSEAAAK	13,513	FLV_P10273_3mutA
GGGGSSPAP	13,514	BAEVM_P10272_3mutA
PAPAPAPAP	13,515	WMSV_P03359_3mut
GGSEAAAKPAP	13,516	PERV_Q4VFZ2_3mut
PAPGGSGGG	13,517	BAEVM_P10272_3mutA
EAAAKEAAAKEAAAKEAAAKEAAAKEAAAK	13,518	MLVMS_P03355_3mut
GGGGSGGGGSGGGGS	13,519	PERV_Q4VFZ2_3mut
GGSGGGPAP	13,520	PERV_Q4VFZ2_3mut
GGGPAPEAAAK	13,521	MLVFF_P26809_3mut
GGGGGSGSS	13,522	MLVMS_P03355_3mutA_WS
GSS		MLVCB_P08361_3mut
GGGGGSPAP	13,524	MLVMS_P03355_PLV919
GGSPAP	13,525	MLVAV_P03356_3mutA
GGGPAPGGS	13,526	KORV_Q9TTC1-Pro_3mutA
PAPGSSGGG	13,527	FLV_P10273_3mutA
PAPGSSGGG	13,528	WMSV_P03359_3mutA
PAPGGS	13,529	MLVBM_Q7SVK7_3mutA_WS
GGGEAAAKGSS	13,530	PERV_Q4VFZ2_3mutA_WS
GGSEAAAKGSS	13,531	MLVBM_Q7SVK7_3mutA_WS
PAPGGSEAAAK	13,532	MLVCB_P08361_3mut
GGSEAAAKGGG	13,533	XMRV6_A1Z651_3mutA
GGSGGGGSS	13,534	WMSV_P03359_3mut
GGGEAAAKPAP	13,535	KORV_Q9TTC1_3mutA
EAAAKGSS	13,536	KORV_Q9TTC1-Pro_3mut
PAPEAAAKGSS	13,537	MLVFF_P26809_3mut
GSAGSAAGSGEF	13,538	PERV_Q4VFZ2_3mut
EAAAKGGGGGS	13,539	WMSV_P03359_3mut
EAAAKGSSPAP	13,540	WMSV_P03359_3mutA
GGGGSEAAAKGGGGS	13,541	XMRV6_A1Z651_3mutA
GSSEAAAKPAP	13,542	SFV3L_P27401-Pro_2mutA
GGGGGG	13,543	PERV_Q4VFZ2_3mutA_WS
PAPGGS	13,544	BAEVM_P10272_3mut
PAP		AVIRE_P03360_3mut
PAPAPAP	13,546	MLVBM_Q7SVK7_3mutA_WS
GGGG	13,547	PERV_Q4VFZ2_3mutA_WS
GSSGGSEAAAK	13,548	MLVBM_Q7SVK7_3mut
GGSGGGGSS	13,549	MLVFF_P26809_3mut

Linker amino acid sequence	SEQ ID NO:	RT domain name
GGGGSSGGS	13,550	AVIRE_P03360_3mutA
GSSPAPGGG	13,551	PERV_Q4VFZ2_3mutA_WS
GGSEAAAKPAP	13,552	MLVMS_P03355_PLV919
PAP		KORV_Q9TTC1-Pro_3mut
GSSGGS	13,554	PERV_Q4VFZ2_3mut
GGGGG	13,555	PERV_Q4VFZ2_3mut
GSSGGGPAP	13,556	FLV_P10273_3mutA
GSSEAAAKGGG	13,557	KORV_Q9TTC1-Pro_3mut
EAAAKEAAAKEAAAKEAAAKEAAAKEAAAK	13,558	MLVCB_P08361_3mut
GGSEAAAKPAP	13,559	MLVCB_P08361_3mut
PAPAPAPAPAPAP	13,560	BAEVM_P10272_3mutA
GGGGSEAAAKGGGGS	13,561	MLVMS_P03355_3mut
EAAAKPAPGSS	13,562	MLVMS_P03355_3mut
GSSGSSGSSGSSGSS	13,563	MLVBM_Q7SVK7_3mutA_WS
PAPEAAAKGSS	13,564	MLVAV_P03356_3mut
AEAAAKEAAAKEAAAKEAAAKALEAEAAAKEAAAKEAAAKEAAAKA	13,565	AVIRE_P03360_3mut
AEAAAKEAAAKEAAAKEAAAKALEAEAAAKEAAAKEAAAKEAAAKA	13,566	PERV_Q4VFZ2_3mut
GGSEAAAKGGG	13,567	PERV_Q4VFZ2_3mutA_WS
GGSGGGGSS	13,568	MLVFF_P26809_3mutA
PAPEAAAKGSS	13,569	MLVCB_P08361_3mut
GGG		PERV_Q4VFZ2_3mutA_WS
GGSGGGEAAAK	13,571	MLVMS_P03355_3mut
EAAAKGGGGSS	13,572	WMSV_P03359_3mut
GSSPAPGGG	13,573	WMSV_P03359_3mutA
EAAAKGSSGGG	13,574	PERV_Q4VFZ2_3mut
GGSGGGEAAAK	13,575	PERV_Q4VFZ2_3mutA_WS
GGSGGSGGSGGSGGS	13,576	PERV_Q4VFZ2_3mutA_WS
EAAAKPAPGGS	13,577	PERV_Q4VFZ2_3mutA_WS
GGGGGSEAAAK	13,578	PERV_Q4VFZ2_3mutA_WS
GSSPAP	13,579	MLVFF_P26809_3mut
GGGEAAAKPAP	13,580	AVIRE_P03360_3mut
GSSGGSEAAAK	13,581	MLVMS_P03355_PLV919
EAAAKPAPGGS	13,582	WMSV_P03359_3mutA
PAPGGG	13,583	KORV_Q9TTC1_3mutA
EAAAKGSSPAP	13,584	KORV_Q9TTC1-Pro_3mut
GSSPAPEAAAK	13,585	MLVFF_P26809_3mut
GGSGGGEAAAK	13,586	MLVFF_P26809_3mutA
GSSGSSGSS	13,587	WMSV_P03359_3mutA
EAAAKGGS	13,588	BAEVM_P10272_3mut
EAAAKPAPGGS	13,589	KORV_Q9TTC1_3mutA

Linker amino acid sequence	SEQ ID NO:	RT domain name
EAAAKPAPGGS	13,590	BAEVM_P10272_3mutA
GSSGGGGGS	13,591	PERV_Q4VFZ2_3mut
PAPGGGGSS	13,592	PERV_Q4VFZ2_3mut
GSSGSSGSS	13,593	WMSV_P03359_3mut
EAAAKEAAAKEAAAKEAAAK	13,594	WMSV_P03359_3mut
GGS		AVIRE_P03360_3mut
EAAAKPAPGSS	13,596	MLVFF_P26809_3mut
EAAAKGGG	13,597	KORV_Q9TTC1_3mut
PAPGSSEAAAK	13,598	MLVMS_P03355_3mut
PAPGSSGGS	13,599	MLVMS_P03355_PLV919
GSSPAPEAAAK	13,600	MLVMS_P03355_3mut
GSSGSSGSSGSSGSSGSS	13,601	WMSV_P03359_3mutA
GGGGS	13,602	BAEVM_P10272_3mut
GSSPAP	13,603	MLVMS_P03355_3mut
EAAAKGGGGSEAAAK	13,604	KORV_Q9TTC1-Pro_3mutA
EAAAKEAAAK	13,605	WMSV_P03359_3mutA
GGGGSSGGS	13,606	MLVCB_P08361_3mutA
PAPGGSEAAAK	13,607	BAEVM_P10272_3mut
EAAAKGGSPAP	13,608	MLVFF_P26809_3mut
GSSGGSGGG	13,609	MLVBM_Q7SVK7_3mutA_WS
GSSGGS	13,610	PERV_Q4VFZ2_3mut
PAPGGSGSS	13,611	PERV_Q4VFZ2_3mutA_WS
EAAAKGGSGSS	13,612	KORV_Q9TTC1-Pro_3mutA
PAPAP	13,613	MLVCB_P08361_3mut
EAAAKGSSPAP	13,614	PERV_Q4VFZ2_3mutA_WS
EAAAKPAPGGG	13,615	MLVMS_P03355_PLV919
GGGGSGGGGSGGGGSGGGGSGGGGSGGGGS	13,616	MLVBM_Q7SVK7_3mut
EAAAKGGGGSS	13,617	MLVMS_P03355_PLV919
PAPEAAAK	13,618	PERV_Q4VFZ2_3mut
EAAAKPAPGSS	13,619	BAEVM_P10272_3mutA
GGSPAP	13,620	PERV_Q4VFZ2_3mutA_WS
GGSGGS	13,621	BAEVM_P10272_3mutA
PAPEAAAKGSS	13,622	KORV_Q9TTC1_3mut
PAPGSS	13,623	MLVMS_P03355_PLV919
PAPAPAPAPAP	13,624	MLVAV_P03356_3mutA
GGG		XMRV6_A1Z651_3mutA
GGGPAP	13,626	PERV_Q4VFZ2_3mutA_WS
GSSPAPEAAAK	13,627	KORV_Q9TTC1_3mutA
PAP		BAEVM_P10272_3mutA
GGSPAP	13,629	BAEVM_P10272_3mutA

Linker amino acid sequence	SEQ ID NO:	RT domain name
PAPEAAAKGGS	13,630	MLVMS_P03355_PLV919
PAPGSSGGS	13,631	PERV_Q4VFZ2_3mutA_WS
PAPAPAPAPAPAP	13,632	PERV_Q4VFZ2_3mut
EAAAKEAAAKEAAAK	13,633	MLVCB_P08361_3mut
GGSGGSGGSGGSGGS	13,634	MLVMS_P03355_PLV919
EAAAKPAPGGS	13,635	MLVMS_P03355_3mut
GGSGGS	13,636	MLVMS_P03355_PLV919
EAAAKPAP	13,637	MLVMS_P03355_3mutA_WS
GGSEAAAK	13,638	XMRV6_A1Z651_3mutA
GGSGGG	13,639	KORV_Q9TTC1_3mut
GGSGGGEAAAK	13,640	PERV_Q4VFZ2_3mut
PAPEAAAKGGG	13,641	AVIRE_P03360
PAPAP	13,642	PERV_Q4VFZ2_3mut
GSS		KORV_Q9TTC1-Pro_3mutA
EAAAKGSSGGG	13,644	MLVAV_P03356_3mutA
GGSPAPGSS	13,645	MLVBM_Q7SVK7_3mutA_WS
PAPEAAAK	13,646	MLVAV_P03356_3mut
EAAAKGGSPAP	13,647	BAEVM_P10272_3mutA
PAPAPAPAP	13,648	WMSV_P03359_3mutA
PAPGGSEAAAK	13,649	MLVMS_P03355_3mut
GGSGGSGGSGGS	13,650	WMSV_P03359_3mut
GGGGGSGSS	13,651	XMRV6_A1Z651_3mut
PAPGGSGGG	13,652	KORV_Q9TTC1_3mutA
GGS		MLVMS_P03355_3mut
EAAAK	13,654	WMSV_P03359_3mut
GGGEAAAKGSS	13,655	MLVBM_Q7SVK7_3mutA_WS
GGSPAPGSS	13,656	MLVCB_P08361_3mut
GGSEAAAKPAP	13,657	PERV_Q4VFZ2_3mut
GGGGSGGGGSGGGGSGGGGSGGGGS	13,658	MLVCB_P08361_3mutA
GGSGSS	13,659	BAEVM_P10272_3mutA
GGGEAAAKGSS	13,660	WMSV_P03359_3mutA
EAAAKGGSPAP	13,661	WMSV_P03359_3mut
GSSPAPEAAAK	13,662	MLVMS_P03355_3mut
GGSGGSGGSGGS	13,663	MLVMS_P03355_PLV919
GSSPAPEAAAK	13,664	WMSV_P03359_3mut
GSSGSSGSSGSS	13,665	PERV_Q4VFZ2
GGSGSSEAAAK	13,666	WMSV_P03359_3mutA
GGSGGG	13,667	MLVFF_P26809_3mut
GGSPAPGGG	13,668	MLVFF_P26809_3mut
GGSGGSGGS	13,669	BAEVM_P10272_3mutA

Linker amino acid sequence	SEQ ID NO:	RT domain name
GGGGSSEAAAK	13,670	MLVBM_Q7SVK7_3mut
GGSPAPGSS	13,671	MLVMS_P03355_3mut
EAAAKPAPGSS	13,672	AVIRE_P03360_3mut
GGGGSSGGS	13,673	FLV_P10273_3mutA
GGSPAPEAAAK	13,674	PERV_Q4VFZ2_3mut
GGSEAAAK	13,675	MLVMS_P03355_3mutA_WS
GSSGSSGSSGSS	13,676	MLVCB_P08361_3mutA
EAAAKEAAAKEAAAKEAAAKEAAAK	13,677	MLVMS_P03355_PLV919
GGGGG	13,678	PERV_Q4VFZ2_3mut
GGSEAAAKGSS	13,679	MLVCB_P08361_3mutA
GSSGGG	13,680	MLVBM_Q7SVK7_3mutA_WS
PAPGSSGGG	13,681	KORV_Q9TTC1-Pro_3mutA
GGSGGS	13,682	BAEVM_P10272_3mut
EAAAKGGGGGS	13,683	MLVBM_Q7SVK7_3mutA_WS
GGSGSSPAP	13,684	MLVCB_P08361_3mut
PAPGSSGGG	13,685	KORV_Q9TTC1
PAPGGSGGG	13,686	MLVMS_P03355_3mut
GGGG	13,687	WMSV_P03359_3mutA
EAAAKGGSPAP	13,688	MLVCB_P08361_3mut
GSSGSS	13,689	FLV_P10273_3mutA
GGSEAAAKPAP	13,690	SFV3L_P27401_2mut
EAAAKGSSGGS	13,691	MLVAV_P03356_3mutA
AEAAAKEAAAKEAAAKEAAAKALEAEAAAKEAAAKEAAAKEAAAKA	13,692	MLVAV_P03356_3mutA
EAAAKGGSGSS	13,693	PERV_Q4VFZ2_3mutA_WS
GGGGG	13,694	MLVCB_P08361_3mut
GGGEAAAK	13,695	BAEVM_P10272_3mut
GGSGGSGGSGGS	13,696	MLVCB_P08361_3mut
EAAAKEAAAKEAAAKEAAAKEAAAKEAAAK	13,697	PERV_Q4VFZ2
PAPAPAPAPAP	13,698	MLVMS_P03355_3mutA_WS
EAAAKEAAAK	13,699	XMRV6_A1Z651_3mut
GSSGGSEAAAK	13,700	PERV_Q4VFZ2_3mutA_WS
PAPGGSEAAAK	13,701	KORV_Q9TTC1-Pro_3mutA
EAAAKGGGPAP	13,702	MLVBM_Q7SVK7_3mutA_WS
PAPGGSGSS	13,703	PERV_Q4VFZ2
SGSETPGTSESATPES	13,704	MLVMS_P03355_3mut
GGSGGS	13,705	MLVMS_P03355_PLV919
EAAAKGGS	13,706	FLV_P10273_3mut
GGSPAPGSS	13,707	MLVMS_P03355_3mutA_WS
EAAAKEAAAKEAAAKEAAAK	13,708	FFV_O93209_2mut
GSSGGSGGG	13,709	MLVMS_P03355_3mutA_WS

Linker amino acid sequence	SEQ ID NO:	RT domain name
PAPGSSEAAAK	13,710	WMSV_P03359_3mut
PAPAPAPAPAPAP	13,711	KORV_Q9TTC1_3mutA
GGGGSS	13,712	BAEVM_P10272_3mut
GGGGSEAAAKGGGGS	13,713	AVIRE_P03360_3mut
GSSPAPEAAAK	13,714	KORV_Q9TTC1-Pro_3mutA
PAPEAAAKGGG	13,715	MLVBM_Q7SVK7_3mut
EAAAKEAAAK	13,716	WMSV_P03359_3mut
EAAAK	13,717	SFV3L_P27401-Pro_2mutA
GSSGGSGGG	13,718	XMRV6_A1Z651_3mutA
GGGEAAAKPAP	13,719	WMSV_P03359_3mutA
GGSGGS	13,720	MLVFF_P26809_3mutA
EAAAKEAAAKEAAAKEAAAKEAAAKEAAAK	13,721	FOAMV_P14350_2mutA
GGGGG	13,722	MLVAV_P03356_3mutA
GSSGGSEAAAK	13,723	BAEVM_P10272_3mut
SGGSSGGSSGSETPGTSESATPESSGGSSGGSS	13,724	SFV1_P23074
GGSGGGPAP	13,725	MLVCB_P08361_3mut
GGSGSS	13,726	PERV_Q4VFZ2_3mut
SGSETPGTSESATPES	13,727	MLVFF_P26809_3mut
EAAAKGGSPAP	13,728	MLVMS_P03355_3mut
PAPAP	13,729	PERV_Q4VFZ2_3mut
AEAAAKEAAAKEAAAKEAAAKALEAEAAAKEAAAKEAAAKEAAAKA	13,730	MLVBM_Q7SVK7_3mut
GGGGGS	13,731	BAEVM_P10272_3mutA
EAAAKEAAAK	13,732	AVIRE_P03360_3mut
GSSGGSEAAAK	13,733	PERV_Q4VFZ2_3mut
GGGEAAAK	13,734	WMSV_P03359_3mut
GSSGGGEAAAK	13,735	AVIRE_P03360_3mutA
GGG		XMRV6_A1Z651_3mut
GGGGSEAAAKGGGGS	13,737	BAEVM_P10272_3mut
GGGG	13,738	MLVMS_P03355_3mut
GGSGGS	13,739	MLVMS_P03355_3mutA_WS
GGSGGGGSS	13,740	MLVBM_Q7SVK7_3mutA_WS
GSSPAPGGS	13,741	PERV_Q4VFZ2_3mut
GSSPAPEAAAK	13,742	PERV_Q4VFZ2_3mutA_WS
EAAAKGGS	13,743	WMSV_P03359_3mut
GGSGGSGGSGGS	13,744	PERV_Q4VFZ2_3mut
GGGGSSEAAAK	13,745	KORV_Q9TTC1-Pro_3mut
PAPAPAPAPAPAP	13,746	MLVAV_P03356_3mut
EAAAKGSSGGG	13,747	MLVMS_P03355_PLV919
GGGGG	13,748	MLVBM_Q7SVK7_3mutA_WS
AEAAAKEAAAKEAAAKEAAAKALEAEAAAKEAAAKEAAAKEAAAKA	13,749	FFV_O93209_2mutA

Linker amino acid sequence	SEQ ID NO:	RT domain name
SGGSSGGSSGSETPGTSESATPESSGGSSGGSS	13,750	KORV_Q9TTC1-Pro_3mut
GGSPAPGGG	13,751	MLVMS_P03355_3mutA_WS
GGGEAAAKGGS	13,752	MLVMS_P03355_3mut
GGGEAAAK	13,753	PERV_Q4VFZ2_3mut
PAPEAAAKGGG	13,754	MLVMS_P03355_3mut
GSSGSSGSSGSSGSSGSS	13,755	BAEVM_P10272_3mutA
AEAAAKEAAAKEAAAKEAAAKALEAEAAAKEAAAKEAAAKEAAAKA	13,756	GALV_P21414_3mutA
EAAAKGGSPAP	13,757	FFV_O93209-Pro
EAAAKEAAAK	13,758	MLVFF_P26809_3mut
GGGGSGGGGSGGGGSGGGGSGGGGSGGGGS	13,759	PERV_Q4VFZ2_3mutA_WS
GGSGGSGGSGGS	13,760	MLVAV_P03356_3mutA
EAAAKEAAAKEAAAKEAAAKEAAAK	13,761	SFV3L_P27401_2mutA
GSSGSSGSSGSSGSSGSS	13,762	BAEVM_P10272_3mut
GGGGS	13,763	MLVMS_P03355_PLV919
AEAAAKEAAAKEAAAKEAAAKALEAEAAAKEAAAKEAAAKEAAAKA	13,764	SFV1_P23074
GGGGSGGGGS	13,765	KORV_Q9TTC1-Pro_3mutA
GGGGSGGGGS	13,766	MLVMS_P03355_3mut
GGSGSS	13,767	KORV_Q9TTC1_3mutA
GSSPAPGGG	13,768	PERV_Q4VFZ2_3mut
GSSGGSPAP	13,769	PERV_Q4VFZ2_3mutA_WS
PAPGGS	13,770	PERV_Q4VFZ2_3mutA_WS
GGSPAPEAAAK	13,771	FOAMV_P14350_2mutA
GGGPAPGGS	13,772	SFV3L_P27401_2mut
PAPGSSGGG	13,773	MLVCB_P08361_3mut
GSSGGGEAAAK	13,774	AVIRE_P03360_3mut
GSSGGG	13,775	XMRV6_A1Z651_3mut
GSSGSS	13,776	PERV_Q4VFZ2_3mut
GSSGGG	13,777	MLVAV_P03356_3mutA
PAPGGGGGS	13,778	PERV_Q4VFZ2_3mut
GSSEAAAK	13,779	MLVMS_P03355_3mut
PAPGGG	13,780	FLV_P10273_3mutA
GGGGSGGGGS	13,781	PERV_Q4VFZ2_3mut
GSSGGS	13,782	MLVMS_P03355_PLV919
GGGGSGGGGS	13,783	SFV3L_P27401_2mut
EAAAKGGSGSS	13,784	FLV_P10273_3mutA
GSSEAAAKGGS	13,785	MLVMS_P03355_3mutA_WS
PAPGSSEAAAK	13,786	SFV3L_P27401_2mutA
GGGGSGGGGS	13,787	SFV3L_P27401-Pro_2mutA
PAPGSSEAAAK	13,788	PERV_Q4VFZ2_3mut
PAPGSSEAAAK	13,789	PERV_Q4VFZ2

Linker amino acid sequence	SEQ ID NO:	RT domain name
GGSPAPGGG	13,790	AVIRE_P03360_3mut
GGGGGS	13,791	PERV_Q4VFZ2_3mutA_WS
GGGGSSGGS	13,792	PERV_Q4VFZ2_3mut
PAPAPAPAP	13,793	AVIRE_P03360_3mutA
GGSGGS	13,794	WMSV_P03359_3mutA
GGGPAPGGS	13,795	PERV_Q4VFZ2_3mut
GGSGGSGGSGGSGGS	13,796	MLVMS_P03355_PLV919
GGSGGG	13,797	PERV_Q4VFZ2_3mut
EAAAKEAAAK	13,798	SFV3L_P27401_2mut
PAPGSS	13,799	XMRV6_A1Z651_3mut
GSSEAAAK	13,800	MLVFF_P26809_3mut
GGSPAPGGG	13,801	MLVMS_P03355_3mut
EAAAKGGG	13,802	WMSV_P03359_3mutA
GSSEAAAKGGS	13,803	PERV_Q4VFZ2_3mutA_WS
GSSGGSPAP	13,804	FFV_O93209
GGGGGS	13,805	KORV_Q9TTC1-Pro_3mut
GSSGGG	13,806	MLVCB_P08361_3mut
GSSGSS	13,807	MLVCB_P08361_3mutA
GGSEAAAKPAP	13,808	BAEVM_P10272_3mut
EAAAKGGGGSS	13,809	MLVCB_P08361_3mut
EAAAKPAPGGS	13,810	KORV_Q9TTC1-Pro_3mutA
GSSGSSGSSGSSGSS	13,811	MLVAV_P03356_3mutA
GGGGSEAAAKGGGGS	13,812	PERV_Q4VFZ2_3mutA_WS
GGSGSS	13,813	KORV_Q9TTC1-Pro_3mut
GSS		SFV3L_P27401-Pro_2mutA
PAPAP	13,815	BAEVM_P10272_3mut
EAAAKPAP	13,816	BAEVM_P10272
EAAAKEAAAKEAAAKEAAAKEAAAK	13,817	KORV_Q9TTC1-Pro_3mut
GGGGGGG	13,818	PERV_Q4VFZ2_3mutA_WS
GGGGS	13,819	MLVMS_P03355_3mut
GSSGGG	13,820	FLV_P10273_3mutA
PAPAPAPAPAP	13,821	FLV_P10273_3mut
EAAAKEAAAKEAAAK	13,822	WMSV_P03359_3mutA
GSSGGS	13,823	MLVBM_Q7SVK7_3mutA_WS
EAAAKPAPGGG	13,824	MLVMS_P03355_3mut
GSSPAPGGS	13,825	WMSV_P03359_3mut
PAPGSSGGG	13,826	PERV_Q4VFZ2_3mutA_WS
GSSGGG	13,827	AVIRE_P03360_3mutA
PAPGGSGSS	13,828	MLVFF_P26809_3mut
PAPGSS	13,829	PERV_Q4VFZ2_3mut

Linker amino acid sequence	SEQ ID NO:	RT domain name
GGGGGSGSS	13,830	WMSV_P03359_3mutA
EAAAKGGGGSS	13,831	MLVBM_Q7SVK7_3mutA_WS
GGGGGGG	13,832	BAEVM_P10272_3mut
PAPEAAAKGSS	13,833	MLVMS_P03355_3mut
GGSGGGEAAAK	13,834	MLVMS_P03355_PLV919
EAAAKGGGGGS	13,835	MLVCB_P08361_3mut
PAPGGS	13,836	KORV_Q9TTC1-Pro_3mut
GGGG	13,837	FLV_P10273_3mutA
EAAAKGGSGSS	13,838	MLVBM_Q7SVK7_3mutA_WS
GGGGSSGGS	13,839	MLVMS_P03355_3mutA_WS
GGGGGGGG	13,840	WMSV_P03359_3mut
GGSGSSGGG	13,841	MLVMS_P03355_PLV919
GSSEAAAKGGS	13,842	KORV_Q9TTC1-Pro_3mutA
EAAAKPAPGSS	13,843	MLVCB_P08361_3mut
GGSPAPGSS	13,844	KORV_Q9TTC1_3mutA
PAPGSSGGG	13,845	BAEVM_P10272_3mut
EAAAKPAPGSS	13,846	WMSV_P03359_3mut
GGSPAPEAAAK	13,847	XMRV6_A1Z651_3mutA
GSSPAP	13,848	FLV_P10273_3mutA
GSS		BAEVM_P10272_3mutA
EAAAKPAPGGS	13,850	FLV_P10273_3mutA
GGSGSSPAP	13,851	FLV_P10273_3mutA
PAPGSSGGS	13,852	MLVMS_P03355_3mut
GSAGSAAGSGEF	13,853	PERV_Q4VFZ2_3mutA_WS
GSSGGSEAAAK	13,854	KORV_Q9TTC1_3mutA
GSSGGS	13,855	MLVMS_P03355_3mutA_WS
EAAAKGGGGSEAAAK	13,856	SFV3L_P27401_2mut
GSSGGS	13,857	PERV_Q4VFZ2_3mutA_WS
GGSPAPEAAAK	13,858	FLV_P10273_3mut
GGSEAAAKGSS	13,859	PERV_Q4VFZ2_3mutA_WS
GSSPAPEAAAK	13,860	PERV_Q4VFZ2_3mutA_WS
GGSGSSGGG	13,861	PERV_Q4VFZ2_3mut
GGGG	13,862	AVIRE_P03360_3mutA
GGSEAAAKPAP	13,863	WMSV_P03359_3mut
GSSGGSPAP	13,864	MLVAV_P03356_3mutA
GSSGGSEAAAK	13,865	MLVMS_P03355_3mut
PAPEAAAKGGS	13,866	KORV_Q9TTC1-Pro_3mut
GGSPAP	13,867	PERV_Q4VFZ2_3mutA_WS
GGSEAAAK	13,868	MLVAV_P03356_3mutA
EAAAKGGGGSEAAAK	13,869	KORV_Q9TTC1-Pro_3mut

Linker amino acid sequence	SEQ ID NO:	RT domain name
SGGSSGGSSGSETPGTSESATPESSGGSSGGSS	13,870	MLVMS_P03355_PLV919
GSSEAAAK	13,871	KORV_Q9TTC1_3mutA
GGG		AVIRE_P03360
GGSEAAAKGSS	13,873	MLVBM_Q7SVK7_3mut
GGSEAAAKGSS	13,874	MLVMS_P03355_3mut
GGSPAPEAAAK	13,875	MLVCB_P08361_3mut
GGSGGGEAAAK	13,876	MLVCB_P08361_3mut
GGSEAAAKPAP	13,877	MLVMS_P03355_3mutA_WS
EAAAKGGSGSS	13,878	KORV_Q9TTC1-Pro_3mut
GGGEAAAKGGS	13,879	MLVCB_P08361_3mut
EAAAKGGGGSEAAAK	13,880	FLV_P10273_3mutA
GGSPAP	13,881	MLVFF_P26809_3mut
GGGGSSGGS	13,882	XMRV6_A1Z651_3mutA
PAP		MLVCB_P08361_3mut
GGS		SFV3L_P27401-Pro_2mutA
GGGGSGGGGS	13,885	MLVMS_P03355_3mut
GGGEAAAKGGS	13,886	MLVAV_P03356_3mutA
GSSGSSGSSGSSGSSGSS	13,887	MLVMS_P03355_PLV919
PAPGSS	13,888	MLVCB_P08361_3mut
GGSGGSGGS	13,889	MLVMS_P03355_PLV919
PAPGGSGGG	13,890	FLV_P10273_3mutA
GGGGSGGGGSGGGGS	13,891	FLV_P10273_3mut
GGSGSSGGG	13,892	KORV_Q9TTC1-Pro_3mutA
GGSGGSGGS	13,893	GALV_P21414_3mutA
GGGEAAAKGGS	13,894	WMSV_P03359_3mut
SGSETPGTSESATPES	13,895	KORV_Q9TTC1_3mutA
EAAAKGGGGGS	13,896	KORV_Q9TTC1-Pro_3mut
EAAAKGSSPAP	13,897	BAEVM_P10272_3mut
GGGG	13,898	MLVCB_P08361_3mut
GGGGSGGGGSGGGGSGGGGSGGGGS	13,899	MLVBM_Q7SVK7_3mut
GSSGGSGGG	13,900	MLVMS_P03355_PLV919
GGSGSS	13,901	MLVFF_P26809_3mut
EAAAKGGS	13,902	AVIRE_P03360_3mutA
GSSEAAAKGGS	13,903	MLVBM_Q7SVK7_3mutA_WS
EAAAKPAPGGG	13,904	WMSV_P03359_3mut
PAPGSSGGG	13,905	MLVCB_P08361_3mutA
GGGGSSEAAAK	13,906	KORV_Q9TTC1-Pro_3mutA
GSSEAAAKPAP	13,907	BAEVM_P10272_3mutA
PAPGGGEAAAK	13,908	MLVBM_Q7SVK7_3mutA_WS
GGSGGGEAAAK	13,909	MLVCB_P08361_3mutA

Linker amino acid sequence	SEQ ID NO:	RT domain name
GGGGSGGGGSGGGGSGGGGSGGGGSGGGGS	13,910	FFV_O93209
EAAAKGGGGGS	13,911	GALV_P21414_3mutA
GGSPAPGGG	13,912	MLVMS_P03355_3mut
GSSGSSGSS	13,913	FLV_P10273_3mutA
EAAAK	13,914	MLVBM_Q7SVK7_3mut
GGGGSSGGS	13,915	MLVMS_P03355_3mut
GGSGSSPAP	13,916	PERV_Q4VFZ2_3mut
EAAAKEAAAKEAAAKEAAAK	13,917	BAEVM_P10272_3mut
GGGPAPGSS	13,918	MLVMS_P03355_3mut
GSSPAPGGS	13,919	PERV_Q4VFZ2_3mutA_WS
PAPAP	13,920	FLV_P10273_3mutA
PAPAPAPAP	13,921	PERV_Q4VFZ2_3mut
GGGGGSEAAAK	13,922	GALV_P21414_3mutA
GGGGGSGSS	13,923	BAEVM_P10272_3mutA
GGGEAAAKGSS	13,924	KORV_Q9TTC1_3mutA
GGGGGSPAP	13,925	AVIRE_P03360_3mut
GGGGGSEAAAK	13,926	SFV3L_P27401_2mutA
GGS		KORV_Q9TTC1_3mutA
GGGGGGG	13,928	PERV_Q4VFZ2_3mut
SGSETPGTSESATPES	13,929	SFV3L_P27401_2mutA
EAAAKGGSGGG	13,930	MLVMS_P03355_3mut
GGGGS	13,931	MLVFF_P26809_3mut
EAAAKGSSGGG	13,932	BAEVM_P10272_3mut
EAAAKPAPGGS	13,933	MLVF5_P26810_3mutA
SGGSSGGSSGSETPGTSESATPESSGGSSGGSS	13,934	SFV3L_P27401_2mutA
GGSPAPGGG	13,935	WMSV_P03359_3mutA
GSAGSAAGSGEF	13,936	MLVFF_P26809_3mut
GGGGSSGGS	13,937	MLVMS_P03355_3mutA_WS
GGGGGGG	13,938	MLVCB_P08361_3mut
GSSEAAAK	13,939	WMSV_P03359_3mut
PAPGSS	13,940	FLV_P10273_3mutA
GSSGGG	13,941	PERV_Q4VFZ2_3mutA_WS
PAPGGG	13,942	MLVFF_P26809_3mut
GGGGGSPAP	13,943	MLVMS_P03355_3mut
GGSEAAAK	13,944	XMRV6_A1Z651_3mut
GSSGGG	13,945	PERV_Q4VFZ2_3mut
GGSGGSGGSGGS	13,946	MLVMS_P03355_3mut
PAPAP	13,947	AVIRE_P03360_3mut
GGSEAAAK	13,948	PERV_Q4VFZ2_3mut
GGGGS	13,949	MLVMS_P03355_PLV919

Linker amino acid sequence	SEQ ID NO:	RT domain name
GGGG	13,950	BAEVM_P10272_3mutA
EAAAKGGGGSS	13,951	MLVCB_P08361_3mutA
EAAAKEAAAKEAAAK	13,952	GALV_P21414_3mutA
PAPGGGEAAAK	13,953	KORV_Q9TTC1
EAAAKGGSPAP	13,954	MLVMS_P03355_3mut
GGSGSSEAAAK	13,955	MLVMS_P03355_3mut
GGSPAPEAAAK	13,956	FLV_P10273_3mutA
GGGGGGG	13,957	PERV_Q4VFZ2_3mut
EAAAKEAAAKEAAAKEAAAKEAAAKEAAAK	13,958	SFV1_P23074_2mutA
EAAAKGSSGGS	13,959	MLVMS_P03355_3mut
GSSEAAAKPAP	13,960	MLVFF_P26809_3mut
GGGGSS	13,961	FLV_P10273_3mutA
EAAAKGGSGGG	13,962	AVIRE_P03360_3mutA
GGSGGS	13,963	PERV_Q4VFZ2_3mutA_WS
GGGGGSPAP	13,964	AVIRE_P03360_3mutA
EAAAKEAAAKEAAAK	13,965	XMRV6_A1Z651_3mut
PAPEAAAKGGS	13,966	FLV_P10273_3mutA
GSSGGSEAAAK	13,967	MLVCB_P08361_3mut
EAAAKGGSGGG	13,968	MLVMS_P03355
GGSGGGPAP	13,969	MLVMS_P03355_3mut
GGS		XMRV6_A1Z651_3mut
GGSEAAAKPAP	13,971	MLVFF_P26809_3mut
EAAAKGGG	13,972	MLVMS_P03355_PLV919
GSSGSSGSSGSS	13,973	WMSV_P03359_3mut
GGSGSSPAP	13,974	PERV_Q4VFZ2_3mut
GGGEAAAK	13,975	MLVMS_P03355_3mutA_WS
GSSPAPGGS	13,976	KORV_Q9TTC1-Pro_3mutA
GSSEAAAKGGG	13,977	SFV3L_P27401_2mut
EAAAKPAPGGS	13,978	MLVCB_P08361_3mut
GGSGGGEAAAK	13,979	PERV_Q4VFZ2
GGSGSS	13,980	MLVCB_P08361_3mut
GGSGGGEAAAK	13,981	MLVBM_Q7SVK7_3mutA_WS
GGSGGSGGSGGSGGSGGS	13,982	FLV_P10273_3mut
PAPEAAAKGSS	13,983	MLVMS_P03355_3mut
EAAAKGSSGGS	13,984	WMSV_P03359_3mutA
GGSGSSEAAAK	13,985	MLVCB_P08361_3mut
GGSGSSEAAAK	13,986	KORV_Q9TTC1_3mutA
GSSGGSGGG	13,987	MLVMS_P03355_PLV919
EAAAKGGSGGG	13,988	SFV3L_P27401-Pro_2mutA
GGSGGS	13,989	AVIRE_P03360_3mutA

Linker amino acid sequence	SEQ ID NO:	RT domain name
GSAGSAAGSGEF	13,990	MLVMS_P03355_PLV919
GGSGSS	13,991	GALV_P21414_3mutA
GGGG	13,992	MLVFF_P26809_3mutA
GGGGSGGGGSGGGGSGGGGS	13,993	WMSV_P03359_3mut
SGSETPGTSESATPES	13,994	BAEVM_P10272_3mut
EAAAKEAAAKEAAAKEAAAK	13,995	FOAMV_P14350_2mutA
GGGEAAAKGGS	13,996	FLV_P10273_3mutA
GSSGGSEAAAK	13,997	MLVFF_P26809_3mut
EAAAKGGGGSS	13,998	MLVAV_P03356_3mut
PAPGGSEAAAK	13,999	KORV_Q9TTC1-Pro_3mut
EAAAK	14,000	XMRV6_A1Z651_3mut
GSSGSSGSSGSSGSSGSS	14,001	PERV_Q4VFZ2_3mut
GGGG	14,002	MLVCB_P08361_3mutA
GSSGSS	14,003	WMSV_P03359_3mutA
GSSGGSPAP	14,004	AVIRE_P03360_3mut
GGSGGSGGS	14,005	MLVCB_P08361_3mut
EAAAKGGGPAP	14,006	FLV_P10273_3mutA
GGGGSGGGGS	14,007	MLVCB_P08361_3mut
GGSEAAAKGSS	14,008	PERV_Q4VFZ2_3mutA_WS
EAAAKEAAAKEAAAKEAAAKEAAAKEAAAK	14,009	SFV3L_P27401_2mutA
GGSGSSEAAAK	14,010	PERV_Q4VFZ2_3mutA_WS
EAAAKEAAAKEAAAKEAAAK	14,011	SFV3L_P27401-Pro_2mutA
GSSEAAAKGGS	14,012	FLV_P10273_3mutA
GGSGSS	14,013	PERV_Q4VFZ2
GGSGSSEAAAK	14,014	SFV3L_P27401-Pro_2mutA
GSSGSSGSS	14,015	XMRV6_A1Z651_3mutA
EAAAKGSSPAP	14,016	KORV_Q9TTC1_3mutA
EAAAKPAP	14,017	FLV_P10273_3mutA
GGSGSSEAAAK	14,018	KORV_Q9TTC1-Pro_3mut
GGGGSGGGGSGGGGSGGGGSGGGGSGGGGS	14,019	KORV_Q9TTC1_3mutA
GGGGSGGGGSGGGGS	14,020	KORV_Q9TTC1-Pro_3mutA
GGGGGGG	14,021	FLV_P10273_3mut
EAAAKGSS	14,022	WMSV_P03359_3mut
EAAAKGGGPAP	14,023	MLVCB_P08361_3mut
GSSGSS	14,024	MLVBM_Q7SVK7_3mutA_WS
EAAAKGGGGGS	14,025	MLVFF_P26809_3mut
GGSGGGEAAAK	14,026	FLV_P10273_3mutA
PAPGSS	14,027	MLVFF_P26809_3mutA
PAPGSS	14,028	BAEVM_P10272_3mutA
GGSPAPGSS	14,029	AVIRE_P03360_3mut

Linker amino acid sequence	SEQ ID NO:	RT domain name
GGGGSSEAAAK	14,030	MLVMS_P03355_3mut
GSSGGGGGS	14,031	FFV_O93209-Pro
EAAAKGSSPAP	14,032	PERV_Q4VFZ2_3mut
GSSPAPGGS	14,033	PERV_Q4VFZ2_3mut
GGGGGG	14,034	BAEVM_P10272_3mut
EAAAKGGGGSS	14,035	PERV_Q4VFZ2_3mutA_WS
PAPGGSEAAAK	14,036	KORV_Q9TTC1_3mutA
SGGSSGGSSGSETPGTSESATPESSGGSSGGSS	14,037	MLVMS_P03355_3mutA_WS
GSSGSSGSSGSS	14,038	MLVMS_P03355_3mut
EAAAKGSSGGG	14,039	MLVMS_P03355_PLV919
GGSEAAAKPAP	14,040	AVIRE_P03360_3mutA
GSSGSSGSSGSSGSS	14,041	WMSV_P03359_3mutA
GGGEAAAKPAP	14,042	FLV_P10273_3mutA
PAPGSSGGG	14,043	KORV_Q9TTC1_3mutA
GSSGSS	14,044	MLVMS_P03355_3mutA_WS
PAPEAAAK	14,045	BAEVM_P10272_3mut
GGGPAPGSS	14,046	PERV_Q4VFZ2
GSSGGSPAP	14,047	MLVFF_P26809_3mut
GGGGSS	14,048	SFV3L_P27401_2mut
PAPEAAAKGSS	14,049	SFV3L_P27401_2mut
GGSGGGPAP	14,050	XMRV6_A1Z651_3mutA
PAPGGS	14,051	BAEVM_P10272_3mutA
EAAAKGGGGGS	14,052	AVIRE_P03360_3mut
GSSGGSPAP	14,053	KORV_Q9TTC1-Pro_3mutA
GSSGGGGGS	14,054	WMSV_P03359_3mut
GGGEAAAKGGS	14,055	AVIRE_P03360_3mut
GGGEAAAKGSS	14,056	BAEVM_P10272_3mut
PAPEAAAKGSS	14,057	MLVAV_P03356_3mutA
GSSGSSGSSGSSGSS	14,058	MLVCB_P08361_3mut
GGSPAPGSS	14,059	FLV_P10273_3mutA
EAAAKGSSPAP	14,060	BAEVM_P10272_3mutA
GGSGGSGGSGGSGGSGGS	14,061	PERV_Q4VFZ2
GGGGSSEAAAK	14,062	FLV_P10273_3mutA
GGGGSSPAP	14,063	FFV_O93209
GSSGGSPAP	14,064	MLVMS_P03355_3mut
GGGPAPGSS	14,065	MLVMS_P03355_PLV919
PAPGSSGGS	14,066	PERV_Q4VFZ2_3mut
GGGGGSPAP	14,067	MLVFF_P26809_3mut
SGSETPGTSESATPES	14,068	MLVMS_P03355_3mutA_WS
GSSGSSGSSGSSGSS	14,069	KORV_Q9TTC1_3mutA

Linker amino acid sequence	SEQ ID NO:	RT domain name
GSSPAPGGG	14,070	WMSV_P03359_3mut
PAPAPAPAPAPAP	14,071	SFV3L_P27401_2mutA
GGGPAPGGS	14,072	MLVMS_P03355_3mut
PAPGGSEAAAK	14,073	WMSV_P03359_3mut
GGGGSSEAAAK	14,074	FFV_O93209-Pro
GGSPAPGGG	14,075	FLV_P10273_3mutA
GSSPAPEAAAK	14,076	AVIRE_P03360_3mut
GGGEAAAK	14,077	FLV_P10273_3mutA
PAPEAAAKGGG	14,078	MLVCB_P08361_3mut
GGSPAPGGG	14,079	MLVCB_P08361_3mut
GGSGGGGSS	14,080	BAEVM_P10272_3mutA
GSSPAPEAAAK	14,081	MLVCB_P08361_3mut
GGSPAPGGG	14,082	KORV_Q9TTC1-Pro_3mutA
PAPGGSGSS	14,083	KORV_Q9TTC1_3mutA
GSSPAP	14,084	KORV_Q9TTC1-Pro_3mutA
SGSETPGTSESATPES	14,085	MLVMS_P03355
GSSGSSGSS	14,086	MLVAV_P03356_3mutA
PAPGSSGGS	14,087	PERV_Q4VFZ2_3mutA_WS
PAPGGS	14,088	KORV_Q9TTC1-Pro_3mutA
PAPEAAAKGGG	14,089	SFV3L_P27401-Pro_2mutA
GGSGGSGGS	14,090	BAEVM_P10272_3mut
PAPGGS	14,091	MLVFF_P26809_3mut
GSSGGSPAP	14,092	MLVMS_P03355_PLV919
GSSGGGGGS	14,093	FLV_P10273_3mutA
GGGGGSPAP	14,094	KORV_Q9TTC1-Pro_3mut
EAAAKPAPGSS	14,095	SFV3L_P27401-Pro_2mutA
EAAAKGGSPAP	14,096	KORV_Q9TTC1-Pro
GGGPAPEAAAK	14,097	MLVMS_P03355_PLV919
GGSEAAAKGSS	14,098	MLVMS_P03355
PAPEAAAKGSS	14,099	KORV_Q9TTC1_3mutA
PAPEAAAKGGS	14,100	WMSV_P03359_3mutA
GSSGGG	14,101	PERV_Q4VFZ2_3mutA_WS
EAAAKGGGGSS	14,102	MLVMS_P03355_PLV919
EAAAKGGSPAP	14,103	AVIRE_P03360_3mutA
GGGGSSGGS	14,104	MLVMS_P03355_PLV919
PAPEAAAKGSS	14,105	PERV_Q4VFZ2_3mutA_WS
EAAAKGGGGGS	14,106	BAEVM_P10272_3mut
GSSGGGGGS	14,107	MLVMS_P03355_3mut
PAPAPAPAP	14,108	KORV_Q9TTC1_3mutA
GGSGGSGGSGGS	14,109	MLVAV_P03356_3mut

Linker amino acid sequence	SEQ ID NO:	RT domain name
PAPAPAPAP	14,110	SFV3L_P27401_2mut
GSSEAAAKPAP	14,111	MLVMS_P03355_3mut
GGSGGGEAAAK	14,112	SFV3L_P27401_2mutA
GSSGGSGGG	14,113	MLVMS_P03355_3mutA_WS
GGGGGSPAP	14,114	MLVCB_P08361_3mutA
GGGEAAAKGSS	14,115	XMRV6_A1Z651_3mutA
GGGGSSPAP	14,116	BAEVM_P10272_3mut
GGSGGG	14,117	PERV_Q4VFZ2_3mut
GGGGSS	14,118	MLVBM_Q7SVK7_3mutA_WS
EAAAKGSSGGS	14,119	PERV_Q4VFZ2_3mutA_WS
GSSGGGGGS	14,120	PERV_Q4VFZ2
EAAAKGSSGGS	14,121	PERV_Q4VFZ2_3mut
EAAAKEAAAK	14,122	MLVAV_P03356_3mut
GSSGGGEAAAK	14,123	MLVAV_P03356_3mut
GSSPAPGGG	14,124	XMRV6_A1Z651_3mut
GGGGSGGGGSGGGGS	14,125	PERV_Q4VFZ2_3mut
EAAAKEAAAKEAAAKEAAAK	14,126	KORV_Q9TTC1_3mutA
EAAAKGGSGSS	14,127	MLVBM_Q7SVK7_3mut
PAPEAAAK	14,128	BLVJ_P03361
GSSGGG	14,129	FFV_O93209-Pro
GGSGGGEAAAK	14,130	KORV_Q9TTC1-Pro_3mutA
EAAAK	14,131	FLV_P10273_3mutA
GGGGSSPAP	14,132	MLVMS_P03355_3mut
GSS		SFV3L_P27401-Pro_2mut
PAPEAAAKGSS	14,134	BAEVM_P10272_3mut
GGGGGSPAP	14,135	PERV_Q4VFZ2_3mut
GSSGSSGSS	14,136	BAEVM_P10272_3mutA
GGGGSGGGGSGGGGSGGGGS	14,137	SFV1_P23074_2mut
GGGGSSEAAAK	14,138	SFV3L_P27401_2mutA
GGGGSGGGGSGGGGSGGGGS	14,139	FOAMV_P14350-Pro_2mut
PAPGSSEAAAK	14,140	MLVBM_Q7SVK7_3mutA_WS
GGGGGSGSS	14,141	MLVFF_P26809_3mutA
GGSEAAAKGGG	14,142	MLVBM_Q7SVK7_3mut
PAPGSSGGG	14,143	PERV_Q4VFZ2
GGS		PERV_Q4VFZ2_3mutA_WS
EAAAKGGSGSS	14,145	FLV_P10273_3mut
GGGEAAAK	14,146	WMSV_P03359_3mutA
GGSEAAAKPAP	14,147	MLVBM_Q7SVK7_3mut
SGSETPGTSESATPES	14,148	FOAMV_P14350-Pro_2mutA
EAAAKPAPGGS	14,149	AVIRE_P03360_3mut

Linker amino acid sequence	SEQ ID NO:	RT domain name
EAAAKGGGGGS	14,150	KORV_Q9TTC1-Pro_3mutA
GGGGS	14,151	PERV_Q4VFZ2_3mut
GGSEAAAKGSS	14,152	MLVFF_P26809_3mutA
GGSEAAAKGGG	14,153	AVIRE_P03360
GGSGGSGGSGGSGGSGGS	14,154	SFV3L_P27401_2mut
GGSEAAAKGSS	14,155	SFV3L_P27401-Pro_2mutA
GGGEAAAKPAP	14,156	MLVCB_P08361_3mut
GGSEAAAK	14,157	MLVMS_P03355_PLV919
GGSPAPGSS	14,158	KORV_Q9TTC1-Pro_3mutA
GSSPAPEAAAK	14,159	WMSV_P03359_3mutA
GGSGSS	14,160	KORV_Q9TTC1-Pro_3mutA
PAPGGGGGS	14,161	AVIRE_P03360_3mut
PAPEAAAKGSS	14,162	FFV_O93209-Pro
GGSGGGEAAAK	14,163	WMSV_P03359_3mut
PAPGGG	14,164	MLVMS_P03355_3mut
EAAAKGGG	14,165	FLV_P10273_3mutA
GSSGSSGSSGSS	14,166	MLVCB_P08361_3mut
EAAAKGGSGGG	14,167	FFV_O93209
GSSPAPGGS	14,168	PERV_Q4VFZ2_3mutA_WS
GSSPAPGGS	14,169	MLVCB_P08361_3mut
GGGPAP	14,170	WMSV_P03359_3mutA
GGGPAP	14,171	KORV_Q9TTC1_3mutA
GGSPAPGSS	14,172	KORV_Q9TTC1-Pro_3mut
PAPAP	14,173	MLVMS_P03355_3mut
GGGGGGG	14,174	MLVMS_P03355_3mut
GGGGG	14,175	KORV_Q9TTC1-Pro_3mut
GSAGSAAGSGEF	14,176	FOAMV_P14350_2mutA
PAPAP	14,177	KORV_Q9TTC1-Pro_3mutA
GGSEAAAKGGG	14,178	SFV3L_P27401-Pro_2mutA
PAPAP	14,179	WMSV_P03359_3mut
GGGGSGGGGSGGGGS	14,180	SFV3L_P27401_2mut
PAPGGS	14,181	KORV_Q9TTC1_3mutA
GGGEAAAKPAP	14,182	FLV_P10273_3mut
GGGGGS	14,183	MLVAV_P03356_3mutA
GSSEAAAKGGG	14,184	WMSV_P03359_3mut
EAAAKGGGGSS	14,185	GALV_P21414_3mutA
GSSGGS	14,186	MLVAV_P03356_3mutA
GSSGGG	14,187	MLVBM_Q7SVK7_3mut
PAPAPAP	14,188	SFV3L_P27401-Pro_2mutA
GGGG	14,189	KORV_Q9TTC1_3mutA

Linker amino acid sequence	SEQ ID NO:	RT domain name
EAAAKPAPGGS	14,190	MLVFF_P26809_3mut
GGGGSGGGGS	14,191	XMRV6_A1Z651_3mut
EAAAKGGG	14,192	MLVCB_P08361_3mut
GGGGSSPAP	14,193	KORV_Q9TTC1_3mutA
GSSEAAAKGGG	14,194	KORV_Q9TTC1-Pro_3mutA
GGGGG	14,195	BLVJ_P03361_2mutB
GGGEAAAKGSS	14,196	FFV_O93209-Pro
GSSGSSGSS	14,197	BAEVM_P10272_3mut
GSSGGSPAP	14,198	PERV_Q4VFZ2_3mut
EAAAKGGS	14,199	KORV_Q9TTC1_3mut
GGSPAPEAAAK	14,200	AVIRE_P03360_3mut
GGSEAAAK	14,201	WMSV_P03359_3mut
GSSGGS	14,202	KORV_Q9TTC1-Pro_3mutA
GGGPAPEAAAK	14,203	KORV_Q9TTC1_3mutA
PAPGSS	14,204	WMSV_P03359_3mutA
GGSEAAAKGSS	14,205	FLV_P10273_3mutA
EAAAKEAAAKEAAAKEAAAKEAAAK	14,206	SFV3L_P27401
GSSEAAAKGGG	14,207	SFV3L_P27401-Pro_2mutA
GGGGSEAAAKGGGGS	14,208	KORV_Q9TTC1-Pro_3mutA
GGSGGSGGS	14,209	WMSV_P03359_3mut
GGGGGSGSS	14,210	KORV_Q9TTC1-Pro
GGGGSGGGGSGGGGSGGGGS	14,211	MLVMS_P03355_3mut
EAAAKGGG	14,212	PERV_Q4VFZ2
GGSEAAAKGGG	14,213	KORV_Q9TTC1-Pro_3mut
GSSGGSGGG	14,214	PERV_Q4VFZ2_3mutA_WS
GGGGGS	14,215	PERV_Q4VFZ2_3mut
GSAGSAAGSGEF	14,216	PERV_Q4VFZ2
PAPEAAAKGSS	14,217	BAEVM_P10272_3mutA
GSSPAPGGG	14,218	MLVCB_P08361_3mut
GGGGSSPAP	14,219	KORV_Q9TTC1-Pro_3mutA
PAPGGSGGG	14,220	MLVFF_P26809_3mut
GSSPAP	14,221	KORV_Q9TTC1_3mutA
PAPGSS	14,222	SFV3L_P27401-Pro_2mut
GGSGGGGSS	14,223	MLVMS_P03355_PLV919
GSSGGS	14,224	WMSV_P03359_3mutA
EAAAKGGGGGS	14,225	PERV_Q4VFZ2
GGGGG	14,226	KORV_Q9TTC1_3mutA
EAAAKGSS	14,227	MLVMS_P03355_PLV919
EAAAKEAAAKEAAAKEAAAKEAAAK	14,228	FLV_P10273_3mut
EAAAKEAAAKEAAAKEAAAK	14,229	SFV3L_P27401-Pro_2mut

Linker amino acid sequence	SEQ ID NO:	RT domain name
GSAGSAAGSGEF	14,230	SFV3L_P27401_2mutA
GGGPAPGGS	14,231	FLV_P10273_3mutA
GGSEAAAKGGG	14,232	MLVCB_P08361_3mut
PAPGGGEAAAK	14,233	BAEVM_P10272_3mut
EAAAKPAPGSS	14,234	FOAMV_P14350_2mut
GGSEAAAK	14,235	KORV_Q9TTC1_3mutA
GGSGSS	14,236	AVIRE_P03360
GGSPAPEAAAK	14,237	MLVMS_P03355_PLV919
GGGGS	14,238	XMRV6_A1Z651_3mut
GGSPAPGGG	14,239	XMRV6_A1Z651_3mut
EAAAKPAPGGS	14,240	PERV_Q4VFZ2
GSSPAP	14,241	BAEVM_P10272_3mut
GGSGSSGGG	14,242	FLV_P10273_3mutA
PAPGGG	14,243	PERV_Q4VFZ2_3mutA_WS
GSSGGSEAAAK	14,244	MLVBM_Q7SVK7_3mut
GGSEAAAK	14,245	MLVMS_P03355_3mut
GGGPAPGGS	14,246	MLVFF_P26809_3mut
GSAGSAAGSGEF	14,247	MLVBM_Q7SVK7_3mutA_WS
EAAAKPAPGGS	14,248	SFVCP_Q87040
PAPGGG	14,249	PERV_Q4VFZ2_3mutA_WS
GSSPAPEAAAK	14,250	MLVBM_Q7SVK7
PAPEAAAK	14,251	MLVBM_Q7SVK7_3mut
PAPGGGGGS	14,252	AVIRE_P03360_3mutA
GGSEAAAKPAP	14,253	MLVBM_Q7SVK7_3mut
EAAAKGSS	14,254	WMSV_P03359_3mutA
GGGEAAAK	14,255	MLVFF_P26809_3mutA
EAAAKEAAAKEAAAK	14,256	MLVMS_P03355_3mut
PAPEAAAKGGG	14,257	BAEVM_P10272_3mut
PAPAPAP	14,258	MLVCB_P08361_3mut
EAAAKPAPGGS	14,259	BAEVM_P10272_3mut
GGGGSGGGGS	14,260	FLV_P10273_3mut
GGGGSEAAAKGGGGS	14,261	KORV_Q9TTC1_3mut
EAAAK	14,262	FLV_P10273_3mut
PAPAPAP	14,263	WMSV_P03359_3mut
GGGGSEAAAKGGGGS	14,264	FFV_O93209-Pro
GGSPAPEAAAK	14,265	MLVMS_P03355_3mut
GGSGSSGGG	14,266	XMRV6_A1Z651_3mut
GGSPAPGSS	14,267	PERV_Q4VFZ2_3mut
SGGSSGGSSGSETPGTSESATPESSGGSSGGSS	14,268	SFV3L_P27401-Pro_2mutA
EAAAKGGGPAP	14,269	BAEVM_P10272_3mutA

Linker amino acid sequence	SEQ ID NO:	RT domain name
GSSGGSEAAAK	14,270	MLVMS_P03355_3mutA_WS
SGSETPGTSESATPES	14,271	PERV_Q4VFZ2_3mutA_WS
EAAAKEAAAKEAAAKEAAAKEAAAK	14,272	KORV_Q9TTC1-Pro_3mutA
GSSGSSGSS	14,273	KORV_Q9TTC1_3mutA
GSSPAPGGG	14,274	SFV3L_P27401-Pro_2mutA
GSSGGGEAAAK	14,275	KORV_Q9TTC1_3mutA
GGSGGGGSS	14,276	PERV_Q4VFZ2_3mutA_WS
GSSGGGEAAAK	14,277	MLVCB_P08361_3mut
GSSEAAAKGGG	14,278	MLVCB_P08361_3mut
GGSGGGGSS	14,279	KORV_Q9TTC1_3mutA
GGSGSSPAP	14,280	PERV_Q4VFZ2_3mutA_WS
GSSPAP	14,281	MLVMS_P03355_3mut
GGGGSSEAAAK	14,282	AVIRE_P03360
GGS		WMSV_P03359_3mut
EAAAKEAAAK	14,284	PERV_Q4VFZ2_3mut
PAPAPAPAP	14,285	MLVAV_P03356_3mut
GGSEAAAKGGG	14,286	KORV_Q9TTC1_3mutA
PAPGGG	14,287	MLVAV_P03356_3mut
EAAAKGSS	14,288	BAEVM_P10272_3mut
GGGGSGGGGS	14,289	WMSV_P03359_3mutA
GGSGGSGGS	14,290	SFV3L_P27401_2mut
EAAAK	14,291	MLVCB_P08361_3mut
GGGGSSGGS	14,292	WMSV_P03359_3mutA
GGGPAPEAAAK	14,293	MLVAV_P03356_3mutA
EAAAKEAAAKEAAAK	14,294	FFV_O93209
GSSEAAAKGGG	14,295	MLVBM_Q7SVK7_3mut
GGGPAPGGS	14,296	FLV_P10273_3mut
GGSEAAAKGGG	14,297	WMSV_P03359_3mut
EAAAKGGGGGS	14,298	XMRV6_A1Z651_3mutA
EAAAKGGSGGG	14,299	FLV_P10273_3mutA
GGSEAAAKGGG	14,300	SFV3L_P27401_2mutA
GGGGS	14,301	PERV_Q4VFZ2_3mutA_WS
GSSGGS	14,302	MLVMS_P03355_3mut
GSSGSS	14,303	MLVAV_P03356_3mutA
GGSPAPGGG	14,304	MLVBM_Q7SVK7_3mutA_WS
GSSGGGGGS	14,305	MLVF5_P26810_3mut
PAPAPAPAP	14,306	MLVCB_P08361_3mut
PAPAP	14,307	PERV_Q4VFZ2_3mutA_WS
PAPGSSGGS	14,308	KORV_Q9TTC1_3mut
PAPGSSGGG	14,309	PERV_Q4VFZ2_3mut

Linker amino acid sequence	SEQ ID NO:	RT domain name
GGGEAAAK	14,310	MLVMS_P03355_PLV919
GGSGGSGGSGGSGGS	14,311	SFV3L_P27401-Pro_2mutA
GGSGGG	14,312	FLV_P10273_3mut
PAPEAAAKGGG	14,313	MLVFF_P26809_3mut
PAP		PERV_Q4VFZ2_3mutA_WS
PAPGGSGSS	14,315	FFV_O93209_2mut
EAAAKEAAAKEAAAKEAAAKEAAAKEAAAK	14,316	FFV_O93209-Pro_2mut
GSSGSSGSSGSS	14,317	FFV_O93209-Pro
GSSGSSGSSGSSGSS	14,318	FLV_P10273_3mutA
GGGEAAAKPAP	14,319	PERV_Q4VFZ2
PAPGSSGGG	14,320	SFV3L_P27401_2mut
PAPGGSGSS	14,321	KORV_Q9TTC1-Pro_3mut
PAPAPAPAPAP	14,322	GALV_P21414_3mutA
GGSGGGEAAAK	14,323	PERV_Q4VFZ2_3mut
GSSPAP	14,324	MLVCB_P08361_3mut
EAAAKPAP	14,325	MLVF5_P26810_3mut
GGGGSGGGGSGGGGSGGGGS	14,326	MLVBM_Q7SVK7_3mut
GGSGGG	14,327	WMSV_P03359_3mut
GGSGGSGGS	14,328	KORV_Q9TTC1_3mut
GGGGGGGG	14,329	MLVFF_P26809_3mut
GGGGSS	14,330	MLVAV_P03356_3mut
GSSGGGGGS	14,331	SFV3L_P27401_2mut
EAAAKEAAAKEAAAKEAAAKEAAAKEAAAK	14,332	GALV_P21414_3mutA
GSSGSSGSS	14,333	PERV_Q4VFZ2_3mut
GSSPAPGGS	14,334	MLVFF_P26809_3mut
PAPAPAP	14,335	AVIRE_P03360_3mutA
EAAAKEAAAKEAAAKEAAAK	14,336	WMSV_P03359_3mutA
PAPAPAPAP	14,337	SFV3L_P27401_2mutA
GGGGSS	14,338	MLVAV_P03356_3mutA
GSSGSSGSSGSSGSS	14,339	SFV3L_P27401_2mutA
PAPGGS	14,340	WMSV_P03359_3mutA
GSSEAAAKGGG	14,341	PERV_Q4VFZ2
GSSGGSPAP	14,342	MLVMS_P03355_PLV919
GSSGSSGSSGSSGSSGSS	14,343	SFV3L_P27401_2mutA
GGSGSSGGG	14,344	MLVCB_P08361_3mut
GGGPAPGSS	14,345	SFV3L_P27401-Pro_2mutA
GSSEAAAKGGS	14,346	WMSV_P03359_3mut
GSSEAAAKGGG	14,347	MLVAV_P03356_3mut
GGSGGGPAP	14,348	FFV_O93209-Pro
GSSGSS	14,349	PERV_Q4VFZ2_3mut

Linker amino acid sequence	SEQ ID NO:	RT domain name
PAPGGGGGS	14,350	GALV_P21414_3mutA
EAAAKPAPGGS	14,351	MLVAV_P03356_3mut
GSSGSS	14,352	MLVMS_P03355_3mut
EAAAKPAPGGS	14,353	FFV_O93209-Pro
GGGPAPEAAAK	14,354	MLVMS_P03355_3mutA_WS
GSSEAAAKGGG	14,355	MLVBM_Q7SVK7_3mut
GGGEAAAKGGS	14,356	BAEVM_P10272_3mut
GSSGSS	14,357	KORV_Q9TTC1-Pro_3mutA
EAAAKEAAAKEAAAK	14,358	SFV1_P23074
PAPGSSGGS	14,359	KORV_Q9TTC1-Pro_3mut
PAPAPAPAPAP	14,360	MLVMS_P03355
GSSEAAAK	14,361	SFV3L_P27401_2mut
PAP		PERV_Q4VFZ2_3mut
GGSEAAAKGGG	14,363	MLVBM_Q7SVK7_3mut
GGSGGGPAP	14,364	MLVBM_Q7SVK7_3mutA_WS
GSSGSS	14,365	MLVMS_P03355_3mut
GGSEAAAK	14,366	MLVMS_P03355
GSSEAAAKGGS	14,367	MLVMS_P03355_PLV919
PAPGGGGGS	14,368	MLVFF_P26809_3mut
GSSGGG	14,369	PERV_Q4VFZ2_3mut
GSSGGS	14,370	PERV_Q4VFZ2_3mutA_WS
PAPGGG	14,371	BAEVM_P10272_3mut
PAPGSSGGG	14,372	MLVBM_Q7SVK7_3mut
GGSEAAAK	14,373	SFV3L_P27401_2mut
GSSPAPEAAAK	14,374	SFV3L_P27401-Pro_2mut
GSSGGSPAP	14,375	BAEVM_P10272_3mut
GGSPAPGSS	14,376	PERV_Q4VFZ2_3mutA_WS
GGSGGSGGS	14,377	PERV_Q4VFZ2
GGSGGGPAP	14,378	FLV_P10273_3mut
GGGPAPEAAAK	14,379	SFV3L_P27401_2mutA
GGGGS	14,380	FLV_P10273_3mutA
GSSGGSGGG	14,381	XMRV6_A1Z651_3mut
EAAAKGGGGSS	14,382	PERV_Q4VFZ2
GGSGSSGGG	14,383	SFV3L_P27401-Pro_2mutA
GGSGGSGGS	14,384	MLVFF_P26809_3mut
GGGPAPEAAAK	14,385	FLV_P10273_3mut
GSSGGGEAAAK	14,386	MLVMS_P03355_3mut
GGG		SFV3L_P27401_2mut
GSAGSAAGSGEF	14,388	WMSV_P03359_3mut
GSSGGGPAP	14,389	MLVMS_P03355_PLV919

Linker amino acid sequence	SEQ ID NO:	RT domain name
GGGGSS	14,390	KORV_Q9TTC1-Pro_3mut
GGGGSSEAAAK	14,391	KORV_Q9TTC1
PAPGGSGGG	14,392	SFV3L_P27401_2mut
GSSGSSGSSGSSGSS	14,393	FFV_O93209
GSSGGSPAP	14,394	MLVMS_P03355_3mut
GGSEAAAK	14,395	KORV_Q9TTC1-Pro_3mutA
GGGGSGGGGS	14,396	BAEVM_P10272_3mut
GSSEAAAKGGG	14,397	AVIRE_P03360_3mut
EAAAKPAPGGG	14,398	FLV_P10273_3mut
EAAAKGGSPAP	14,399	SFV3L_P27401-Pro_2mutA
GSSEAAAKPAP	14,400	MLVBM_Q7SVK7_3mut
GGGPAPGGS	14,401	MLVCB_P08361_3mut
GGG		SFV3L_P27401_2mutA
EAAAKGGGGSEAAAK	14,403	SFV3L_P27401_2mutA
GGSGSSGGG	14,404	MLVBM_Q7SVK7_3mut
GSAGSAAGSGEF	14,405	BAEVM_P10272_3mut
GGGEAAAK	14,406	FOAMV_P14350_2mutA
PAPEAAAKGGS	14,407	WMSV_P03359_3mut
PAPAPAPAPAPAP	14,408	MLVF5_P26810_3mutA
GGSGGGGSS	14,409	FLV_P10273_3mutA
PAPGSSGGS	14,410	BAEVM_P10272_3mut
PAPEAAAK	14,411	WMSV_P03359_3mutA
GSSGSSGSSGSSGSSGSS	14,412	FFV_O93209-Pro_2mut
GGGGGSGSS	14,413	FFV_O93209-Pro
GGGGGGGG	14,414	SFV3L_P27401-Pro_2mutA
GGGGGG	14,415	FLV_P10273_3mut
GSSGGSGGG	14,416	MLVAV_P03356_3mutA
GGGGSS	14,417	SFV3L_P27401-Pro_2mutA
GGSGGGPAP	14,418	FOAMV_P14350_2mut
GSSGSS	14,419	AVIRE_P03360_3mutA
EAAAKEAAAKEAAAKEAAAKEAAAK	14,420	SFV3L_P27401-Pro_2mutA
EAAAKEAAAK	14,421	BAEVM_P10272_3mut
GSSPAPEAAAK	14,422	GALV_P21414_3mutA
GGSEAAAKPAP	14,423	SFV3L_P27401_2mutA
GGSGGGEAAAK	14,424	SFV3L_P27401-Pro_2mutA
EAAAKGSSPAP	14,425	FOAMV_P14350_2mut
GGSGSSEAAAK	14,426	SFV3L_P27401_2mut
GGG		PERV_Q4VFZ2
GGGGGSGSS	14,428	FOAMV_P14350_2mut
GGSGGGEAAAK	14,429	KORV_Q9TTC1-Pro_3mut

Linker amino acid sequence	SEQ ID NO:	RT domain name
GSSGGSGGG	14,430	AVIRE_P03360_3mutA
EAAAKPAPGGG	14,431	SFV3L_P27401_2mutA
PAPGGSGGG	14,432	KORV_Q9TTC1-Pro_3mut
PAPAPAP	14,433	WMSV_P03359_3mutA
GSSEAAAKPAP	14,434	SFV1_P23074
SGGSSGGSSGSETPGTSESATPESSGGSSGGSS	14,435	SRV2_P51517
GSSGGSGGG	14,436	PERV_Q4VFZ2_3mutA_WS
GSSGSSGSSGSSGSSGSS	14,437	FFV_O93209
GSSGGGPAP	14,438	WMSV_P03359_3mut
PAPAPAPAPAPAP	14,439	MLVBM_Q7SVK7_3mut
GGGGGSPAP	14,440	KORV_Q9TTC1-Pro_3mutA
PAPGSS	14,441	MLVBM_Q7SVK7_3mutA_WS
PAPEAAAKGGS	14,442	SFV3L_P27401-Pro_2mut
GGGGSSPAP	14,443	MLVMS_P03355_3mut
GGSEAAAK	14,444	FFV_O93209-Pro
EAAAKPAPGGS	14,445	AVIRE_P03360_3mutA
PAPGSS	14,446	WMSV_P03359_3mut
PAPGSSGGG	14,447	SFV3L_P27401-Pro_2mutA
EAAAKEAAAKEAAAK	14,448	SFV3L_P27401_2mut
GGS		MLVRD_P11227_3mut
GGGGS	14,450	KORV_Q9TTC1-Pro_3mut
GGSGGGGSS	14,451	KORV_Q9TTC1
GGSGGG	14,452	MLVMS_P03355_3mutA_WS
GGGEAAAKPAP	14,453	BAEVM_P10272_3mut
EAAAKEAAAKEAAAKEAAAKEAAAK	14,454	FLV_P10273
PAPGGSGGG	14,455	KORV_Q9TTC1-Pro_3mutA
GSSGSSGSSGSSGSSGSS	14,456	HTL1L_P0C211
GGGEAAAKPAP	14,457	WMSV_P03359
GSSGGSPAP	14,458	FFV_O93209-Pro
PAPAPAPAPAP	14,459	SFV3L_P27401-Pro_2mutA
GSSGGSEAAAK	14,460	SFV3L_P27401_2mutA
GGSPAPGSS	14,461	SFV3L_P27401_2mut
GGSGGSGGS	14,462	KORV_Q9TTC1-Pro_3mut
PAPEAAAKGSS	14,463	KORV_Q9TTC1-Pro_3mut
EAAAKGGS	14,464	KORV_Q9TTC1_3mutA
EAAAKGGGGSEAAAK	14,465	SFV3L_P27401-Pro_2mut
GGGGSSPAP	14,466	FFV_O93209-Pro
EAAAK	14,467	SFV3L_P27401_2mut
EAAAKGGGGSS	14,468	BAEVM_P10272_3mut
GGGGGSEAAAK	14,469	MLVBM_Q7SVK7_3mut

Linker amino acid sequence	SEQ ID NO:	RT domain name
GGGG	14,470	PERV_Q4VFZ2
GGGGGSEAAAK	14,471	FLV_P10273_3mut
EAAAKGGGPAP	14,472	KORV_Q9TTC1-Pro
GGGGSGGGGSGGGGSGGGGS	14,473	FFV_O93209_2mutA
GSSGGSGGG	14,474	PERV_Q4VFZ2_3mut
GGGGSGGGGSGGGGS	14,475	GALV_P21414_3mutA
GGSGGGEAAAK	14,476	AVIRE_P03360_3mutA
PAPEAAAKGGG	14,477	SFV3L_P27401_2mut
GGGGSGGGGS	14,478	AVIRE_P03360
GSSGGGEAAAK	14,479	SFV3L_P27401_2mutA
GGGGG	14,480	AVIRE_P03360_3mutA
GGSGSS	14,481	KORV_Q9TTC1_3mut
PAPAPAPAPAPAP	14,482	FOAMV_P14350_2mut
GGSEAAAKPAP	14,483	KORV_Q9TTC1-Pro_3mut
GGGGGG	14,484	PERV_Q4VFZ2_3mut
GSSGGGEAAAK	14,485	MLVBM_Q7SVK7
SGGSSGGSSGSETPGTSESATPESSGGSSGGSS	14,486	MLVAV_P03356
GGSPAPGSS	14,487	BAEVM_P10272_3mut
GGGGSSPAP	14,488	BAEVM_P10272
GGGGSEAAAKGGGGS	14,489	SFV3L_P27401_2mut
GGGGGGGG	14,490	GALV_P21414_3mutA
PAPAP	14,491	MLVAV_P03356_3mut
GGGEAAAK	14,492	PERV_Q4VFZ2_3mutA_WS
GSSPAPGGG	14,493	FFV_O93209_2mut
GGSGGSGGSGGSGGS	14,494	BAEVM_P10272
GGGGGS	14,495	MLVF5_P26810_3mutA
PAPGGGGSS	14,496	FLV_P10273_3mutA
GGGEAAAK	14,497	MLVBM_Q7SVK7_3mut
PAPEAAAKGGG	14,498	WMSV_P03359_3mut
GSSEAAAK	14,499	MLVBM_Q7SVK7_3mut
EAAAKEAAAK	14,500	AVIRE_P03360
EAAAKGGGGGS	14,501	MLVBM_Q7SVK7_3mut
GGGEAAAKGGS	14,502	SFV3L_P27401-Pro_2mutA
PAPAPAPAPAP	14,503	MLVF5_P26810_3mut
PAPGSSEAAAK	14,504	SFV3L_P27401-Pro_2mutA
EAAAKEAAAKEAAAK	14,505	BAEVM_P10272_3mutA
GGSPAPGSS	14,506	MLVMS_P03355
PAPGSSGGS	14,507	FLV_P10273_3mutA
EAAAKEAAAKEAAAKEAAAK	14,508	FOAMV_P14350-Pro_2mut
EAAAKGGG	14,509	KORV_Q9TTC1_3mutA

Linker amino acid sequence	SEQ ID NO:	RT domain name
EAAAKGGSGGG	14,510	MLVBM_Q7SVK7_3mut
GGGGGS	14,511	KORV_Q9TTC1-Pro_3mutA
PAPGGSGGG	14,512	WMSV_P03359_3mut
GGGPAPGGS	14,513	KORV_Q9TTC1_3mutA
GSS		FFV_O93209
GGSGGSGGS	14,515	PERV_Q4VFZ2_3mut
GGGGS	14,516	GALV_P21414_3mutA
GGGG	14,517	MLVF5_P26810_3mut
GGSEAAAKPAP	14,518	FFV_O93209-Pro_2mut
PAPAPAPAP	14,519	FFV_O93209-Pro
PAP		MLVF5_P26810_3mut
EAAAKEAAAKEAAAK	14,521	FFV_O93209_2mut
EAAAKGSS	14,522	MLVCB_P08361_3mut
EAAAKGGG	14,523	MLVBM_Q7SVK7_3mut
PAPEAAAKGGG	14,524	FFV_O93209_2mut
GSSGGGEAAAK	14,525	SFV1_P23074-Pro_2mut
PAPGGGEAAAK	14,526	GALV_P21414_3mutA
GGGGSGGGGSGGGGSGGGGS	14,527	FOAMV_P14350-Pro_2mutA
GSSGGG	14,528	FOAMV_P14350_2mut
GGGGSGGGGSGGGGSGGGGS	14,529	SFV3L_P27401_2mutA
GGSGSS	14,530	AVIRE_P03360_3mut
GGSGSSEAAAK	14,531	MMTVB_P03365_WS
PAPAPAP	14,532	MLVAV_P03356_3mutA
GSSGGSPAP	14,533	SFV3L_P27401-Pro_2mut
GGSPAP	14,534	AVIRE_P03360
GGSGGGPAP	14,535	FFV_O93209
GSSEAAAK	14,536	PERV_Q4VFZ2
GSSGGGPAP	14,537	PERV_Q4VFZ2_3mutA_WS
GGGGSSEAAAK	14,538	KORV_Q9TTC1_3mutA
GGSEAAAKPAP	14,539	SFVCP_Q87040
GGSGGGPAP	14,540	FOAMV_P14350_2mutA
GGGGSGGGGSGGGGSGGGGS	14,541	BLVJ_P03361_2mutB
GGGGSSPAP	14,542	SFV3L_P27401_2mutA
EAAAKGGS	14,543	MLVF5_P26810_3mut
GGSEAAAKGSS	14,544	MLVCB_P08361_3mut
GGGGSSEAAAK	14,545	SFV3L_P27401_2mut
EAAAKGGSGGG	14,546	FOAMV_P14350_2mut
GGSGGS	14,547	FLV_P10273_3mut
EAAAKGGG	14,548	FFV_O93209-Pro
GSSGSSGSSGSSGSS	14,549	SFV3L_P27401

Linker amino acid sequence	SEQ ID NO:	RT domain name
GSSGGGPAP	14,550	PERV_Q4VFZ2_3mutA_WS
PAPGGSEAAAK	14,551	SFV3L_P27401-Pro_2mutA
GGSPAP	14,552	KORV_Q9TTC1
EAAAKPAPGSS	14,553	KORV_Q9TTC1_3mutA
SGSETPGTSESATPES	14,554	SFV1_P23074
GSSPAP	14,555	SFV3L_P27401-Pro_2mutA
GSSPAPGGG	14,556	SFV3L_P27401_2mut
GGGEAAAKGSS	14,557	SFV1_P23074_2mut
GGGPAPGGS	14,558	BAEVM_P10272_3mut
EAAAKGGG	14,559	KORV_Q9TTC1-Pro_3mutA
GSSGGG	14,560	SFV3L_P27401-Pro_2mut
GGSPAPEAAAK	14,561	BAEVM_P10272_3mut
EAAAKGSSPAP	14,562	FFV_O93209
EAAAKGGGGSEAAAK	14,563	SFV3L_P27401-Pro_2mutA
GSSGSSGSSGSSGSS	14,564	SFV1_P23074_2mut
EAAAKGGSPAP	14,565	FOAMV_P14350_2mut
GGSGGS	14,566	KORV_Q9TTC1-Pro_3mutA
EAAAKGSSGGS	14,567	GALV_P21414
GSSGGGPAP	14,568	MLVAV_P03356
PAPEAAAKGGS	14,569	FOAMV_P14350_2mut
EAAAKPAPGGG	14,570	AVIRE_P03360_3mut
GGSPAP	14,571	SFV3L_P27401_2mutA
GGGGSGGGGS	14,572	SFV3L_P27401_2mutA
GGGGSS	14,573	AVIRE_P03360_3mutA
GGSPAPGGG	14,574	SFV3L_P27401-Pro_2mutA
EAAAKPAPGSS	14,575	SFV3L_P27401
EAAAKPAP	14,576	FOAMV_P14350-Pro_2mut
PAPEAAAKGSS	14,577	PERV_Q4VFZ2_3mutA_WS
EAAAKGGSGSS	14,578	SFV3L_P27401_2mutA
GGGEAAAKGSS	14,579	GALV_P21414_3mutA
GGGGSEAAAKGGGGS	14,580	PERV_Q4VFZ2_3mut
PAPGGSGSS	14,581	FFV_O93209-Pro_2mutA
GGSEAAAKPAP	14,582	GALV_P21414_3mutA
GGSGGSGGSGGSGGS	14,583	FFV_O93209-Pro
GSSGGSEAAAK	14,584	SFV3L_P27401-Pro_2mut
GGS		GALV_P21414_3mutA
PAPGGSEAAAK	14,586	MLVMS_P03355
PAPEAAAKGGS	14,587	BAEVM_P10272_3mutA
GGSGSSPAP	14,588	SFV3L_P27401-Pro_2mutA
GSSPAP	14,589	WMSV_P03359_3mut

Linker amino acid sequence	SEQ ID NO:	RT domain name
GGGEAAAK	14,590	MMTVB_P03365
GGGGSS	14,591	PERV_Q4VFZ2_3mut
GGSPAPGSS	14,592	SFV3L_P27401-Pro_2mut
PAPGGS	14,593	MLVBM_Q7SVK7_3mut
EAAAKGSSPAP	14,594	MLVBM_Q7SVK7_3mut
GGGGSSGGS	14,595	PERV_Q4VFZ2_3mut
PAPAPAPAPAPAP	14,596	SFV1_P23074
GGSEAAAKGGG	14,597	SFV3L_P27401-Pro_2mut
GGSGGS	14,598	SFV1_P23074_2mut
GSSGGGGGS	14,599	MLVF5_P26810_3mutA
EAAAKGGGPAP	14,600	SFV3L_P27401
EAAAKEAAAKEAAAKEAAAK	14,601	FOAMV_P14350-Pro_2mutA
GGGPAPGSS	14,602	SFV3L_P27401_2mutA
GGGGSGGGGSGGGGSGGGGS	14,603	SFV3L_P27401_2mut
EAAAKEAAAKEAAAKEAAAK	14,604	MMTVB_P03365_WS
PAPGSSGGS	14,605	KORV_Q9TTC1-Pro_3mutA
PAPGSSEAAAK	14,606	FOAMV_P14350-Pro_2mut
GSSPAPEAAAK	14,607	BAEVM_P10272_3mut
EAAAKGGGGSEAAAK	14,608	FFV_O93209-Pro
GGSPAP	14,609	PERV_Q4VFZ2
GGSGSSEAAAK	14,610	XMRV6_A1Z651_3mut
GGSEAAAKGGG	14,611	GALV_P21414_3mutA
PAPGGGGSS	14,612	AVIRE_P03360_3mutA
GGSGGSGGSGGS	14,613	PERV_Q4VFZ2
GGGGSSGGS	14,614	PERV_Q4VFZ2_3mutA_WS
SGGSSGGSSGSETPGTSESATPESSGGSSGGSS	14,615	BAEVM_P10272_3mutA
GGGPAP	14,616	MLVAV_P03356_3mut
GGGGSGGGGSGGGGSGGGGS	14,617	FFV_O93209_2mut
GSSEAAAK	14,618	FFV_O93209
GGSPAPEAAAK	14,619	FOAMV_P14350_2mut
GGGGGSEAAAK	14,620	FOAMV_P14350_2mut
GSSPAPGGS	14,621	MLVBM_Q7SVK7_3mut
GSS		SFVCP_Q87040_2mut
EAAAKPAP	14,623	FOAMV_P14350-Pro
EAAAKGGG	14,624	SFV3L_P27401_2mut
GGGEAAAK	14,625	AVIRE_P03360_3mutA
PAPGSSGGG	14,626	WMSV_P03359_3mut
EAAAKGGSPAP	14,627	SFV3L_P27401
GSSGGSGGG	14,628	SFV3L_P27401-Pro_2mutA
GSSGGGEAAAK	14,629	GALV_P21414_3mutA

Linker amino acid sequence	SEQ ID NO:	RT domain name
GGGPAPGSS	14,630	MLVBM_Q7SVK7_3mutA_WS
PAPGGGEAAAK	14,631	FFV_O93209-Pro_2mut
GSSGSSGSSGSS	14,632	SFV1_P23074_2mut
GGSEAAAK	14,633	PERV_Q4VFZ2_3mutA_WS
GGGEAAAKPAP	14,634	SFV3L_P27401_2mut
EAAAKGGGPAP	14,635	SFV3L_P27401_2mut
GGGGSSPAP	14,636	FLV_P10273_3mut
EAAAKPAPGSS	14,637	FFV_O93209_2mut
GGGGSSPAP	14,638	SFV3L_P27401_2mut
GSSGSS	14,639	KORV_Q9TTC1_3mutA
GGGGSGGGGSGGGGSGGGGSGGGGS	14,640	BLVJ_P03361_2mut
GGGGSSGGS	14,641	GALV_P21414_3mutA
EAAAKGGSGSS	14,642	FFV_O93209-Pro
EAAAKPAP	14,643	PERV_Q4VFZ2
GSSGGGEAAAK	14,644	MLVBM_Q7SVK7_3mut
PAPGGSGGG	14,645	BAEVM_P10272
EAAAKGGGPAP	14,646	MLVF5_P26810
GSSGSSGSS	14,647	MLVBM_Q7SVK7_3mut
GSSGGS	14,648	AVIRE_P03360_3mutA
GGSEAAAKGGG	14,649	FOAMV_P14350_2mut
EAAAKGGS	14,650	MLVF5_P26810_3mutA
GGSGSSGGG	14,651	WMSV_P03359_3mut
EAAAK	14,652	SFV1_P23074_2mut
GSSGGSPAP	14,653	SFV3L_P27401-Pro_2mutA
GGGGSSGGS	14,654	KORV_Q9TTC1_3mut
PAPGGSGGG	14,655	FFV_O93209-Pro_2mut
GGGPAPGGS	14,656	SFV3L_P27401_2mutA
GSSPAPEAAAK	14,657	FLV_P10273_3mut
GGSGSSPAP	14,658	SFV3L_P27401_2mut
GSSEAAAKGGS	14,659	SFV3L_P27401_2mut
PAPGGG	14,660	SFV3L_P27401_2mutA
SGSETPGTSESATPES	14,661	KORV_Q9TTC1-Pro_3mut
GGGGS	14,662	SFV1_P23074-Pro_2mutA
GSSGGGEAAAK	14,663	WMSV_P03359
EAAAKGGGGSEAAAK	14,664	MLVF5_P26810_3mutA
GSSEAAAKPAP	14,665	FFV_O93209
GGGGGG	14,666	SFV1_P23074_2mutA
EAAAKEAAAKEAAAK	14,667	MMTVB_P03365-Pro
EAAAKPAPGSS	14,668	MLVBM_Q7SVK7_3mut
GGSGSSEAAAK	14,669	SFV3L_P27401_2mutA

Linker amino acid sequence	SEQ ID NO:	RT domain name
GGSEAAAK	14,670	MLVMS_P03355_3mut
GGSPAPEAAAK	14,671	SFV3L_P27401_2mut
GGGPAPGSS	14,672	SFV1_P23074
GGGGGSEAAAK	14,673	MLVBM_Q7SVK7_3mutA_WS
EAAAKPAPGSS	14,674	KORV_Q9TTC1-Pro
GSSGSSGSSGSS	14,675	SFV3L_P27401_2mut
EAAAKPAP	14,676	SFV3L_P27401_2mut
GGGEAAAK	14,677	PERV_Q4VFZ2_3mut
GGSGGS	14,678	SFV3L_P27401_2mutA
EAAAKGSSGGS	14,679	MMTVB_P03365
SGSETPGTSESATPES	14,680	SFV3L_P27401
EAAAKGSSGGG	14,681	PERV_Q4VFZ2
EAAAKEAAAKEAAAKEAAAKEAAAKEAAAK	14,682	MMTVB_P03365
GGSGGGPAP	14,683	KORV_Q9TTC1_3mutA
PAPAPAPAP	14,684	SFV3L_P27401
GGGEAAAKGGS	14,685	SFV1_P23074_2mut
GSSGGSGGG	14,686	PERV_Q4VFZ2_3mut
PAPEAAAKGGS	14,687	FOAMV_P14350_2mutA
GGGEAAAKGSS	14,688	SFV3L_P27401_2mut
GGGGSGGGGSGGGGSGGGGS	14,689	MLVBM_Q7SVK7
PAPGSSGGG	14,690	FLV_P10273
GGSGSSGGG	14,691	FFV_O93209
EAAAKPAPGSS	14,692	MLVBM_Q7SVK7
GSSEAAAKGGG	14,693	SFV3L_P27401_2mutA
GGSGGSGGSGGSGGS	14,694	MLVF5_P26810
GGSEAAAKPAP	14,695	SFV3L_P27401-Pro_2mutA
EAAAKGGSPAP	14,696	SFV3L_P27401_2mutA
EAAAKGGGGGS	14,697	SFV3L_P27401_2mut
GSSPAPEAAAK	14,698	SFV3L_P27401_2mutA
PAPAP	14,699	MLVBM_Q7SVK7_3mut
PAPGGSEAAAK	14,700	KORV_Q9TTC1-Pro
GGSGSS	14,701	MLVF5_P26810_3mutA
GGSEAAAKPAP	14,702	FFV_O93209_2mut
GSS		MLVMS_P03355
SGGSSGGSSGSETPGTSESATPESSGGSSGGSS	14,704	SFV3L_P27401-Pro
PAPGGGEAAAK	14,705	SFV3L_P27401_2mut
PAPGGGGGS	14,706	SFV3L_P27401-Pro_2mut
PAPGGSGSS	14,707	BAEVM_P10272_3mut
GSSGGGEAAAK	14,708	FFV_O93209
GGSEAAAKPAP	14,709	SFV1_P23074_2mut

Linker amino acid sequence	SEQ ID NO:	RT domain name
GGGGG	14,710	FLV_P10273_3mut
GGGEAAAKGSS	14,711	SFV3L_P27401
GSSGSSGSSGSSGSS	14,712	SFV1_P23074-Pro
SGSETPGTSESATPES	14,713	AVIRE_P03360
PAPGSSGGG	14,714	MLVBM_Q7SVK7_3mut
GGGGSSPAP	14,715	HTL3P_Q4U0X6_2mut
GGGEAAAK	14,716	SFV1_P23074
GGSGGG	14,717	AVIRE_P03360
EAAAKGSSGGG	14,718	SFV3L_P27401_2mutA
GSSPAPEAAAK	14,719	FOAMV_P14350-Pro_2mutA
GGGPAPGSS	14,720	WMSV_P03359
EAAAKGSSGGG	14,721	MLVMS_P03355
GGGGGSEAAAK	14,722	MLVMS_P03355
EAAAKPAPGGS	14,723	SFV3L_P27401
EAAAKGSSPAP	14,724	SFV3L_P27401
GGGGGGG	14,725	FOAMV_P14350_2mutA
EAAAKEAAAKEAAAK	14,726	SFV3L_P27401
GSSPAPGGS	14,727	FFV_O93209_2mutA
GGGGSSEAAAK	14,728	SFV3L_P27401-Pro_2mutA
GGSEAAAKGSS	14,729	GALV_P21414_3mutA
GGSEAAAKGSS	14,730	BAEVM_P10272_3mutA
EAAAKPAPGGG	14,731	MLVCB_P08361
GSSGSSGSSGSSGSSGSS	14,732	SFV1_P23074-Pro
GGGGSEAAAKGGGGS	14,733	FOAMV_P14350_2mut
GSSPAPGGS	14,734	MLVMS_P03355_PLV919
GGGGSGGGGS	14,735	FFV_O93209-Pro
GSSGGSPAP	14,736	KORV_Q9TTC1_3mutA
GGSGGS	14,737	GALV_P21414_3mutA
PAPGSSEAAAK	14,738	WMSV_P03359
PAPGGGGSS	14,739	MMTVB_P03365-Pro
GGGGSSGGS	14,740	PERV_Q4VFZ2_3mutA_WS
GGGGSGGGGS	14,741	FFV_O93209_2mut
GGGGSGGGGSGGGGSGGGGS	14,742	XMRV6_A1Z651
GGSGSSEAAAK	14,743	SFV1_P23074_2mut
GGSGGGGSS	14,744	GALV_P21414_3mutA
GGSEAAAKPAP	14,745	MLVBM_Q7SVK7
EAAAKGGSPAP	14,746	SFV1_P23074_2mutA
PAPAPAPAP	14,747	FFV_O93209
GSSGGSPAP	14,748	MMTVB_P03365-Pro
GGGGGSPAP	14,749	KORV_Q9TTC1_3mutA

Linker amino acid sequence	SEQ ID NO:	RT domain name
EAAAKGGGPAP	14,750	PERV_Q4VFZ2
GSSGGSPAP	14,751	BAEVM_P10272
GGGGG	14,752	FFV_O93209
GGGGGS	14,753	FLV_P10273_3mutA
EAAAKEAAAKEAAAK	14,754	FOAMV_P14350
PAPGGG	14,755	MLVCB_P08361_3mut
GSSGGSEAAAK	14,756	FOAMV_P14350_2mutA
GGSPAPGGG	14,757	FLV_P10273_3mut
GSSGSSGSSGSSGSSGSS	14,758	SFV1_P23074-Pro_2mutA
GGSPAPEAAAK	14,759	SFV3L_P27401
PAPGGGGSS	14,760	HTL3P_Q4U0X6_2mutB
GGGGSSEAAAK	14,761	MMTVB_P03365_2mut_WS
PAPGGS	14,762	MLVRD_P11227_3mut
GGSGGSGGSGGSGGS	14,763	MMTVB_P03365
GSAGSAAGSGEF	14,764	AVIRE_P03360
GSSGGS	14,765	BAEVM_P10272_3mutA
GGSGGGGSS	14,766	MMTVB_P03365
GGSGGGGSS	14,767	WMSV_P03359
PAPEAAAKGSS	14,768	SFV1_P23074
GSSGSSGSSGSS	14,769	SFV1_P23074-Pro_2mutA
PAPAPAPAPAPAP	14,770	SFV3L_P27401
PAPGSSGGG	14,771	FLV_P10273_3mut
GGSGSSPAP	14,772	MLVMS_P03355
GGSGGGPAP	14,773	FOAMV_P14350
PAPGGGGGS	14,774	KORV_Q9TTC1_3mutA
EAAAKGSSPAP	14,775	GALV_P21414_3mutA
GGSGSSPAP	14,776	MLVBM_Q7SVK7_3mut
EAAAKGSS	14,777	SFV3L_P27401_2mut
GGGGGSEAAAK	14,778	WMSV_P03359
GGGGGGGG	14,779	SFV1_P23074-Pro
EAAAKEAAAK	14,780	MLVBM_Q7SVK7
GGGEAAAKGGS	14,781	MLVBM_Q7SVK7
EAAAKGGSPAP	14,782	SFV3L_P27401_2mut
GSSEAAAK	14,783	XMRV6_A1Z651
PAPGGGEAAAK	14,784	MMTVB_P03365_WS
GGSPAP	14,785	GALV_P21414_3mutA
GSSPAPGGG	14,786	MLVBM_Q7SVK7_3mutA_WS
GGSGSSPAP	14,787	SFV1_P23074_2mutA
GGS		HTL32_Q0R5R2_2mut
GGSGGGGSS	14,789	MMTVB_P03365-Pro

Linker amino acid sequence	SEQ ID NO:	RT domain name
GGGGSGGGGSGGGGSGGGGS	14,790	SFVCP_Q87040_2mutA
EAAAKGGGPAP	14,791	FOAMV_P14350_2mut
GSSGGGEAAAK	14,792	MMTVB_P03365
SGGSSGGSSGSETPGTSESATPESSGGSSGGSS	14,793	MLVBM_Q7SVK7_3mutA_WS
AEAAAKEAAAKEAAAKEAAAKALEAEAAAKEAAAKEAAAKEAAAKA	14,794	MMTVB_P03365_WS
EAAAKEAAAK	14,795	FOAMV_P14350-Pro_2mut
GSSPAPEAAAK	14,796	FOAMV_P14350_2mutA
EAAAKPAPGGS	14,797	GALV_P21414_3mutA
GSSGGSPAP	14,798	KORV_Q9TTC1-Pro_3mut
GGGPAPEAAAK	14,799	MLVAV_P03356
GGGEAAAKPAP	14,800	SFV1_P23074-Pro_2mut
GGGGGSEAAAK	14,801	SFV3L_P27401_2mut
GGGPAPGSS	14,802	SFV3L_P27401_2mut
GGSEAAAKPAP	14,803	AVIRE_P03360
GSSGSSGSSGSSGSSGSS	14,804	SFV1_P23074-Pro_2mut
EAAAKGSSGGS	14,805	FOAMV_P14350_2mutA
GGGGGG	14,806	MLVBM_Q7SVK7_3mut
GSSPAPGGS	14,807	PERV_Q4VFZ2
GGSGSSPAP	14,808	GALV_P21414_3mutA
GGGPAPEAAAK	14,809	SFV3L_P27401
GGSGGGEAAAK	14,810	WMSV_P03359
GSAGSAAGSGEF	14,811	SFV1_P23074_2mut
GSSGGGEAAAK	14,812	MLVMS_P03355
GGG		MMTVB_P03365-Pro
PAPGSSGGS	14,814	FOAMV_P14350_2mut
GGGGSSPAP	14,815	FFV_O93209_2mut
SGGSSGGSSGSETPGTSESATPESSGGSSGGSS	14,816	MMTVB_P03365_WS
GGGGGGG	14,817	XMRV6_A1Z651
PAPAPAPAPAP	14,818	FOAMV_P14350
GGGGSGGGGSGGGGSGGGGS	14,819	MMTVB_P03365_2mut_WS
GGSGGGPAP	14,820	SFV3L_P27401_2mut
GGGGGG	14,821	SFV1_P23074-Pro
EAAAKPAPGSS	14,822	SFV3L_P27401_2mut
GGGGSSGGS	14,823	HTL3P_Q4U0X6_2mut
PAPGSSEAAAK	14,824	MMTVB_P03365-Pro
GGGGSSPAP	14,825	FOAMV_P14350-Pro_2mut
PAPGSSGGS	14,826	MMTVB_P03365
AEAAAKEAAAKEAAAKEAAAKALEAEAAAKEAAAKEAAAKEAAAKA	14,827	SRV2_P51517
PAPAPAP	14,828	MMTVB_P03365_2mut_WS
PAPGGGGGS	14,829	MMTVB_P03365_2mutB

Linker amino acid sequence	SEQ ID NO:	RT domain name
GGGGSS	14,830	SFV1_P23074-Pro_2mutA
EAAAKEAAAKEAAAKEAAAK	14,831	SFV3L_P27401-Pro
GGSGGSGGSGGSGGS	14,832	MMTVB_P03365-Pro
GGGGGGG	14,833	SFV3L_P27401_2mut
PAPGGGEAAAK	14,834	SFV3L_P27401
PAPGSS	14,835	FOAMV_P14350_2mutA
GGGGSGGGGS	14,836	SFVCP_Q87040_2mutA
GSSGGSGGG	14,837	XMRV6_A1Z651
GGGGSGGGGSGGGGSGGGGSGGGGSGGGGS	14,838	MLVBM_Q7SVK7
GSSEAAAKGGG	14,839	FFV_O93209-Pro_2mut
GGSEAAAKPAP	14,840	SFV3L_P27401-Pro
GSSGGSGGG	14,841	SFV1_P23074_2mut
EAAAKGGGGSS	14,842	FOAMV_P14350_2mutA
GGGGGG	14,843	SFV3L_P27401_2mut
GGGGG	14,844	MLVBM_Q7SVK7_3mut
PAPEAAAKGGG	14,845	SFV3L_P27401
EAAAKGGSPAP	14,846	KORV_Q9TTC1_3mutA
GGGEAAAKPAP	14,847	SFV1_P23074_2mut
GSSGSSGSSGSSGSSGSS	14,848	KORV_Q9TTC1-Pro
EAAAKEAAAKEAAAKEAAAK	14,849	SFVCP_Q87040
PAPGSSEAAAK	14,850	MLVBM_Q7SVK7
GSSGSSGSS	14,851	FFV_O93209-Pro_2mut
GSSGGGPAP	14,852	SFV3L_P27401-Pro_2mut
GGGPAPEAAAK	14,853	WMSV_P03359_3mut
GGGEAAAK	14,854	MMTVB_P03365-Pro
GSSGSSGSSGSS	14,855	SFV3L_P27401-Pro_2mutA
PAPAPAPAPAP	14,856	FFV_O93209-Pro
GGSPAPEAAAK	14,857	FFV_O93209-Pro_2mut
GSSGSSGSSGSSGSSGSS	14,858	GALV_P21414
EAAAKEAAAKEAAAKEAAAKEAAAK	14,859	FOAMV_P14350
GGGPAPEAAAK	14,860	MMTVB_P03365-Pro
PAPGGSGGG	14,861	MLVF5_P26810_3mutA
PAPGGSGGG	14,862	FLV_P10273_3mut
GGGEAAAKGGS	14,863	SFV3L_P27401
GSAGSAAGSGEF	14,864	MLVBM_Q7SVK7_3mut
GSSPAPGGG	14,865	MPMV_P07572_2mutB
GSSGSSGSSGSSGSSGSS	14,866	FOAMV_P14350
GGSGGGGSS	14,867	BLVJ_P03361_2mut
PAPEAAAKGSS	14,868	SFV1_P23074-Pro
GGG		FFV_O93209

Linker amino acid sequence	SEQ ID NO:	RT domain name
EAAAKGGGGSS	14,870	SFV1_P23074_2mut
EAAAKEAAAKEAAAKEAAAKEAAAKEAAAK	14,871	SRV2_P51517
GGGGSGGGGSGGGGSGGGGSGGGGSGGGGS	14,872	MMTVB_P03365
GGGEAAAKGGS	14,873	MMTVB_P03365_WS
GSSGSS	14,874	SFV1_P23074
GSSGGGGGS	14,875	SFV3L_P27401
GGGGSSEAAAK	14,876	SFV1_P23074
EAAAKGSSGGS	14,877	HTL1A_P03362_2mutB
GSSEAAAKGGS	14,878	GALV_P21414_3mutA
EAAAKGSSPAP	14,879	SFV1_P23074
EAAAKPAPGSS	14,880	SFV3L_P27401_2mutA
PAPGSSGGG	14,881	SFV3L_P27401-Pro_2mut
GGGGSGGGGSGGGGSGGGGSGGGGSGGGGS	14,882	SFV3L_P27401-Pro
EAAAKEAAAKEAAAKEAAAKEAAAK	14,883	MMTVB_P03365_WS
GGGGSSEAAAK	14,884	MLVF5_P26810_3mutA
EAAAKGGSPAP	14,885	GALV_P21414
PAPEAAAKGSS	14,886	MMTVB_P03365_WS
GSSGGGGGS	14,887	SFVCP_Q87040_2mut
GGGGSSPAP	14,888	SFV1_P23074
EAAAKGGGGSS	14,889	XMRV6_A1Z651
PAPAPAPAP	14,890	MMTVB_P03365
GGSEAAAKGSS	14,891	SFV3L_P27401_2mutA
GSSPAPGGG	14,892	MMTVB_P03365_WS
GGGGGG	14,893	SFV3L_P27401-Pro
GGSGGSGGS	14,894	FOAMV_P14350-Pro_2mut
PAPAPAPAPAPAP	14,895	WMSV_P03359
GSSPAP	14,896	MLVBM_Q7SVK7
GGGGGSGSS	14,897	MMTVB_P03365_2mut_WS
EAAAKGSSGGS	14,898	MMTVB_P03365_2mutB_WS
EAAAK	14,899	FFV_O93209_2mutA
PAPEAAAK	14,900	SFV1_P23074-Pro
EAAAKGGSGSS	14,901	SFV3L_P27401
GGSGGSGGS	14,902	FFV_O93209-Pro
GSSGGGEAAAK	14,903	MMTVB_P03365
SGGSSGGSSGSETPGTSESATPESSGGSSGGSS	14,904	MLVFF_P26809_3mutA
GGSGGSGGSGGSGGSGGS	14,905	HTL1L_P0C211_2mutB
GGGEAAAK	14,906	SFV3L_P27401-Pro_2mutA
GGGGGSGSS	14,907	MMTVB_P03365
GSSPAPGGS	14,908	FOAMV_P14350_2mutA
EAAAKGSS	14,909	MLVMS_P03355

Linker amino acid sequence	SEQ ID NO:	RT domain name
GSSGGSGGG	14,910	FFV_O93209-Pro
GGSGGGGSS	14,911	MMTVB_P03365-Pro_2mut
GGSPAPGSS	14,912	FOAMV_P14350_2mut
GGSGGSGGSGGSGGSGGS	14,913	SFVCP_Q87040-Pro_2mut
GSSEAAAKGGG	14,914	FOAMV_P14350_2mutA
GGSGGSGGS	14,915	MMTVB_P03365-Pro
GSSGSSGSSGSSGSSGSS	14,916	MMTVB_P03365_2mut_WS
GSSGSSGSSGSSGSS	14,917	MMTVB_P03365-Pro
PAPEAAAK	14,918	WDSV_O92815
GSSGSSGSSGSSGSS	14,919	FFV_O93209-Pro_2mut
EAAAKGGGGSEAAAK	14,920	MMTVB_P03365-Pro
GGSPAPEAAAK	14,921	FOAMV_P14350
GSSGSS	14,922	PERV_Q4VFZ2
GGG		MMTVB_P03365-Pro
GGGGSGGGGSGGGGS	14,924	FFV_O93209_2mut
EAAAKEAAAKEAAAKEAAAKEAAAKEAAAK	14,925	MMTVB_P03365-Pro
GGSGSSPAP	14,926	WMSV_P03359
GGGGGGGG	14,927	SFV3L_P27401_2mut
PAPGSSEAAAK	14,928	FOAMV_P14350-Pro_2mutA
GGGGSSPAP	14,929	FOAMV_P14350_2mut
GSSGGSPAP	14,930	MLVBM_Q7SVK7_3mut
GSSGGGGGS	14,931	GALV_P21414_3mutA
EAAAKEAAAKEAAAKEAAAKEAAAK	14,932	MMTVB_P03365
GSSGGGGGS	14,933	SFV1_P23074_2mut
GGGGSEAAAKGGGGS	14,934	SFV1_P23074
GGGEAAAKPAP	14,935	FFV_O93209
PAPGGGEAAAK	14,936	SFV1_P23074
GGSGGGEAAAK	14,937	PERV_Q4VFZ2_3mutA_WS
GSSGGG	14,938	MMTVB_P03365-Pro
EAAAKGSSGGS	14,939	FFV_O93209_2mut
GGGGG	14,940	SFV1_P23074_2mut
GGGPAP	14,941	SFV3L_P27401
GSSGGSEAAAK	14,942	FFV_O93209
SGGSSGGSSGSETPGTSESATPESSGGSSGGSS	14,943	MMTVB_P03365-Pro
GSSGGGEAAAK	14,944	SFV1_P23074_2mutA
GSSGSSGSSGSSGSS	14,945	SFV3L_P27401_2mut
GGSEAAAKPAP	14,946	FLV_P10273
GGGGSGGGGS	14,947	FOAMV_P14350-Pro_2mutA
GSSEAAAKPAP	14,948	SFV3L_P27401
GGGGSEAAAKGGGGS	14,949	MMTVB_P03365-Pro

Linker amino acid sequence	SEQ ID NO:	RT domain name
PAPGSSEAAAK	14,950	MLVF5_P26810_3mut
EAAAKGGSGGG	14,951	SFV3L_P27401
GGGPAPGGS	14,952	SFV3L_P27401
GSSEAAAKGGS	14,953	FOAMV_P14350_2mutA
EAAAKGGSGGG	14,954	HTL1L_P0C211
GSSGGSPAP	14,955	SFV3L_P27401_2mutA
PAPAP	14,956	FFV_O93209
PAPGGSGSS	14,957	MMTVB_P03365_WS
EAAAKGGGGGS	14,958	FOAMV_P14350_2mut
PAPEAAAKGGS	14,959	SFV3L_P27401_2mut
GSSEAAAKPAP	14,960	MMTVB_P03365-Pro
GGSGGS	14,961	PERV_Q4VFZ2_3mut
GSSEAAAKGGG	14,962	FFV_O93209-Pro_2mutA
EAAAK	14,963	HTL1L_P0C211
GSSPAP	14,964	MLVMS_P03355
EAAAKPAPGGG	14,965	FFV_O93209-Pro_2mut
GGGGSEAAAKGGGGS	14,966	SFV1_P23074-Pro_2mut
EAAAKGSSGGS	14,967	SFV3L_P27401
GSAGSAAGSGEF	14,968	FFV_O93209_2mutA
PAPEAAAKGGS	14,969	MMTVB_P03365_2mutB_WS
EAAAKEAAAKEAAAKEAAAKEAAAKEAAAK	14,970	MMTVB_P03365
GGS		MMTVB_P03365
GGSEAAAKPAP	14,972	SFV1_P23074
EAAAKGSSGGG	14,973	HTLV2_P03363_2mut
GGSEAAAKGGG	14,974	MMTVB_P03365_WS
GGSGGS	14,975	FFV_O93209-Pro
GSSEAAAKGGS	14,976	MMTVB_P03365-Pro
PAPAPAPAPAP	14,977	SFV1_P23074_2mutA
GGSEAAAKGGG	14,978	MMTVB_P03365_2mutB_WS
PAPAPAPAP	14,979	MMTVB_P03365_WS
GGGGSGGGGSGGGGSGGGGSGGGGS	14,980	HTL3P_Q4U0X6_2mut
PAPGGSEAAAK	14,981	SFV1_P23074-Pro_2mut
GGSGGGPAP	14,982	MMTVB_P03365
GSSGSSGSSGSSGSSGSS	14,983	MMTVB_P03365-Pro
GGSEAAAKPAP	14,984	SFV1_P23074-Pro
GGGEAAAKGSS	14,985	SFV3L_P27401_2mutA
GGGPAPGGS	14,986	AVIRE_P03360
PAPGGG	14,987	MLVRD_P11227
GGSEAAAKGSS	14,988	SFV3L_P27401_2mut
GGGEAAAKGSS	14,989	FOAMV_P14350_2mut

Linker amino acid sequence	SEQ ID NO:	RT domain name
GGGEAAAKGSS	14,990	SFV1_P23074-Pro
EAAAKEAAAKEAAAKEAAAK	14,991	MLVAV_P03356
EAAAKGGGPAP	14,992	JSRV_P31623_2mutB
EAAAKGGGGSS	14,993	FOAMV_P14350_2mut
EAAAKEAAAKEAAAKEAAAKEAAAK	14,994	SRV2_P51517
GSSGGGGGS	14,995	FFV_O93209
PAPAPAP	14,996	FOAMV_P14350_2mutA
GGSGGSGGSGGS	14,997	FOAMV_P14350
GGGEAAAK	14,998	MMTVB_P03365_WS
GGGGGS	14,999	SFV1_P23074_2mutA
GGSGGS	15,000	WMSV_P03359_3mut
EAAAKGGS	15,001	MMTVB_P03365-Pro
GGGGSS	15,002	BLVJ_P03361_2mut
PAPAP	15,003	MMTVB_P03365-Pro_2mut
PAPGGG	15,004	SMRVH_P03364
EAAAKGGGGSS	15,005	SFV3L_P27401
PAPAPAPAPAP	15,006	MMTVB_P03365
GGGPAP	15,007	MMTVB_P03365-Pro
GSSGGSGGG	15,008	MMTVB_P03365
EAAAKGGGPAP	15,009	FOAMV_P14350_2mutA
GSSGSSGSSGSS	15,010	SFV1_P23074
GGGGSGGGGS	15,011	SFV3L_P27401
GSSGGSGGG	15,012	MLVF5_P26810
GGGEAAAKPAP	15,013	MMTVB_P03365-Pro
PAPEAAAK	15,014	HTLV2_P03363_2mut
GSSGSSGSSGSS	15,015	FOAMV_P14350_2mut
GSSEAAAKPAP	15,016	MMTVB_P03365-Pro
PAPEAAAKGGG	15,017	HTL3P_Q4U0X6_2mut
GGSEAAAKGSS	15,018	MMTVB_P03365-Pro
EAAAKPAPGGS	15,019	MMTVB_P03365_2mut_WS
GSSGGSEAAAK	15,020	MLVF5_P26810_3mutA
GGGGSGGGGSGGGGSGGGGSGGGGSGGGGS	15,021	MLVF5_P26810_3mut
EAAAKGGGGSS	15,022	MMTVB_P03365-Pro
GGGGGSGSS	15,023	HTL1A_P03362_2mutB
PAPAP	15,024	FFV_O93209-Pro_2mut
GGGGGSPAP	15,025	HTL1C_P14078_2mut
GGGPAP	15,026	HTLV2_P03363_2mut
EAAAKGGGGSEAAAK	15,027	SFVCP_Q87040
GGSEAAAKGGG	15,028	FFV_O93209-Pro_2mutA
GSSPAPGGS	15,029	FOAMV_P14350-Pro_2mut

Linker amino acid sequence	SEQ ID NO:	RT domain name
GGGGGGG	15,030	MMTVB_P03365-Pro
EAAAKGSS	15,031	SFV3L_P27401_2mutA
EAAAKGGGGSEAAAK	15,032	MMTVB_P03365-Pro
GGGGSEAAAKGGGGS	15,033	SFV1_P23074-Pro_2mutA
EAAAKGGGGSS	15,034	MMTVB_P03365
GGGEAAAKGGS	15,035	SFV1_P23074
PAPEAAAKGGG	15,036	MLVF5_P26810
GGGGSSGGS	15,037	MMTVB_P03365
GGSGSS	15,038	MMTVB_P03365
PAPAPAPAPAPAP	15,039	KORV_Q9TTC1
EAAAKGGG	15,040	SFV1_P23074-Pro_2mut
PAPAPAPAPAPAP	15,041	SRV2_P51517
GSSGSSGSSGSSGSS	15,042	FFV_O93209-Pro_2mutA
GGGGSS	15,043	FOAMV_P14350_2mut
PAPGGGEAAAK	15,044	MMTVB_P03365_WS
GGSGGGEAAAK	15,045	FFV_O93209-Pro_2mut
PAPAPAPAPAP	15,046	MMTVB_P03365_WS
GGGEAAAKGGS	15,047	MMTVB_P03365-Pro
GGGEAAAKGSS	15,048	MMTVB_P03365_2mutB
GSSPAPEAAAK	15,049	MMTVB_P03365_WS
EAAAKEAAAKEAAAKEAAAKEAAAK	15,050	SFV1_P23074-Pro_2mutA
PAPGGG	15,051	SFV3L_P27401
GSSEAAAKGGG	15,052	MMTVB_P03365_WS
GGGGSSEAAAK	15,053	FOAMV_P14350_2mut
PAPGSSGGS	15,054	SFV1_P23074-Pro_2mut
GSSGSSGSSGSSGSSGSS	15,055	SFV3L_P27401
EAAAKGSSGGG	15,056	MMTVB_P03365
PAPGGGGSS	15,057	WDSV_O92815_2mutA
GGSPAP	15,058	MMTVB_P03365-Pro
GGSGGSGGSGGSGGS	15,059	SFVCP_Q87040-Pro_2mut
PAPAPAPAP	15,060	MMTVB_P03365-Pro
GGGGG	15,061	HTL1A_P03362
GGSGGSGGSGGS	15,062	SFV1_P23074_2mutA
GSSGSSGSSGSSGSS	15,063	FOAMV_P14350-Pro_2mut
PAPGGSEAAAK	15,064	MMTVB_P03365_2mutB_WS
PAPAPAPAP	15,065	SFV1_P23074_2mut
PAPGGGGSS	15,066	MMTVB_P03365
GGSGSS	15,067	SFV3L_P27401_2mut
EAAAKEAAAKEAAAKEAAAK	15,068	MMTVB_P03365_2mut
EAAAKGGSGGG	15,069	HTL3P_Q4U0X6_2mut

Linker amino acid sequence	SEQ ID NO:	RT domain name
PAPGGGGSS	15,070	SFVCP_Q87040-Pro_2mutA
EAAAKGGGGGS	15,071	MLVAV_P03356
GGGGGS	15,072	FOAMV_P14350_2mut
GGGEAAAKGGS	15,073	FFV_O93209-Pro_2mutA
EAAAKPAPGGG	15,074	MMTVB_P03365_2mutB
GGSGGGPAP	15,075	FFV_O93209_2mut
GSSEAAAKPAP	15,076	MMTVB_P03365
PAPAPAPAPAPAP	15,077	SFV1_P23074_2mut
GGSPAPGGG	15,078	MMTVB_P03365-Pro
GGSGGGEAAAK	15,079	MMTVB_P03365
PAPAP	15,080	SFVCP_Q87040
GSSEAAAK	15,081	SFVCP_Q87040
GGGGSGGGGSGGGGS	15,082	MMTVB_P03365-Pro
GSSGSSGSS	15,083	SFV3L_P27401
EAAAKGGSGGG	15,084	MMTVB_P03365-Pro
GSSPAP	15,085	SFV1_P23074_2mut
GGGEAAAK	15,086	SFV1_P23074-Pro
AEAAAKEAAAKEAAAKEAAAKALEAEAAAKEAAAKEAAAKEAAAKA	15,087	MMTVB_P03365-Pro
PAPGGS	15,088	HTL1C_P14078_2mut
PAPGSSGGS	15,089	SFV1_P23074_2mut
PAPEAAAK	15,090	MMTVB_P03365_WS
PAPAP	15,091	MMTVB_P03365-Pro
EAAAKGGS	15,092	HTL1A_P03362_2mut
GGGGSEAAAKGGGGS	15,093	HTL1C_P14078
EAAAKGSSGGS	15,094	FOAMV_P14350-Pro
PAPGGSGSS	15,095	MMTVB_P03365-Pro
PAPGGSEAAAK	15,096	SFV1_P23074_2mut
PAPGSSEAAAK	15,097	FFV_O93209-Pro_2mut
PAPGSSGGG	15,098	FOAMV_P14350-Pro_2mutA
GSSGGGEAAAK	15,099	AVIRE_P03360
GGGGGG	15,100	SMRVH_P03364_2mut
PAPEAAAKGGG	15,101	MMTVB_P03365-Pro
GGGEAAAKGGS	15,102	SFVCP_Q87040_2mutA
PAPAPAPAPAP	15,103	SRV2_P51517
GSSGSSGSSGSSGSSGSS	15,104	MMTVB_P03365
EAAAKGGGPAP	15,105	MLVAV_P03356
PAPAPAPAPAP	15,106	FOAMV_P14350-Pro_2mutA
PAPGGSEAAAK	15,107	FOAMV_P14350
GSSGGGPAP	15,108	HTL32_Q0R5R2_2mutB
GGGGGSPAP	15,109	HTL3P_Q4U0X6_2mutB

Linker amino acid sequence	SEQ ID NO:	RT domain name
GSSGGSGGG	15,110	MMTVB_P03365-Pro
PAPAP	15,111	SFVCP_Q87040-Pro
GSSGGGPAP	15,112	MMTVB_P03365-Pro
GGSGSS	15,113	MMTVB_P03365-Pro_2mut
GGSPAPEAAAK	15,114	SFV1_P23074-Pro_2mut
EAAAKGGSGGG	15,115	SFV3L_P27401_2mut
GGGGSSEAAAK	15,116	MMTVB_P03365_WS
GGGGGSGSS	15,117	MMTVB_P03365_2mut
GGGGSSGGS	15,118	SFV1_P23074-Pro_2mutA
EAAAKGGGGSEAAAK	15,119	MMTVB_P03365_WS
PAPGGGEAAAK	15,120	SFV1_P23074-Pro
PAPEAAAKGGG	15,121	MMTVB_P03365
AEAAAKEAAAKEAAAKEAAAKALEAEAAAKEAAAKEAAAKEAAAKA	15,122	MMTVB_P03365
GSSGGSEAAAK	15,123	FOAMV_P14350-Pro_2mut
GGSPAP	15,124	MLVBM_Q7SVK7_3mut
GSSEAAAK	15,125	FOAMV_P14350
GSSEAAAK	15,126	MMTVB_P03365-Pro
EAAAKGSSGGS	15,127	HTL1A_P03362_2mut
GGGEAAAKPAP	15,128	FOAMV_P14350-Pro_2mut
EAAAKGGSPAP	15,129	FOAMV_P14350
GSSEAAAKPAP	15,130	MMTVB_P03365_WS
GSSGSSGSS	15,131	FOAMV_P14350_2mut
EAAAKEAAAKEAAAKEAAAK	15,132	MMTVB_P03365_WS
EAAAK	15,133	MMTVB_P03365
PAPGSS	15,134	BAEVM_P10272
PAPGGS	15,135	FFV_O93209-Pro_2mut
GGSGGS	15,136	SFV1_P23074-Pro_2mutA
SGGSSGGSSGSETPGTSESATPESSGGSSGGSS	15,137	HTLV2_P03363_2mut
GGSGGGEAAAK	15,138	MMTVB_P03365_WS
PAPGSSGGG	15,139	HTL1A_P03362
GGSGGS	15,140	SFV3L_P27401-Pro
GSSGSS	15,141	SFV1_P23074-Pro
PAPGGSEAAAK	15,142	MMTVB_P03365
GSAGSAAGSGEF	15,143	MMTVB_P03365-Pro
PAPGGG	15,144	FOAMV_P14350_2mut
EAAAKGGSGSS	15,145	MMTVB_P03365_WS
GSSGGGEAAAK	15,146	SFV3L_P27401-Pro
GGSGGGPAP	15,147	FOAMV_P14350-Pro_2mut
PAPAPAPAPAPAP	15,148	WDSV_O92815
SGSETPGTSESATPES	15,149	SFVCP_Q87040-Pro_2mutA

Linker amino acid sequence	SEQ ID NO:	RT domain name
GGSGGSGGS	15,150	SFV1_P23074
GGGGSS	15,151	SFVCP_Q87040_2mut
GGGGGSEAAAK	15,152	MMTVB_P03365
SGSETPGTSESATPES	15,153	MMTVB_P03365_WS
PAPAPAP	15,154	SFV3L_P27401
PAPEAAAKGSS	15,155	MMTVB_P03365_2mutB_WS
GSSGSSGSSGSSGSS	15,156	SRV2_P51517
GGGPAPGSS	15,157	HTL32_Q0R5R2_2mutB
GGSGGGGSS	15,158	MMTVB_P03365-Pro
SGSETPGTSESATPES	15,159	SRV2_P51517
EAAAKGSSGGS	15,160	MMTVB_P03365-Pro
GSSPAPEAAAK	15,161	MMTVB_P03365-Pro
GSSPAPEAAAK	15,162	SRV2_P51517
GGGGSSPAP	15,163	MMTVB_P03365-Pro
PAPGGGEAAAK	15,164	SFV1_P23074-Pro_2mutA
PAPEAAAKGGS	15,165	MMTVB_P03365
GSSGSSGSSGSSGSSGSS	15,166	FOAMV_P14350-Pro
GGSPAPGSS	15,167	SFV3L_P27401
GGGPAPGGS	15,168	SFV1_P23074-Pro_2mutA
GGGPAPGSS	15,169	MMTVB_P03365-Pro
EAAAKPAP	15,170	MLVBM_Q7SVK7
EAAAKEAAAKEAAAK	15,171	HTL1C_P14078
GSSGGSEAAAK	15,172	SRV2_P51517
PAPGGGGGS	15,173	SRV2_P51517
GGGEAAAK	15,174	FFV_O93209-Pro_2mut
EAAAKGGGPAP	15,175	HTL32_Q0R5R2
GGSGSSGGG	15,176	MMTVB_P03365
PAPEAAAKGSS	15,177	MMTVB_P03365-Pro
PAPGGGGGS	15,178	MMTVB_P03365-Pro
EAAAKGGGGGS	15,179	MMTVB_P03365_WS
GGGGGS	15,180	MMTVB_P03365-Pro
GGGGSGGGGSGGGGSGGGGSGGGGS	15,181	HTL1C_P14078
EAAAKGGSPAP	15,182	MMTVB_P03365
GGGGSSPAP	15,183	FFV_O93209-Pro_2mut
GGGGSSGGS	15,184	MMTVB_P03365-Pro
PAPGSSGGS	15,185	MMTVB_P03365-Pro
GGGGGS	15,186	SRV2_P51517
GGSGSSGGG	15,187	MMTVB_P03365
GSSGGSEAAAK	15,188	MMTVB_P03365-Pro
EAAAKEAAAKEAAAKEAAAK	15,189	GALV_P21414

Linker amino acid sequence	SEQ ID NO:	RT domain name
GGSEAAAKGGG	15,190	MMTVB_P03365-Pro
SGGSSGGSSGSETPGTSESATPESSGGSSGGSS	15,191	MMTVB_P03365-Pro
GSSEAAAKGGS	15,192	MMTVB_P03365
GGGGSGGGGSGGGGSGGGGSGGGGSGGGGS	15,193	HTL3P_Q4U0X6_2mutB
GGGEAAAK	15,194	MMTVB_P03365-Pro
PAPAPAPAP	15,195	MMTVB_P03365-Pro
PAPGSSGGG	15,196	MMTVB_P03365
GSSGSSGSSGSSGSS	15,197	GALV_P21414
GGSPAP	15,198	MMTVB_P03365_WS
GGGGSGGGGSGGGGSGGGGSGGGGSGGGGS	15,199	MMTVB_P03365-Pro
PAPEAAAK	15,200	MMTVB_P03365-Pro
PAPGSSGGG	15,201	SFV1_P23074-Pro_2mutA
GGGGGSEAAAK	15,202	MMTVB_P03365_2mutB_WS
PAPAPAPAPAP	15,203	MMTVB_P03365-Pro
EAAAKGGSGSS	15,204	MMTVB_P03365-Pro
EAAAKEAAAKEAAAKEAAAK	15,205	MLVRD_P11227_3mut
PAPAPAPAP	15,206	FOAMV_P14350_2mutA
GGGPAPGSS	15,207	SFVCP_Q87040_2mut
PAPEAAAKGSS	15,208	SFVCP_Q87040_2mut
GGSPAPGGG	15,209	MMTVB_P03365-Pro
GGGGSGGGGSGGGGSGGGGS	15,210	MMTVB_P03365
EAAAKGGS	15,211	HTL3P_Q4U0X6_2mut
PAPGSSGGS	15,212	MMTVB_P03365_WS
GGGGSGGGGS	15,213	MMTVB_P03365
GGSGGS	15,214	FOAMV_P14350
EAAAKGGGGSEAAAK	15,215	SFVCP_Q87040-Pro_2mut
EAAAKEAAAKEAAAKEAAAK	15,216	MMTVB_P03365-Pro_2mutB
PAPGGGEAAAK	15,217	SFVCP_Q87040-Pro
GSSGSS	15,218	JSRV_P31623_2mutB
EAAAKGGGGGS	15,219	MMTVB_P03365_2mut_WS
GSSPAPEAAAK	15,220	MMTVB_P03365-Pro
GGGEAAAK	15,221	HTL1C_P14078
PAPEAAAKGSS	15,222	HTL32_Q0R5R2_2mutB
GGGGSSEAAAK	15,223	MMTVB_P03365-Pro
PAPGSSGGS	15,224	MMTVB_P03365-Pro
EAAAKGGGGGS	15,225	MMTVB_P03365
GGGGSGGGGSGGGGSGGGGS	15,226	MMTVB_P03365
EAAAKGGGGSS	15,227	HTL3P_Q4U0X6_2mut
GGGEAAAKGGS	15,228	SFVCP_Q87040-Pro
GGGGGSPAP	15,229	MMTVB_P03365-Pro_2mutB

Linker amino acid sequence	SEQ ID NO:	RT domain name
GGSGGGEAAAK	15,230	SFV3L_P27401-Pro
PAPGGGGGS	15,231	SFV3L_P27401-Pro
EAAAKGGGGSEAAAK	15,232	MMTVB_P03365
PAPEAAAKGSS	15,233	MMTVB_P03365-Pro
GGSEAAAKGGG	15,234	MMTVB_P03365-Pro
GGSGGSGGSGGSGGS	15,235	SMRVH_P03364_2mutB
GGSGGSGGSGGSGGS	15,236	HTL1L_P0C211_2mut
GGGGGG	15,237	WDSV_O92815
GGGGGSGSS	15,238	MMTVB_P03365-Pro
GGSEAAAKPAP	15,239	SFV3L_P27401-Pro_2mut
GGGPAPGSS	15,240	MMTVB_P03365_2mut_WS
GGGGGS	15,241	MMTVB_P03365_WS
GGSPAPEAAAK	15,242	MMTVB_P03365
PAPEAAAKGGS	15,243	HTL1A_P03362
EAAAKGGSGSS	15,244	MMTVB_P03365_2mut_WS
GGGPAPEAAAK	15,245	SFV3L_P27401-Pro_2mut
PAPGGGGSS	15,246	HTL32_Q0R5R2_2mut
GSSPAPGGG	15,247	HTL3P_Q4U0X6_2mut
GGGGSSGGS	15,248	BLVAU_P25059_2mut
EAAAKGGGGGS	15,249	HTL1L_P0C211
GGSEAAAKGSS	15,250	JSRV_P31623_2mutB
GSSGGG	15,251	JSRV_P31623
GGSGGSGGSGGS	15,252	MMTVB_P03365-Pro
EAAAKPAP	15,253	SFV1_P23074-Pro_2mutA
GGGGSSGGS	15,254	MMTVB_P03365_WS
GGSGGS	15,255	MMTVB_P03365_WS
EAAAKGGGGGS	15,256	MMTVB_P03365-Pro
GGGGSGGGGSGGGGSGGGGSGGGGSGGGGS	15,257	MMTVB_P03365
GGSGGSGGS	15,258	MMTVB_P03365
GGGGGSEAAAK	15,259	MLVBM_Q7SVK7
GGSGSSPAP	15,260	MMTVB_P03365_WS
EAAAKEAAAKEAAAK	15,261	JSRV_P31623
PAPEAAAKGGS	15,262	MMTVB_P03365-Pro
GGSGSSEAAAK	15,263	FOAMV_P14350
GGGGGSGSS	15,264	MMTVB_P03365-Pro_2mut
GGGPAPGGS	15,265	MMTVB_P03365
SGSETPGTSESATPES	15,266	SFVCP_Q87040_2mut
GSSPAPGGS	15,267	SFV1_P23074-Pro_2mutA
GSSGSSGSSGSSGSS	15,268	MMTVB_P03365
EAAAKGGGPAP	15,269	MMTVB_P03365

Linker amino acid sequence	SEQ ID NO:	RT domain name
GSSGGG	15,270	MMTVB_P03365_2mut_WS
GGGEAAAKPAP	15,271	MMTVB_P03365
PAPGGSGGG	15,272	MMTVB_P03365-Pro
GSSGGSGGG	15,273	WDSV_O92815_2mut
GGSGGG	15,274	HTL32_Q0R5R2_2mut
EAAAKGGSPAP	15,275	HTLV2_P03363_2mut
GGSPAPEAAAK	15,276	MMTVB_P03365-Pro
GSSGGSEAAAK	15,277	MMTVB_P03365_2mut
GSAGSAAGSGEF	15,278	MMTVB_P03365_WS
PAPGGSGSS	15,279	FFV_O93209
GGSEAAAKGGG	15,280	MMTVB_P03365
GGSPAPGSS	15,281	MMTVB_P03365-Pro
GSSGGSGGG	15,282	SFV3L_P27401
PAPEAAAKGGG	15,283	HTL1A_P03362_2mutB
GGGEAAAKPAP	15,284	MMTVB_P03365-Pro
GGSEAAAK	15,285	HTL32_Q0R5R2_2mutB
GGGEAAAKGSS	15,286	MPMV_P07572
GGGGGSEAAAK	15,287	MMTVB_P03365-Pro
PAPAPAPAPAP	15,288	SFVCP_Q87040-Pro_2mutA
PAPAPAPAPAP	15,289	HTL1L_P0C211_2mut
GGGGSSGGS	15,290	HTL3P_Q4U0X6
PAPGGSEAAAK	15,291	MMTVB_P03365_2mut_WS
PAPAPAPAPAP	15,292	HTL1A_P03362
EAAAKPAPGGG	15,293	MMTVB_P03365_2mut_WS
GGSEAAAK	15,294	MMTVB_P03365_2mut_WS
GGGEAAAKGSS	15,295	SFV1_P23074-Pro_2mutA
GGSPAPGSS	15,296	MMTVB_P03365-Pro
GGSEAAAKPAP	15,297	MLVBM_Q7SVK7
PAPEAAAKGGG	15,298	MMTVB_P03365_2mut_WS
GSSEAAAKPAP	15,299	MMTVB_P03365-Pro_2mutB
GGGGSEAAAKGGGGS	15,300	MMTVB_P03365-Pro_2mut
GSSEAAAKGGS	15,301	MMTVB_P03365-Pro_2mutB
GSSGSSGSSGSSGSS	15,302	SRV2_P51517_2mutB
GGGGGSPAP	15,303	HTL1L_P0C211_2mut
GGSEAAAK	15,304	MMTVB_P03365
GSSPAPEAAAK	15,305	SMRVH_P03364_2mutB
GGGPAPGGS	15,306	HTL1C_P14078_2mut
GGSPAPEAAAK	15,307	MMTVB_P03365_WS
GGSEAAAKPAP	15,308	HTL1A_P03362_2mut
PAPAPAPAP	15,309	HTLV2_P03363_2mut

Linker amino acid sequence	SEQ ID NO:	RT domain name
GSSPAPGGG	15,310	MMTVB_P03365
GSSGSSGSSGSS	15,311	MMTVB_P03365-Pro
GGSEAAAKGSS	15,312	MMTVB_P03365_WS
GGSGSSGGG	15,313	MMTVB_P03365_2mutB
GSSGSSGSSGSSGSSGSS	15,314	JSRV_P31623_2mutB
GGSEAAAKPAP	15,315	MMTVB_P03365-Pro
GSSGGSGGG	15,316	HTLV2_P03363_2mut
AEAAAKEAAAKEAAAKEAAAKALEAEAAAKEAAAKEAAAKEAAAKA	15,317	WDSV_O92815_2mut
GGSPAPEAAAK	15,318	MMTVB_P03365
GGGGSSEAAAK	15,319	MMTVB_P03365
GGSGGGEAAAK	15,320	SFV1_P23074-Pro_2mutA
GGGGSEAAAKGGGGS	15,321	WDSV_O92815_2mut
GGSGSSEAAAK	15,322	MMTVB_P03365_2mutB_WS
GGSEAAAKPAP	15,323	MMTVB_P03365_WS
GSSGGGEAAAK	15,324	SFVCP_Q87040-Pro
GSSGGS	15,325	SFVCP_Q87040-Pro_2mut
GGSEAAAKPAP	15,326	SFVCP_Q87040_2mut
GSSGGSEAAAK	15,327	SFVCP_Q87040_2mut
GSSPAPEAAAK	15,328	SRV2_P51517_2mutB
GGSGGSGGSGGSGGSGGS	15,329	BLVAU_P25059
GSSGSSGSSGSSGSS	15,330	HTL1C_P14078_2mut
EAAAKGGGGSS	15,331	MMTVB_P03365_2mutB
GGGEAAAKGSS	15,332	SFVCP_Q87040-Pro

Example 3: Quantifying activity of a gene editing polypeptide and template for rewriting the endogenous FAH locus achieved in primary mouse hepatocytes

This example demonstrates the use of a gene modifying system containing a gene modifying polypeptide and a template RNA, to convert an A nucleotide to a G nucleotide in the endogenous *Fah* locus in mouse primary hepatocytes derived from a Fah5981SB mouse. The Fah5981SB mouse model harbors a G to A point mutation in the last nucleotide of exon 8 of the *Fah* gene, leading to aberrant mRNA splicing and subsequent mRNA degradation, without the production of Fah protein and, and thus serves as a mouse model of hereditary tyrosinemia type I.

In this example, the template RNA contained:

(1) a gRNA spacer;

(2) a gRNA scaffold;

(3) a heterologous object sequence; and

(4) a primer binding site (PBS) sequence.

More specifically, the template RNA (including chemical modification pattern) comprised the following sequences:

FAH1_R14_P12_Heavy RNACS048-001

mG*mG*mA*rUrGrGrUrCrCrUrCrArUrGrArArCrGrArCrGrUrUrUrUrArGrAmGmCmUmAmGmAmAmAmUmAmGmCrArArGrUrUrArArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmUmGmAmAmAmAmAmAmGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrUrUrArCrCrGrCrUrCrCrArGrUrCrGrUrUrCrArUrGrArG*mG*mA*mC (SEQ ID NO: 30421)

FAH1_R15_P10_Heavy RNACS049-001

mG*mG*mA*rUrGrGrUrCrCrUrCrArUrGrArArCrGrArCrGrUrUrUrUrArGrAmGmCmUmAmGmAmAmAmUmAmGmCrArArGrUrUrArArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmUmGmAmAmAmAmAmAmGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrArUrUrArCrCrGrCrUrCrCrArGrUrCrGrUrUrCrArUrG*mA*mG*Mg (SEQ ID NO:30422)

FAH2_R19_P11_MUT_Heavy RNACS052-001

mU*mC*mA*rGrArGrGrArArGrCrUrGrGrGrCrCrArCrCrGrUrUrUrUrArGrAmGmCmUmAmGmAmAmAmUmAmGmCrArArGrUrUrArArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmUmGmAmAmAmAmAmAmGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrUrGrGrArGrCrGrGrUrArArUrGrGrCrUrGrGrUrGrGrCrCrCrArGrC*mU*mU*mC (SEQ ID NO: 30423)

FAH2_R19_P13_MUT_Heavy RNACS053-001

mU*mC*mA*rGrArGrGrArArGrCrUrGrGrGrCrCrArCrCrGrUrUrUrUrArGrAmGmCmUmAmGmAmAmAmUmAmGmCrArArGrUrUrArArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmUmGmAmAmAmAmAmAmGmUmGmGmCmAmCmCmGmAm

GmUmCmGmGmUmGmCrUrGrGrArGrCrGrGrUrArArUrGrGrCrUrGrGrUrGrGrCrCrCrA rGrCrUrU*mC*mC*mU (SEQ ID NO: 30424)

Additional exemplary template RNAs that could be utilized in this experiment include the following:

FAH1 RNACS050

mG*mG*mA*rUrGrGrUrCrCrUrCrArUrGrArArCrGrArCrGrUrUrUrUrArGrAmGmCmUmAm GmAmAmAmUmAmGmCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUr CrAmAmCmUmUmGmAmAmAmAmAmGmUmGmGmCmAmCmCmGmAmGmUmCmGmG mUmGmCrArGrGrCrArUrUrArCrCrGrCrUrCrCrArGrUrCrGrUrUrCrArUrGrArG*mG*mA*m C (SEQ ID NO: 30425)

FAH1 RNACS051

mG*mG*mA*rUrGrGrUrCrCrUrCrArUrGrArArCrGrArCrGrUrUrUrUrArGrAmGmCmUmAm GmAmAmAmUmAmGmCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUr CrAmAmCmUmUmGmAmAmAmAmAmGmUmGmGmCmAmCmCmGmAmGmUmCmGmG mUmGmCrArGrGrCrArUrUrArCrCrGrCrUrCrCrArGrUrCrGrUrUrCrArUrG*mA*mG*mG (SEQ ID NO: 30426)

In the sequences above m=2’-O-methyl ribonucleotide, r=ribose and *=phosphorothioate bond.

The gene modifying polypeptides tested comprised sequence of: RNAV209 (nCas9-RT) and RNAV214 (wtCas9-RT). Specifically, the nCas9-RT and the wtCas9-RT had the following amino acid sequences:

nCas9-RT (RNAV209):

MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLI GALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRLEESFLVE EDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHF LIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQL PGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYAD

LFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYK
EIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNG
SIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKS
EETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVK
YVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRF
NASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKV
MKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKE
DIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMAR
ENQTTQKGQKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMY
VDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDK**A**RGKSDNVPSEEVVKKMKN
YWRQLLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMN
TKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK
KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRK
RPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKESILPKRNSDKL
IARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNP
IDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYL
ASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHR
DKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRI
DLSQLGGDSGGSSGGSSGSETPGTSESATPESSGGSSGGSSTLNIEDEYRLHETSKEPDVS
LGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQR
LLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGL
PPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTL
FNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAK
KAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPG
FAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQG
YAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPL
VILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEG
LQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIW
AKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTS
EGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPD
TSTLLIENSSPSGGSKRTADGSEFEKRTADGSEFESPKKKAKVE (SEQ ID NO: 30427)

wtCas9-RT (RNAV214-040):

MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLI
GALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRLEESFLVE
EDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHF
LIEGDLNPDNSDVDKLFIQLVQTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQL
PGEKKNGLFGNLIALSLGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYAD
LFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYK
EIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNG
SIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIPYYVGPLARGNSRFAWMTRKS
EETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLYEYFTVYNELTKVK
YVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRF
NASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKV
MKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFKE
DIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMAR
ENQTTQKGQKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMY
VDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKNRGKSDNVPSEEVVKKMKN
YWRQLLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMN
TKYDENDKLIREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIK
KYPKLESEFVYGDYKVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRK
RPLIETNGETGEIVWDKGRDFATVRKVLSMPQVNIVKKTEVQTGGFSKESILPKRNSDKL
IARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNP
IDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASAGELQKGNELALPSKYVNFLYL
ASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADANLDKVLSAYNKHR
DKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDATLIHQSITGLYETRI
DLSQLGGDSGGSSGGSSGSETPGTSESATPESSGGSSGGSSTLNIEDEYRLHETSKEPDVS
LGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQR
LLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGL
PPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTL
FNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAK
KAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPG
FAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQG

YAKGVLTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPL
VILAPHAVEALVKQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEG
LQHNCLDILAEAHGTRPDLTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIW
AKALPAGTSAQRAELIALTQALKMAEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTS
EGKEIKNKDEILALLKALFLPKRLSIIHCPGHQKGHSAEARGNRMADQAARKAAITETPD
TSTLLIENSSPSGGSKRTADGSEFEKRTADGSEFESPKKKAKVE (SEQ ID NO: 30428)

Underlining indicates the residue that differs between the nickase and wild-type sequences.

The gene modifying system comprising the gene modifying polypeptides listed above and the template RNA described above were transfected into primary mouse hepatocytes. The gene modifying polypeptide and the template RNA were delivered by nucleofection in the RNA format. Specifically, 4 µg of gene modifying polypeptide mRNA were combined with 10 µg of chemically synthesized template RNA in 5 µL of water. The transfection mix was added to 100,000 mouse primary hepatocytes in Buffer P3 [Lonza], and cells were nucleofected using program DG-138. After nucleofection, cells were grown at 37˚C, 5% CO_2 for 3 days prior to cell lysis and genomic DNA extraction. To analyze gene editing activity, primers flanking the target insertion site locus were used to amplify across the locus. Amplicons were analyzed via short read sequencing using an Illumina MiSeq. Conversion of terminal A to G sequence in exon 8 of *fah* gene indicates successful editing.

As shown in FIG. 2, for FAH2 templates, perfect rewrite levels (conversion of A to G with no unwanted mutations detected) of 4-8% were detected with RNAV209 but not with RNAV214. Indel levels of 4.4 to 6.6% were observed with RNAV209. Furthermore, the amount of WT *Fah* mRNA was measured using quantitative RT-PCR using primers that bind to exons 7 and 8. As shown in FIG. 3, FAH2 templates result in an increase in the abundance of *Fah* mRNA relative to WT by up to 12% when FAH2 template is tested with RNAV209 mRNA. These results demonstrate the use of a gene modifying system to reverse a mutation in the *Fah* gene, resulting in partial restoration of the expression of wild-type *Fah* mRNA.

Example 4: Quantifying activity of a gene editing polypeptide and template in vivo for rewriting the endogenous FAH locus achieved in mouse liver

This example demonstrates the use of a gene modifying system containing a gene modifying polypeptide and a template RNA, to convert an A nucleotide to a G nucleotide in the Fah5981SB mouse model into the endogenous *Fah* locus in mouse liver. The Fah5981SB mouse model harbors a G to A point mutation in the last nucleotide of exon 8 of the *Fah* gene, leading to aberrant mRNA splicing and subsequent mRNA degradation, without the production of Fah protein and serves as a mouse model of hereditary tyrosinemia type I.

In this example, the template RNA contained:

(1) a gRNA spacer;
(2) a gRNA scaffold;
(3) a heterologous object sequence; and
(4) a primer binding site (PBS) sequence.

More specifically, the template RNA comprised the following sequences:

FAH1_R14_P12_Heavy RNACS048-001

mG*mG*mA*rUrGrGrUrCrCrUrCrArUrGrArArCrGrArCrGrUrUrUrUrArGrAmGmCmUmAmGmAmAmAmUmAmGmCrArArGrUrUrArArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmUmGmAmAmAmAmAmGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrUrUrArCrCrGrCrUrCrCrArGrUrCrGrUrUrCrArUrGrArG*mG*mA*mC (SEQ ID NO: 30429)

FAH1_R15_P10_Heavy RNACS049-001

mG*mG*mA*rUrGrGrUrCrCrUrCrArUrGrArArCrGrArCrGrUrUrUrUrArGrAmGmCmUmAmGmAmAmAmUmAmGmCrArArGrUrUrArArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmUmGmAmAmAmAmAmGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrArUrUrArCrCrGrCrUrCrCrArGrUrCrGrUrUrCrArUrG*mA*mG*mG (SEQ ID NO: 30430)

FAH2_R19_P11_MUT_Heavy RNACS052-001

mU*mC*mA*rGrArGrGrArArGrCrUrGrGrGrCrCrArCrCrGrUrUrUrUrArGrAmGmCm UmAmGmAmAmAmUmAmGmCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrG rUrUrArUrCrAmAmCmUmUmGmAmAmAmAmAmGmUmGmGmCmAmCmCmGmAm GmUmCmGmGmUmGmCrUrGrGrArGrCrGrGrUrArArUrGrGrCrUrGrGrUrGrGrCrCrCrA rGrC*mU*mU*mC (SEQ ID NO:30431)

FAH2_R19_P13_MUT_Heavy RNACS053-001

mU*mC*mA*rGrArGrGrArArGrCrUrGrGrGrCrCrArCrCrGrUrUrUrUrArGrAmGmCm UmAmGmAmAmAmUmAmGmCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrG rUrUrArUrCrAmAmCmUmUmGmAmAmAmAmAmGmUmGmGmCmAmCmCmGmAm GmUmCmGmGmUmGmCrUrGrGrArGrCrGrGrUrArArUrGrGrCrUrGrGrUrGrGrCrCrCrA rGrCrUrU*mC*mC*mU (SEQ ID NO: 30432)

The gene modifying polypeptides tested comprised a sequence of: RNAV209 and RNAV214, the sequences of which are each provided in Example 3.

The gene modifying system comprising the gene modifying polypeptides and the template RNA described above was formulated in LNP and delivered to mice. Specifically, 2mg/kg of total RNA equivalent formulated in LNPs, combined at 1:1 (w/w) of template RNA and mRNA, were dosed intravenously in 7 to 9-week-old, mixed gender Fah5981SB mice. Six hours or 6 days post-dosing, animals were sacrificed, and their liver collected for analyses. To determine the expression distribution of the gene modifying polypeptide in the liver, 6-hr liver samples were subjected to immunohistochemistry using an anti-Cas9 antibody. Upon staining, quantification of Cas9-positive hepatocytes was determined by QuPath Markup. As shown in FIG.4, the expression of the gene modifying polypeptide was observed in 82-91% of hepatocytes.

To analyze gene editing activity, primers flanking the target insertion site locus were used to amplify across the locus in the genomic DNA of liver samples collected 6 days post-dosing. Amplicons were analyzed via short read sequencing using an Illumina MiSeq. Conversion of an A nucleotide to a G nucleotide indicates successful editing. As shown in FIG.5, perfect rewrite

levels (conversion of A to G with no unwanted mutations detected) of 0.1% - 1.9% were detected across the different groups. Indel levels were in the range of 0.2% - 0.4%.

To determine the phenotypic correction caused by the gene editing activity, the restoration of wild-type FAH mRNA was determined by real-time qRT-PCR, and the restoration of Fah protein expression determined by immunohistochemistry using an anti-Fah antibody. As shown in FIG.6, wild-type mRNA restoration of 0.1% - 6%, relative to littermate heterozygous mice, was detected across the different groups. As shown in FIG. 7, Fah protein was detected in 0.1% - 7% of liver cross-sectional area across the different groups. These results demonstrate the use of a gene modifying system to reverse a mutation in the *Fah* gene in an *in vivo* mouse model for hereditary tyrosinemia type I, resulting in partial restoration of expression of wild-type *Fah* mRNA and Fah protein.

Example 5. Gene editing at the TTR locus in an in vivo mouse model

This Example demonstrates successful delivery of an mRNA and guide using Cas9-mediated gene editing using the protospacer sequence ACACAAAUACCAGUCCAGCG (SEQ ID NO: 37641) that targets the TTR locus using a gene modifying polypeptide and RNA in a C57Blk/6 mouse.

RNAs were prepared as follows. An mRNA encoding a gene modifying polypeptide having the sequence shown in Table 5A1 below was produced by in vitro transcription and the purified mRNA was dissolved in 1 mM sodium citrate, pH 6, to a final concentration of RNA of 1-2 mg/mL. Similarly, a guide RNA having a sequence shown in Table 5A1 below was produced by chemical synthesis and dissolved in water or aqueous buffer, to a final concentration of RNA of 1-2 mg/mL.

Table 5A1. Sequences of Example 5

Name	SEQ ID NO	Nucleic acid sequence
Cas9-RT gene	30433	AUGCCUGCGGCUAAGCGGGUAAAAUUGGAUGGUGGGGACAAG AAGUACAGCAUCGGCCUGGACAUCGGCACCAACUCUGUGGGCU GGGCCGUGAUCACCGACGAGUACAAGGUGCCCAGCAAGAAAUU CAAGGUGCUGGGCAACACCGACCGGCACAGCAUCAAGAAGAAC

modifying polypeptide		CUGAUCGGAGCCCUGCUGUUCGACAGCGGCGAAACAGCCGAGG CCACCCGGCUGAAGAGAACCGCCAGAAGAAGAUACACCAGACG GAAGAACCGGAUCUGCUAUCUGCAAGAGAUCUUCAGCAACGAG AUGGCCAAGGUGGACGACAGCUUCUUCCACAGACUGGAAGAGU CCUUCCUGGUGGAAGAGGAUAAGAAGCACGAGCGGCACCCCAU CUUCGGCAACAUCGUGGACGAGGUGGCCUACCACGAGAAGUAC CCCACCAUCUACCACCUGAGAAAGAAACUGGUGGACAGCACCG ACAAGGCCGACCUGCGGCUGAUCUAUCUGGCCCUGGCCCACAU GAUCAAGUUCCGGGGCCACUUCCUGAUCGAGGGCGACCUGAAC CCCGACAACAGCGACGUGGACAAGCUGUUCAUCCAGCUGGUGC AGACCUACAACCAGCUGUUCGAGGAAAACCCCAUCAACGCCAG CGGCGUGGACGCCAAGGCCAUCCUGUCUGCCAGACUGAGCAAG AGCAGACGGCUGGAAAAUCUGAUCGCCCAGCUGCCCGGCGAGA AGAAGAAUGGCCUGUUCGGAAACCUGAUUGCCCUGAGCCUGGG CCUGACCCCCAACUUCAAGAGCAACUUCGACCUGGCCGAGGAU GCCAAACUGCAGCUGAGCAAGGACACCUACGACGACGACCUGG ACAACCUGCUGGCCCAGAUCGGCGACCAGUACGCCGACCUGUU UCUGGCCGCCAAGAACCUGUCCGACGCCAUCCUGCUGAGCGAC AUCCUGAGAGUGAACACCGAGAUCACCAAGGCCCCCCUGAGCG CCUCUAUGAUCAAGAGAUACGACGAGCACCACCAGGACCUGAC CCUGCUGAAAGCUCUCGUGCGGCAGCAGCUGCCUGAGAAGUAC AAAGAGAUUUUCUUCGACCAGAGCAAGAACGGCUACGCCGGCU ACAUUGACGGCGGAGCCAGCCAGGAAGAGUUCUACAAGUUCAU CAAGCCCAUCCUGGAAAAGAUGGACGGCACCGAGGAACUGCUC GUGAAGCUGAACAGAGAGGACCUGCUGCGGAAGCAGCGGACCU UCGACAACGGCAGCAUCCCCCACCAGAUCCACCUGGGAGAGCU GCACGCCAUUCUGCGGCGGCAGGAAGAUUUUUACCCAUUCCUG AAGGACAACCGGGAAAAGAUCGAGAAGAUCCUGACCUUCCGCA UCCCCUACUACGUGGGCCCUCUGGCCAGGGGAAACAGCAGAUU CGCCUGGAUGACCAGAAAGAGCGAGGAAACCAUCACCCCCUGG AACUUCGAGGAAGUGGUGGACAAGGGCGCUUCCGCCCAGAGCU UCAUCGAGCGGAUGACCAACUUCGAUAAGAACCUGCCCAACGA GAAGGUGCUGCCCAAGCACAGCCUGCUGUACGAGUACUUCACC GUGUAUAACGAGCUGACCAAAGUGAAAUACGUGACCGAGGGA AUGAGAAAGCCCGCCUUCCUGAGCGGCGAGCAGAAAAAGGCCA UCGUGGACCUGCUGUUCAAGACCAACCGGAAAGUGACCGUGAA GCAGCUGAAAGAGGACUACUUCAAGAAAAUCGAGUGCUUCGAC UCCGUGGAAAUCUCCGGCGUGGAAGAUCGGUUCAACGCCUCCC UGGGCACAUACCACGAUCUGCUGAAAAUUAUCAAGGACAAGGA CUUCCUGGACAAUGAGGAAAACGAGGACAUUCUGGAAGAUAU CGUGCUGACCCUGACACUGUUUGAGGACAGAGAGAUGAUCGAG GAACGGCUGAAAACCUAUGCCCACCUGUUCGACGACAAAGUGA UGAAGCAGCUGAAGCGGCGGAGAUACACCGGCUGGGGCAGGCU GAGCCGGAAGCUGAUCAACGGCAUCCGGGACAAGCAGUCCGGC AAGACAAUCCUGGAUUUCCUGAAGUCCGACGGCUUCGCCAACA GAAACUUCAUGCAGCUGAUCCACGACGACAGCCUGACCUUUAA

		AGAGGACAUCCAGAAAGCCCAGGUGUCCGGCCAGGGCGAUAGC CUGCACGAGCACAUUGCCAAUCUGGCCGGCAGCCCCGCCAUUA AGAAGGGCAUCCUGCAGACAGUGAAGGUGGUGGACGAGCUCG UGAAAGUGAUGGGCCGGCACAAGCCCGAGAACAUCGUGAUCGA AAUGGCCAGAGAGAACCAGACCACCCAGAAGGGACAGAAGAAC AGCCGCGAGAGAAUGAAGCGGAUCGAAGAGGGCAUCAAAGAG CUGGGCAGCCAGAUCCUGAAAGAACACCCCGUGGAAAACACCC AGCUGCAGAACGAGAAGCUGUACCUGUACUACCUGCAGAAUGG GCGGGAUAUGUACGUGGACCAGGAACUGGACAUCAACCGGCUG UCCGACUACGAUGUGGACCAUAUCGUGCCUCAGAGCUUUCUGA AGGACGACUCCAUCGACAACAAGGUGCUGACCAGAAGCGACAA GAAUCGGGGCAAGAGCGACAACGUGCCCUCCGAAGAGGUCGUG AAGAAGAUGAAGAACUACUGGCGGCAGCUGCUGAACGCCAAGC UGAUUACCCAGAGAAAGUUCGACAAUCUGACCAAGGCCGAGAG AGGCGGCCUGAGCGAACUGGAUAAGGCCGGCUUCAUCAAGAGA CAGCUGGUGGAAACCCGGCAGAUCACAAAGCACGUGGCACAGA UCCUGGACUCCCGGAUGAACACUAAGUACGACGAGAAUGACAA GCUGAUCCGGGAAGUGAAAGUGAUCACCCUGAAGUCCAAGCUG GUGUCCGAUUUCCGGAAGGAUUUCCAGUUUUACAAAGUGCGCG AGAUCAACAACUACCACCACGCCCACGACGCCUACCUGAACGC CGUCGUGGGAACCGCCCUGAUCAAAAAGUACCCUAAGCUGGAA AGCGAGUUCGUGUACGGCGACUACAAGGUGUACGACGUGCGGA AGAUGAUCGCCAAGAGCGAGCAGGAAAUCGGCAAGGCUACCGC CAAGUACUUCUUCUACAGCAACAUCAUGAACUUUUUCAAGACC GAGAUUACCCUGGCCAACGGCGAGAUCCGGAAGCGGCCUCUGA UCGAGACAAACGGCGAAACCGGGGAGAUCGUGUGGGAUAAGG GCCGGGAUUUUGCCACCGUGCGGAAAGUGCUGAGCAUGCCCCA AGUGAAUAUCGUGAAAAAGACCGAGGUGCAGACAGGCGGCUU CAGCAAAGAGUCUAUCCUGCCCAAGAGGAACAGCGAUAAGCUG AUCGCCAGAAAGAAGGACUGGGACCCUAAGAAGUACGGCGGCU UCGACAGCCCCACCGUGGCCUAUUCUGUGCUGGUGGUGGCCAA AGUGGAAAAGGGCAAGUCCAAGAAACUGAAGAGUGUGAAAGA GCUGCUGGGGAUCACCAUCAUGGAAAGAAGCAGCUUCGAGAAG AAUCCCAUCGACUUUCUGGAAGCCAAGGGCUACAAAGAAGUGA AAAAGGACCUGAUCAUCAAGCUGCCUAAGUACUCCCUGUUCGA GCUGGAAAACGGCCGGAAGAGAAUGCUGGCCUCUGCCGGCGAA CUGCAGAAGGGAAACGAACUGGCCCUGCCCUCCAAAUAUGUGA ACUUCCUGUACCUGGCCAGCCACUAUGAGAAGCUGAAGGGCUC CCCCGAGGAUAAUGAGCAGAAACAGCUGUUUGUGGAACAGCAC AAGCACUACCUGGACGAGAUCAUCGAGCAGAUCAGCGAGUUCU CCAAGAGAGUGAUCCUGGCCGACGCUAAUCUGGACAAAGUGCU GUCCGCCUACAACAAGCACCGGGAUAAGCCCAUCAGAGAGCAG GCCGAGAAUAUCAUCCACCUGUUUACCCUGACCAAUCUGGGAG CCCCUGCCGCCUUCAAGUACUUUGACACCACCAUCGACCGGAA GAGGUACACCAGCACCAAAGAGGUGCUGGACGCCACCCUGAUC CACCAGAGCAUCACCGGCCUGUACGAGACACGGAUCGACCUGU

		CUCAGCUGGGAGGUGACUCUGGAGGAUCUAGCGGAGGAUCCUC UGGCAGCGAGACACCAGGAACAAGCGAGUCAGCAACACCAGAG AGCAGUGGCGGCAGCAGCGGCGGCAGCAGCACCCUAAAUAUAG AAGAUGAGUAUCGGCUACAUGAGACCUCAAAAGAGCCAGAUG UUUCUCUAGGGUCCACAUGGCUGUCUGAUUUUCCUCAGGCCUG GGCGGAAACCGGGGGCAUGGGACUGGCAGUUCGCCAAGCUCCU CUGAUCAUACCUCUGAAAGCAACCUCUACCCCCGUGUCCAUAA AACAAUACCCCAUGUCACAAGAAGCCAGACUGGGGAUCAAGCC CCACAUACAGAGACUGUUGGACCAGGGAAUACUGGUACCCUGC CAGUCCCCCUGGAACACGCCCCUGCUACCCGUUAAGAAACCAG GGACUAAUGAUUAUAGGCCUGUCCAGGAUCUGAGAGAAGUCA ACAAGCGGGUGGAGGACAUCCACCCCACCGUGCCCAACCCUUA CAACCUCUUGAGCGGGCUCCCACCGUCCCACCAGUGGUACACU GUGCUUGAUUUAAAGGAUGCCUUUUUCUGCCUGAGACUCCACC CCACCAGUCAGCCUCUCUUCGCCUUUGAGUGGAGAGAUCCAGA GAUGGGAAUCUCAGGACAAUUGACCUGGACCAGACUCCCACAG GGUUUCAAAAACAGUCCCACCCUGUUUAAUGAGGCACUGCACA GAGACCUAGCAGACUUCCGGAUCCAGCACCCAGACUUGAUCCU GCUACAGUACGUGGAUGACUUACUGCUGGCCGCCACUUCUGAG CUAGACUGCCAACAAGGUACUCGGGCCCUGUUACAAACCCUAG GGAACCUCGGGUAUCGGGCCUCGGCCAAGAAAGCCCAAAUUUG CCAGAAACAGGUCAAGUAUCUGGGGUAUCUUCUAAAAGAGGG UCAGAGAUGGCUGACUGAGGCCAGAAAAGAGACUGUGAUGGG GCAGCCUACUCCGAAGACCCCUCGACAACUAAGGGAGUUCCUA GGGAAGGCAGGCUUCUGUCGCCUCUUCAUCCCUGGGUUUGCAG AAAUGGCAGCCCCCCUGUACCCUCUCACCAAACCGGGGACUCU GUUUAAUUGGGGCCCAGACCAACAAAAGGCCUAUCAAGAAAUC AAGCAAGCCCUUCUAACUGCCCCAGCCCUGGGGUUGCCAGAUU UGACUAAGCCCUUUGAACUCUUUGUCGACGAGAAGCAGGGCUA CGCCAAAGGUGUCCUAACGCAAAAACUGGGACCUUGGCGUCGG CCGGUGGCCUACCUGUCCAAAAAGCUAGACCCAGUAGCAGCUG GGUGGCCCCCUUGCCUACGGAUGGUAGCAGCCAUUGCCGUACU GACAAAGGAUGCAGGCAAGCUAACCAUGGGACAGCCACUAGUC AUUCUGGCCCCCCAUGCAGUAGAGGCACUAGUCAAACAACCCC CCGACCGCUGGCUUUCCAACGCCCGGAUGACUCACUAUCAGGC CUUGCUUUUGGACACGGACCGGGUCCAGUUCGGACCGGUGGUA GCCCUGAACCCGGCUACGCUGCUCCCACUGCCUGAGGAAGGGC UGCAACACAACUGCCUUGAUAUCCUGGCCGAAGCCCACGGAAC CCGACCCGACCUAACGGACCAGCCGCUCCCAGACGCCGACCACA CCUGGUACACGGAUGGAAGCAGUCUCUUACAAGAGGGACAGCG UAAGGCGGGAGCUGCGGUGACCACCGAGACCGAGGUAAUCUGG GCUAAAGCCCUGCCAGCCGGGACAUCCGCUCAGCGGGCUGAAC UGAUAGCACUCACCCAGGCCCUAAAGAUGGCAGAAGGUAAGAA GCUAAAUGUUUAUACUGAUAGCCGUUAUGCUUUUGCUACUGCC CAUAUCCAUGGAGAAAUAUACAGAAGGCGUGGGUGGCUCACA UCAGAAGGCAAAGAGAUCAAAAAUAAAGACGAGAUCUUGGCC

		CUACUAAAAGCCCUCUUUCUGCCCAAAAGACUUAGCAUAAUCC AUUGUCCAGGACAUCAAAAGGGACACAGCGCCGAGGCUAGAGG CAACCGGAUGGCUGACCAAGCGGCCCGAAAGGCAGCCAUCACA GAGACUCCAGACACCUCUACCCUCCUCAUAGAAAAUUCAUCAC CCUCUGGCGGCUCAAAAAGAACCGCCGACGGCAGCGAAUUCGA GAAAAGGACGGCGGAUGGUAGCGAAUUCGAGAGCCCUAAAAA GAAGGCCAAGGUAGAGUAA
guide RNA	30434	mA*mC*mA*CAAAUACCAGUCCAGCGGUUUUAGAmGmCmUmAm GmAmAmAmUmAmGmCAAGUUAAAAUAAGGCUAGUCCGUUAUC AmAmCmUmUmGmAmAmAmAmGmUmGmGmCmAmCmCmGmA mGmUmCmGmGmUmGmCmU*mU*mU*mU m=2′OMethyl, *=phosphorothioate linkage

Lipid nanoparticle (LNP) components (ionizable lipid, helper lipid, sterol, PEG) were dissolved in 100% ethanol with the lipid component molar ratios of 47:8:43.5:1.5, respectively. RNA (guide and mRNA) was combined in a 1:1 weight ratio and diluted to a concentration of 0.05-0.2 mg/mL in sodium acetate buffer, pH 5. RNA was formulated into distinct LNPs with a lipid amine to total RNA phosphate (N:P) molar ratio of 4.0. The LNPs were formed by microfluidic or turbulent mixing of the lipid and RNA solutions. A 3:1 ratio of aqueous to organic solvent was maintained during mixing using differential flow rates. After mixing, the LNPs were diluted, collected and buffer exchanged into 50 mM Tris, 9% sucrose buffer using tangential flow filtration. Formulations were concentrated to 1.0 mg/mL or higher then filtered through 0.2 μm sterile filter. The final LNP were stored at −80˚C until further use.

The LNP formulations were delivered intravenously by bolus tail vein injection to C57Blk/6 mice that were approximately 8 weeks old at concentrations ranging from 1-0.1 mg/kg. The expression of the Cas9-RT was measured by 6 hours after injection by euthanizing animals and collecting livers during necropsy. Animals were euthanized at 5 days after injection where liver was collected upon necropsy to which the activity of gene editing of the TTR locus was assessed. Expression of the Cas9-RT gene editing polypeptide in liver was measured by Western blot where Cas9 was detected by a mouse monoclonal antibody (7A9-3A3, Cell Signaling Technology) and GAPDH (Cell Signaling Technology) was used as a loading control. (FIG. 8). Editing of the TTR locus was quantified by Sanger sequencing followed by TIDE analysis of an amplicon of the TTR locus near the binding site of the protospacer. Editing of the

TTR locus was observed, as shown in FIG. 9. TTR protein levels in serum were quantified by an ELISA using a standard curve (Aviva Biosciences). TTR protein levels in serum declined in treated animals, as shown in FIG. 10. These experiments demonstrate that the Cas9-RT polypeptide can be expressed *in vivo*, and can edit the TTR locus, resulting in a decrease in TTR protein levels in serum.

Example 6. Gene editing at the TTR locus in an in vivo cynomolgus macaque model

This Example demonstrates successful delivery of an mRNA and guide using Cas9-mediated gene editing using the protospacer sequence ACACAAAUACCAGUCCAGCG (SEQ ID NO: 37641) that targets the TTR locus using a gene modifying polypeptide and RNA in a cynomolgus model.

RNAs were prepared as follows. An mRNA encoding a gene modifying polypeptide having the sequence shown in Table 6A1 below was produced by in vitro transcription and the purified mRNA was dissolved in 1 mM sodium citrate, pH 6, to a final concentration of RNA of 1-2 mg/mL. Similarly, a guide RNA having a sequence shown in Table 6A1 below was produced by chemical synthesis and dissolved in water or aqueous buffer, to a final concentration of RNA of 1-2 mg/mL.

Table 6A1. Sequences of Example 6

Name	SEQ ID NO	Nucleic acid sequence
Cas9-RT gene modifying polypeptide	30435	AUGCCUGCGGCUAAGCGGGUAAAAUUGGAUGGUGGGGACAAGA AGUACAGCAUCGGCCUGGACAUCGGCACCAACUCUGUGGGCUGG GCCGUGAUCACCGACGAGUACAAGGUGCCCAGCAAGAAAUUCAA GGUGCUGGGCAACACCGACCGGCACAGCAUCAAGAAGAACCUGA UCGGAGCCCUGCUGUUCGACAGCGGCGAAACAGCCGAGGCCACC CGGCUGAAGAGAACCGCCAGAAGAAGAUACACCAGACGGAAGAA CCGGAUCUGCUAUCUGCAAGAGAUCUUCAGCAACGAGAUGGCCA AGGUGGACGACAGCUUCUUCCACAGACUGGAAGAGUCCUUCCUG GUGGAAGAGGAUAAGAAGCACGAGCGGCACCCCAUCUUCGGCAA CAUCGUGGACGAGGUGGCCUACCACGAGAAGUACCCCACCAUCU ACCACCUGAGAAAGAAACUGGUGGACAGCACCGACAAGGCCGAC CUGCGGCUGAUCUAUCUGGCCCUGGCCCACAUGAUCAAGUUCCG GGGCCACUUCCUGAUCGAGGGCGACCUGAACCCCGACAACAGCG ACGUGGACAAGCUGUUCAUCCAGCUGGUGCAGACCUACAACCAG CUGUUCGAGGAAAACCCCAUCAACGCCAGCGGCGUGGACGCCAA GGCCAUCCUGUCUGCCAGACUGAGCAAGAGCAGACGGCUGGAAA AUCUGAUCGCCCAGCUGCCCGGCGAGAAGAAGAAUGGCCUGUUC

		GGAAACCUGAUUGCCCUGAGCCUGGGCCUGACCCCCAACUUCAA GAGCAACUUCGACCUGGCCGAGGAUGCCAAACUGCAGCUGAGCA AGGACACCUACGACGACGACCUGGACAACCUGCUGGCCCAGAUC GGCGACCAGUACGCCGACCUGUUUCUGGCCGCCAAGAACCUGUC CGACGCCAUCCUGCUGAGCGACAUCCUGAGAGUGAACACCGAGA UCACCAAGGCCCCCCUGAGCGCCUCUAUGAUCAAGAGAUACGAC GAGCACCACCAGGACCUGACCCUGCUGAAAGCUCUCGUGCGGCA GCAGCUGCCUGAGAAGUACAAAGAGAUUUUCUUCGACCAGAGCA AGAACGGCUACGCCGGCUACAUUGACGGCGGAGCCAGCCAGGAA GAGUUCUACAAGUUCAUCAAGCCCAUCCUGGAAAAGAUGGACGG CACCGAGGAACUGCUCGUGAAGCUGAACAGAGAGGACCUGCUGC GGAAGCAGCGGACCUUCGACAACGGCAGCAUCCCCCACCAGAUC CACCUGGGAGAGCUGCACGCCAUUCUGCGGCGGCAGGAAGAUUU UUACCCAUUCCUGAAGGACAACCGGGAAAAGAUCGAGAAGAUCC UGACCUUCCGCAUCCCCUACUACGUGGGCCCUCUGGCCAGGGGA AACAGCAGAUUCGCCUGGAUGACCAGAAAGAGCGAGGAAACCAU CACCCCCUGGAACUUCGAGGAAGUGGUGGACAAGGGCGCUUCCG CCCAGAGCUUCAUCGAGCGGAUGACCAACUUCGAUAAGAACCUG CCCAACGAGAAGGUGCUGCCCAAGCACAGCCUGCUGUACGAGUA CUUCACCGUGUAUAACGAGCUGACCAAAGUGAAAUACGUGACCG AGGGAAUGAGAAAGCCCGCCUUCCUGAGCGGCGAGCAGAAAAAG GCCAUCGUGGACCUGCUGUUCAAGACCAACCGGAAAGUGACCGU GAAGCAGCUGAAAGAGGACUACUUCAAGAAAAUCGAGUGCUUC GACUCCGUGGAAAUCUCCGGCGUGGAAGAUCGGUUCAACGCCUC CCUGGGCACAUACCACGAUCUGCUGAAAAUUAUCAAGGACAAGG ACUUCCUGGACAAUGAGGAAAACGAGGACAUUCUGGAAGAUAU CGUGCUGACCCUGACACUGUUUGAGGACAGAGAGAUGAUCGAGG AACGGCUGAAAACCUAUGCCCACCUGUUCGACGACAAAGUGAUG AAGCAGCUGAAGCGGCGGAGAUACACCGGCUGGGGCAGGCUGAG CCGGAAGCUGAUCAACGGCAUCCGGGACAAGCAGUCCGGCAAGA CAAUCCUGGAUUUCCUGAAGUCCGACGGCUUCGCCAACAGAAAC UUCAUGCAGCUGAUCCACGACGACAGCCUGACCUUUAAAGAGGA CAUCCAGAAAGCCCAGGUGUCCGGCCAGGGCGAUAGCCUGCACG AGCACAUUGCCAAUCUGGCCGGCAGCCCCGCCAUUAAGAAGGGC AUCCUGCAGACAGUGAAGGUGGUGGACGAGCUCGUGAAAGUGA UGGGCCGGCACAAGCCCGAGAACAUCGUGAUCGAAAUGGCCAGA GAGAACCAGACCACCCAGAAGGGACAGAAGAACAGCCGCGAGAG AAUGAAGCGGAUCGAAGAGGGCAUCAAAGAGCUGGGCAGCCAG AUCCUGAAAGAACACCCCGUGGAAAACACCCAGCUGCAGAACGA GAAGCUGUACCUGUACUACCUGCAGAAUGGGCGGGAUAUGUACG UGGACCAGGAACUGGACAUCAACCGGCUGUCCGACUACGAUGUG GACCAUAUCGUGCCUCAGAGCUUUCUGAAGGACGACUCCAUCGA CAACAAGGUGCUGACCAGAAGCGACAAGAAUCGGGGCAAGAGCG ACAACGUGCCCUCCGAAGAGGUCGUGAAGAAGAUGAAGAACUAC UGGCGGCAGCUGCUGAACGCCAAGCUGAUUACCCAGAGAAAGUU CGACAAUCUGACCAAGGCCGAGAGAGGCGGCCUGAGCGAACUGG

		AUAAGGCCGGCUUCAUCAAGAGACAGCUGGUGGAAACCCGGCAG AUCACAAAGCACGUGGCACAGAUCCUGGACUCCCGGAUGAACAC UAAGUACGACGAGAAUGACAAGCUGAUCCGGGAAGUGAAAGUG AUCACCCUGAAGUCCAAGCUGGUGUCCGAUUUCCGGAAGGAUUU CCAGUUUUACAAAGUGCGCGAGAUCAACAACUACCACCACGCCC ACGACGCCUACCUGAACGCCGUCGUGGGAACCGCCCUGAUCAAA AAGUACCCUAAGCUGGAAAGCGAGUUCGUGUACGGCGACUACAA GGUGUACGACGUGCGGAAGAUGAUCGCCAAGAGCGAGCAGGAA AUCGGCAAGGCUACCGCCAAGUACUUCUUCUACAGCAACAUCAU GAACUUUUUCAAGACCGAGAUUACCCUGGCCAACGGCGAGAUCC GGAAGCGGCCUCUGAUCGAGACAAACGGCGAAACCGGGGAGAUC GUGUGGGAUAAGGGCCGGGAUUUUGCCACCGUGCGGAAAGUGC UGAGCAUGCCCCAAGUGAAUAUCGUGAAAAAGACCGAGGUGCAG ACAGGCGGCUUCAGCAAAGAGUCUAUCCUGCCCAAGAGGAACAG CGAUAAGCUGAUCGCCAGAAAGAAGGACUGGGACCCUAAGAAGU ACGGCGGCUUCGACAGCCCCACCGUGGCCUAUUCUGUGCUGGUG GUGGCCAAAGUGGAAAAGGGCAAGUCCAAGAAACUGAAGAGUG UGAAAGAGCUGCUGGGGAUCACCAUCAUGGAAAGAAGCAGCUUC GAGAAGAAUCCCAUCGACUUUCUGGAAGCCAAGGGCUACAAAGA AGUGAAAAAGGACCUGAUCAUCAAGCUGCCUAAGUACUCCCUGU UCGAGCUGGAAAACGGCCGGAAGAGAAUGCUGGCCUCUGCCGGC GAACUGCAGAAGGGAAACGAACUGGCCCUGCCCUCCAAAUAUGU GAACUUCCUGUACCUGGCCAGCCACUAUGAGAAGCUGAAGGGCU CCCCCGAGGAUAAUGAGCAGAAACAGCUGUUUGUGGAACAGCAC AAGCACUACCUGGACGAGAUCAUCGAGCAGAUCAGCGAGUUCUC CAAGAGAGUGAUCCUGGCCGACGCUAAUCUGGACAAAGUGCUGU CCGCCUACAACAAGCACCGGGAUAAGCCCAUCAGAGAGCAGGCC GAGAAUAUCAUCCACCUGUUUACCCUGACCAAUCUGGGAGCCCC UGCCGCCUUCAAGUACUUUGACACCACCAUCGACCGGAAGAGGU ACACCAGCACCAAAGAGGUGCUGGACGCCACCCUGAUCCACCAG AGCAUCACCGGCCUGUACGAGACACGGAUCGACCUGUCUCAGCU GGGAGGUGACUCUGGAGGAUCUAGCGGAGGAUCCUCUGGCAGCG AGACACCAGGAACAAGCGAGUCAGCAACACCAGAGAGCAGUGGC GGCAGCAGCGGCGGCAGCAGCACCCUAAAUAUAGAAGAUGAGUA UCGGCUACAUGAGACCUCAAAAGAGCCAGAUGUUUCUCUAGGGU CCACAUGGCUGUCUGAUUUUCCUCAGGCCUGGGCGGAAACCGGG GGCAUGGGACUGGCAGUUCGCCAAGCUCCUCUGAUCAUACCUCU GAAAGCAACCUCUACCCCCGUGUCCAUAAAACAAUACCCCAUGU CACAAGAAGCCAGACUGGGGAUCAAGCCCCACAUACAGAGACUG UUGGACCAGGGAAUACUGGUACCCUGCCAGUCCCCCUGGAACAC GCCCCUGCUACCCGUUAAGAAACCAGGGACUAAUGAUUAUAGGC CUGUCCAGGAUCUGAGAGAAGUCAACAAGCGGGUGGAGGACAUC CACCCCACCGUGCCCAACCCUUACAACCUCUUGAGCGGGCUCCCA CCGUCCCACCAGUGGUACACUGUGCUUGAUUUAAAGGAUGCCUU UUUCUGCCUGAGACUCCACCCCACCAGUCAGCCUCUCUUCGCCU UUGAGUGGAGAGAUCCAGAGAUGGGAAUCUCAGGACAAUUGAC

		CUGGACCAGACUCCCACAGGGUUUCAAAAACAGUCCCACCCUGU UUAAUGAGGCACUGCACAGAGACCUAGCAGACUUCCGGAUCCAG CACCCAGACUUGAUCCUGCUACAGUACGUGGAUGACUUACUGCU GGCCGCCACUUCUGAGCUAGACUGCCAACAAGGUACUCGGGCCC UGUUACAAACCCUAGGGAACCUCGGGUAUCGGGCCUCGGCCAAG AAAGCCCAAAUUUGCCAGAAACAGGUCAAGUAUCUGGGGUAUCU UCUAAAAGAGGGUCAGAGAUGGCUGACUGAGGCCAGAAAAGAG ACUGUGAUGGGGCAGCCUACUCCGAAGACCCCUCGACAACUAAG GGAGUUCCUAGGGAAGGCAGGCUUCUGUCGCCUCUUCAUCCCUG GGUUUGCAGAAAUGGCAGCCCCCCUGUACCCUCUCACCAAACCG GGGACUCUGUUUAAUUGGGGCCCAGACCAACAAAAGGCCUAUCA AGAAAUCAAGCAAGCCCUUCUAACUGCCCCAGCCCUGGGGUUGC CAGAUUUGACUAAGCCCUUUGAACUCUUUGUCGACGAGAAGCAG GGCUACGCCAAAGGUGUCCUAACGCAAAAACUGGGACCUUGGCG UCGGCCGGUGGCCUACCUGUCCAAAAAGCUAGACCCAGUAGCAG CUGGGUGGCCCCCUUGCCUACGGAUGGUAGCAGCCAUUGCCGUA CUGACAAAGGAUGCAGGCAAGCUAACCAUGGGACAGCCACUAGU CAUUCUGGCCCCCCAUGCAGUAGAGGCACUAGUCAAACAACCCC CCGACCGCUGGCUUUCCAACGCCCGGAUGACUCACUAUCAGGCC UUGCUUUUGGACACGGACCGGGUCCAGUUCGGACCGGUGGUAGC CCUGAACCCGGCUACGCUGCUCCCACUGCCUGAGGAAGGGCUGC AACACAACUGCCUUGAUAUCCUGGCCGAAGCCCACGGAACCCGA CCCGACCUAACGGACCAGCCGCUCCCAGACGCCGACCACACCUGG UACACGGAUGGAAGCAGUCUCUUACAAGAGGGACAGCGUAAGGC GGGAGCUGCGGUGACCACCGAGACCGAGGUAAUCUGGGCUAAAG CCCUGCCAGCCGGGACAUCCGCUCAGCGGGCUGAACUGAUAGCA CUCACCCAGGCCCUAAAGAUGGCAGAAGGUAAGAAGCUAAAUGU UUAUACUGAUAGCCGUUAUGCUUUUGCUACUGCCCAUAUCCAUG GAGAAAUAUACAGAAGGCGUGGGUGGCUCACAUCAGAAGGCAA AGAGAUCAAAAAUAAAGACGAGAUCUUGGCCCUACUAAAAGCCC UCUUUCUGCCCAAAAGACUUAGCAUAAUCCAUUGUCCAGGACAU CAAAAGGGACACAGCGCCGAGGCUAGAGGCAACCGGAUGGCUGA CCAAGCGGCCCGAAAGGCAGCCAUCACAGAGACUCCAGACACCU CUACCCUCCUCAUAGAAAAUUCAUCACCCUCUGGCGGCUCAAAA AGAACCGCCGACGGCAGCGAAUUCGAGAAAAGGACGGCGGAUGG UAGCGAAUUCGAGAGCCCUAAAAAGAAGGCCAAGGUAGAGUAA
guide RNA	30436	mA*mC*mA*CAAAUACCAGUCCAGCGGUUUUAGAmGmCmUmAmG mAmAmAmUmAmGmCAAGUUAAAAUAAGGCUAGUCCGUUAUCAm AmCmUmUmGmAmAmAmAmAmGmUmGmGmCmAmCmCmGmAmGm UmCmGmGmUmGmCmU*mU*mU*mU m=2′OMethyl, *=phosphorothioate linkage

Lipid nanoparticle (LNP) components (ionizable lipid, helper lipid, sterol, PEG) were dissolved in 100% ethanol with the lipid component molar ratios of 47:8:43.5:1.5, respectively. RNA (guide and mRNA) was combined in a 1:1 weight ratio and diluted to a concentration of 0.05-0.2 mg/mL in sodium acetate buffer, pH 5. RNA was formulated into distinct LNPs with a lipid amine to total RNA phosphate (N:P) molar ratio of 4.0. The LNPs were formed by microfluidic or turbulent mixing of the lipid and RNA solutions. A 3:1 ratio of aqueous to organic solvent was maintained during mixing using differential flow rates. After mixing, the LNPs were diluted, collected and buffer exchanged into 50 mM Tris, 9% sucrose buffer using tangential flow filtration. Formulations were concentrated to 1.0 mg/mL or higher then filtered through 0.2 μm sterile filter. The final LNP were stored at −80˚C until further use. The LNP formulations were delivered intravenously by infusion over the course of 1 hour at 2 mg/kg where the volume of the infusion was 5 ml/kg. Cynomolgus macaques from mainland Asia were given dexamethasone 2 mg/kg bolus via intramuscular injection 1.5-2 h prior to intravenous infusion using a syringe pump. Animals were monitored after infusion and the expression of the Cas9-RT was measured by laparoscopic biopsies taken from the liver 8-12 h, 24 h, and 48 h after infusion. Animals were euthanized 14 days after infusion and liver was harvested by dividing the organ up into 8 different segments to which the activity of gene editing of the TTR locus was assessed. Expression of the Cas9-RT gene editing polypeptide in liver was quantified by capillary electrophoresis western blot using the ProteinSimple Jess system (bio-techne) where Cas9 was detected by a mouse monoclonal antibody (7A9-3A3, Cell Signaling Technology). Relative expression of the Cas9-RT gene editing polypeptide was measured by an area under curve analysis, as shown in FIG. 11. Editing of the TTR locus was quantified by amplicon-sequencing of the TTR locus near the binding site of the protospacer. Editing of the TTR locus was observed, as shown in FIG. 12. These experiments demonstrate that the Cas9-RT polypeptide can be expressed *in vivo* in a non-human primate model and can edit the TTR locus.

Example 7: Evaluating rewrite efficiency of exemplary template RNAs and second strand-nicking gRNAs with an exemplary gene modifying polypeptide in correcting an F263S mutation in a murine Pah gene in murine hepatocyte cells

This example describes the use of exemplary gene modifying systems containing either of two gene modifying polypeptides and template RNAs comprising varied lengths of

heterologous object sequences and PBS sequences to quantify the activity of template RNAs for correction of an F263S mutation (corresponding to a T835C base change) in the murine ***Pah*** gene. In this example, a template RNA contained:

(1) a gRNA spacer;
(2) a gRNA scaffold;
(3) a heterologous object sequence; and
(4) a primer binding site (PBS) sequence.

Exemplary template RNAs generated are given in Table E1. Two different versions of each template RNA were produced and tested (EM and HM), one with a first level and distributions of nucleotide modifications (e.g., phosphorothioate linkages denoted by an asterisk and/or 2'-O-methyl groups denoted by an 'm' preceding a nucleotide) and one with a second level and distribution.

In Examples 7-8, unless otherwise noted the HM version of a template RNA was used in the described experiments.

Table E1 – Exemplary Template RNAs and Sequences

RNACS	Name	Sequence	SEQ ID NO
RNACS1205	EM_mPKU5_R19_P9	mC*mC*mU*rArArUrGrUrArCrUrGrUrGrUrGrCrArGrUrGrUrUrUrUrArGrArGrCrUrArGrArArArUrArGrCrArArCrArArGrUrArArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrArArCrUrUrGrArArArArArGrUrGrGrCrArCrCrGrArGrUrCrGrGrUrGrCrGrCrCrUrUrCrCrGrArGrUrCrUrUrCrCrArCrUrGrCrArCrArC*mA*mG*mU	30437
RNACS1256	EM_mPKU5_R29_P8	mC*mC*mU*rArArUrGrUrArCrUrGrUrGrUrGrCrArGrUrGrUrUrUrUrArGrArGrCrUrArGrArArArUrArGrCrArArCrArArGrUrArArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrArArCrUrUrGrArArArArArGrUrGrGrCrArCrCrGrArGrUrCrGrGrUrGrCrGrCrCrUrUrCrCrGrArGrUrCrUrUrCrCrArCrUrGrCrArCrArA*mC*mA*mG	30438
RNACS1184	EM_mPKU5_R15_P10	mC*mC*mU*rArArUrGrUrArCrUrGrUrGrUrGrCrArGrUrGrUrUrUrUrArGrArGrCrUrArGrArArArUrArGrCrArArCrArArGrUrArArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrArArCrUrUrGrArArArArArGrUrGrGrCrArCrCrGrArGrUrCrGrGrUrGrCrGrCrCrUrUrCrCrGrArGrUrCrUrUrCrCrArCrUrGrCrArCrArA*mG*mU*mA	30439
RNACS1216	EM_mPKU5_R21_P8	mC*mC*mU*rArArUrGrUrArCrUrGrUrGrUrGrCrArGrUrGrUrUrUrUrArGrArGrCrUrArGrArArArUrArGrCrArArCrArArGrUrArArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrArArCrUrUrGrArArArArArGrUrGrGrCrArCrCrGrArGrUrCrGrGrUrGrCrGrCrCrUrUrCrCrGrArGrUrCrUrUrCrCrArCrUrGrCrArCrArA*mC*mA*mG	30440
RNACS1215	EM_mPKU5_R21_P9	mC*mC*mU*rArArUrGrUrArCrUrGrUrGrUrGrCrArGrUrGrUrUrUrUrArGrArGrCrUrArGrArArArUrArGrCrArArCrArArGrUrArArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrArArCrUrUrGrArArArArArGrUrGrGrCrArCrCrGrArGrUrCrGrGrUrGrCrGrCrCrUrUrCrCrGrArGrUrCrUrUrCrCrArCrUrGrCrArCrArC*mA*mG*mU	30441
RNACS1204	EM_mPKU5_R19_P10	mC*mC*mU*rArArUrGrUrArCrUrGrUrGrUrGrCrArGrUrGrUrUrUrUrArGrArGrCrUrArGrArArArUrArGrCrArArCrArArGrUrArArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrArArCrUrUrGrArArArArArGrUrGrGrCrArCrCrGrArGrUrCrGrGrUrGrCrGrCrCrUrUrCrCrGrArGrUrCrUrUrCrCrArCrUrGrCrArCrArA*mG*mU*mA	30442

RNACS1195	EM_mPKU5_R17_P9	mC*mC*mU*rArArUrGrUrArCrUrGrUrGrUrGrCrArGrUrGrUrUrUrUrArGrArGrCrUrArGrArArArUrArGrCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrArArCrUrUrGrArArArArArGrUrGrGrCrArCrCrGrArGrUrCrGrGrUrGrCrCrUrUrCrCrGrArGrUrCrUrUrCrCrArCrUrGrCrArCrArC*mA*mG*mU	30443
RNACS1206	EM_mPKU5_R19_P8	mC*mC*mU*rArArUrGrUrArCrUrGrUrGrUrGrCrArGrUrGrUrUrUrUrArGrArGrCrUrArGrArArArUrArGrCrArArGrUrGrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrArArCrUrUrGrArArArArArGrUrGrGrCrArCrCrGrArGrUrCrGrGrUrGrCrGrCrCrUrUrCrCrGrArGrUrCrUrUrCrCrArCrUrGrCrArCrA*mC*mA*mG	30444
RNACS1166	EM_mPKU5_R11_P8	mC*mC*mU*rArArUrGrUrArCrUrGrUrGrUrGrCrArGrUrGrUrUrUrUrArGrArGrCrUrArGrArArArUrArGrCrArArGrUrGrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrArArCrUrUrGrArArArArArGrUrGrGrCrArCrCrGrArGrUrCrGrGrUrGrCrArGrUrCrUrUrCrCrArCrUrGrGrCrArCrA*mC*mA*mG	30445
RNACS1196	EM_mPKU5_R17_P8	mC*mC*mU*rArArUrGrUrArCrUrGrUrGrUrGrCrArGrUrGrUrUrUrUrArGrArGrCrUrArGrArArArUrArGrCrArArGrUrGrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrArArCrUrUrGrArArArArArGrUrGrGrCrArCrCrGrArGrUrCrGrGrUrGrCrCrUrUrCrCrGrArGrUrCrUrUrCrCrArCrUrGrCrArCrA*mC*mA*mG	30446
RNACS1214	EM_mPKU5_R21_P10	mC*mC*mU*rArArUrGrUrArCrUrGrUrGrUrGrCrArGrUrGrUrUrUrUrArGrArGrCrUrArGrArArArUrArGrCrArArGrUrGrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrArArCrUrUrGrArArArArArGrUrGrGrCrArCrCrGrArGrUrCrGrGrUrGrCrUrGrGrCrCrUrUrCrCrGrArGrUrCrUrUrCrCrArCrUrGrCrArCrA*mG*mU*mA	30447
RNACS1186	EM_mPKU5_R15_P8	mC*mC*mU*rArArUrGrUrArCrUrGrUrGrUrGrCrArGrUrGrUrUrUrUrArGrArGrCrUrArGrArArArUrArGrCrArArGrUrGrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrArArCrUrUrGrArArArArArGrUrGrGrCrArCrCrGrArGrUrCrGrGrUrGrCrUrGrCrCrUrUrCrCrGrArGrUrCrUrUrCrCrArCrUrGrCrArCrA*mC*mA*mG	30448
RNACS1185	EM_mPKU5_R15_P9	mC*mC*mU*rArArUrGrUrArCrUrGrUrGrUrGrCrArGrUrGrUrUrUrUrArGrArGrCrUrArGrArArArUrArGrCrArArGrUrGrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrArArCrUrUrGrArArArArArGrUrGrGrCrArCrCrGrArGrUrCrGrGrUrGrCrUrGrCrCrUrUrCrCrGrArGrUrCrUrUrCrCrArCrUrGrCrArCrA*mA*mG*mU	30449

RNACS1174	EM_mPKU5_R13_P10	mC*mC*mU*rArArUrGrUrArCrUrGrUrGrUrGrCrArGrUrGrUrUrUrUrArGrArGrCrUrArGrArArArUrArGrCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrArArCrUrUrGrArArArArArGrUrGrGrCrArCrCrGrArGrUrCrGrGrUrGrCrCrGrArGrUrCrUrUrCrCrArCrUrGrCrArCrArCrA*mG*mU*mA	30450
RNACS1175	EM_mPKU5_R13_P9	mC*mC*mU*rArArUrGrUrArCrUrGrUrGrUrGrCrArGrUrGrUrUrUrUrArGrArGrCrUrArGrArArArUrArGrCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrArArCrUrUrGrArArArArArGrUrGrGrCrArCrCrGrArGrUrCrGrGrUrGrCrCrGrArGrUrCrUrUrCrCrArCrUrGrCrArCrArC*mA*mG*mU	30451
RNACS425	EM_mPKU5_2.1	mC*mC*mU*rArArUrGrUrArCrUrGrUrGrUrGrCrArGrUrGrUrUrUrUrArGrArGrCrUrArGrArArArUrArGrCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrArArCrUrUrGrArArArArArGrUrGrGrCrArCrCrGrArGrUrCrGrGrUrGrCrCrGrArGrUrCrUrUrCrCrArCrUrGrCrArCrArCrArGrUrA*mC*mA*mU	30452
RNACS1375	EM_mPKU6_R18_P9	mG*mC*mC*rUrArArUrGrUrArCrUrGrUrGrUrGrCrArGrGrUrUrUrUrArGrArGrCrUrArGrArArArUrArGrCrArArGrUrGrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrArArCrUrUrGrArArArArArGrUrGrGrCrArCrCrGrArGrUrCrGrGrUrGrCrCrUrUrCrCrGrArGrUrCrUrUrCrCrArCrUrGrCrArCrArCrA*mG*mU*mA	30453
RNACS1385	EM_mPKU6_R20_P9	mG*mC*mC*rUrArArUrGrUrArCrUrGrUrGrUrGrCrArGrGrUrUrUrUrArGrArGrCrUrArGrArArArUrArGrCrArArGrUrGrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrArArCrUrUrGrArArArArArGrUrGrGrCrArCrCrGrArGrUrCrGrGrUrGrCrCrUrUrCrCrGrArGrUrCrUrUrCrCrArCrUrGrCrArCrArCrArCrA*mG*mU*mA	30454
RNACS1355	EM_mPKU6_R14_P9	mG*mC*mC*rUrArArUrGrUrArCrUrGrUrGrUrGrCrArGrGrUrUrUrUrArGrArGrCrUrArGrArArArUrArGrCrArArGrUrGrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrArArCrUrUrGrArArArArArGrUrGrGrCrArCrCrGrArGrUrCrGrGrUrGrCrCrGrArGrUrCrUrUrCrCrArCrUrGrCrArCrArCrA*mG*mU*mA	30455
RNACS3664	EM_mPKU6_1.2	mG*mC*mC*rUrArArUrGrUrArCrUrGrUrGrUrGrCrArGrGrUrUrUrUrArGrArGrCrUrArGrArArArUrArGrCrArArGrUrGrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrArArCrUrUrGrArArArArArGrUrGrGrCrArCrCrGrArGrUrCrGrGrUrGrCrCrUrUrCrCrGrArGrUrCrUrUrCrCrArCrUrGrCrArCrArCrArGrUrArC*mA*mU*mU	30456

RNACS3665	HM_mPKU5_R19_P9	mC*mC*mU*rArArUrGrUrArCrUrGrUrGrUrGrCrArGrUrGrUrUrUrUrArGrAmGmCmUmAmGmAmAmAmUmAmGmCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmUmGmAmAmAmAmAmGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrGrCrCrUrUrCrCrGrArGrUrCrUrUrUrCrCrArCrUrGrCrArCrArC*mA*mG*mU	30457
RNACS3666	HM_mPKU5_R29_P8	mC*mC*mU*rArArUrGrUrArCrUrGrUrGrUrGrCrArGrUrGrUrUrUrUrArGrAmGmCmUmAmGmAmAmAmUmAmGmCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmUmGmAmAmAmAmAmGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrGrGrGrUrGrGrCrCrUrGrGrCrCrUrUrCrCrGrArGrUrCrUrUrCrCrArCrArC*mC*mA*mG	30458
RNACS3460	HM_mPKU5_R15_P10	mC*mC*mU*rArArUrGrUrArCrUrGrUrGrUrGrCrArGrUrGrUrUrUrUrArGrAmGmCmUmAmGmAmAmAmUmAmGmCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmUmGmAmAmAmAmAmGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrUrGrCrArCrArCrA*mG*mU*mA	30459
RNACS3667	HM_mPKU5_R21_P8	mC*mC*mU*rArArUrGrUrArCrUrGrUrGrUrGrCrArGrUrGrUrUrUrUrArGrAmGmCmUmAmGmAmAmAmUmAmGmCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmUmGmAmAmAmAmAmGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrUrGrGrCrCrUrUrCrCrGrArGrUrCrUrUrCrCrArCrArC*mC*mA*mG	30460
RNACS3668	HM_mPKU5_R21_P9	mC*mC*mU*rArArUrGrUrArCrUrGrUrGrUrGrCrArGrUrGrUrUrUrUrArGrAmGmCmUmAmGmAmAmAmUmAmGmCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmUmGmAmAmAmAmAmGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrUrGrGrCrCrUrUrCrCrGrArGrUrCrUrUrCrCrArCrArC*mA*mG*mU	30461
RNACS3669	HM_mPKU5_R19_P10	mC*mC*mU*rArArUrGrUrArCrUrGrUrGrUrGrCrArGrUrGrUrUrUrUrArGrAmGmCmUmAmGmAmAmAmUmAmGmCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmUmGmAmAmAmAmAmGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrGrCrCrUrUrCrCrGrArGrUrCrUrUrCrCrArCrArC*mG*mU*mA	30462
RNACS2302	HM_mPKU5_R17_P9	mC*mC*mU*rArArUrGrUrArCrUrGrUrGrUrGrCrArGrUrGrUrUrUrUrArGrAmGmCmUmAmGmAmAmAmUmAmGmCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmUmGmAmAmAmAmAmGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrCrUrUrGrCrCrGrArGrUrCrUrUrCrCrArCrArC*mA*mG*mU	30463

RNACS3670	HM_mPKU5_R19_P8	mC*mC*mU*rArArUrGrUrArCrUrGrUrGrUrGrCrArGrUrGrUrUrUrUrArGrAmGmCmUmAmGmAmAmAmUmAmGmCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmUmGmAmAmAmAmAmGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrGrCrCrUrUrCrCrGrArGrUrCrUrUrUrCrCrArCrUrGrCrArCrA*mC*mA*mG	30464
RNACS1855	HM_mPKU5_R11_P8	mC*mC*mU*rArArUrGrUrArCrUrGrUrGrUrGrCrArGrUrGrUrUrUrUrArGrAmGmCmUmAmGmAmAmAmUmAmGmCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmUmGmAmAmAmAmAmGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrArGrUrCrUrUrCrCrArCrUrGrCrCrArCrA*mC*mA*mG	30465
RNACS3671	HM_mPKU5_R17_P8	mC*mC*mU*rArArUrGrUrArCrUrGrUrGrUrGrCrArGrUrGrUrUrUrUrArGrAmGmCmUmAmGmAmAmAmUmAmGmCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmUmGmAmAmAmAmAmGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrCrUrUrCrCrGrArGrUrCrUrUrCrCrArCrUrGrCrArCrA*mC*mA*mG	30466
RNACS3672	HM_mPKU5_R21_P10	mC*mC*mU*rArArUrGrUrArCrUrGrUrGrUrGrCrArGrUrGrUrUrUrUrArGrAmGmCmUmAmGmAmAmAmUmAmGmCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmUmGmAmAmAmAmAmGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrUrGrGrCrCrUrUrCrCrGrArGrUrCrUrUrCrCrArCrArCrA*mG*mU*mA	30467
RNACS1862	HM_mPKU5_R15_P8	mC*mC*mU*rArArUrGrUrArCrUrGrUrGrUrGrCrArGrUrGrUrUrUrUrArGrAmGmCmUmAmGmAmAmAmUmAmGmCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmUmGmAmAmAmAmAmGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrUrCrCrGrArGrUrCrUrUrUrCrCrArCrUrGrCrArCrA*mC*mA*mG	30468
RNACS2103	HM_mPKU5_R15_P9	mC*mC*mU*rArArUrGrUrArCrUrGrUrGrUrGrCrArGrUrGrUrUrUrUrArGrAmGmCmUmAmGmAmAmAmUmAmGmCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmUmGmAmAmAmAmAmGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrUrCrCrGrArGrUrCrUrUrUrCrCrArCrUrGrCrArCrA*mA*mG*mU	30469
RNACS2104	HM_mPKU5_R13_P10	mC*mC*mU*rArArUrGrUrArCrUrGrUrGrUrGrCrArGrUrGrUrUrUrUrArGrAmGmCmUmAmGmAmAmAmUmAmGmCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmUmGmAmAmAmAmAmGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrCrGrArGrUrCrUrUrCrCrArCrUrGrCrArCrA*mG*mU*mA	30470

RNACS2099	HM_mPKU5_R13_P9	mC*mC*mU*rArArUrGrUrArCrUrGrUrGrUrGrCrArGrUrGrUrUrUrUrArGrAmGmCmUmAmGmAmAmAmUmAmGmCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmUmGmAmAmAmAmAmGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrCrGrArGrUrCrUrUrCrCrArCrUrGrCrArCrArC*mA*mG*mU	30471
RNACS3673	HM_mPKU5_2.1	mC*mC*mU*rArArUrGrUrArCrUrGrUrGrUrGrCrArGrUrGrUrUrUrUrArGrAmGmCmUmAmGmAmAmAmUmAmGmCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmUmGmAmAmAmAmAmGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrUrUrCrCrGrArGrUrCrUrUrCrCrArCrUrGrCrArCrArCrArGrUrA*mC*mA*mU	30472
RNACS1869	HM_mPKU6_R18_P9	mG*mC*mC*rUrArArUrGrUrArCrUrGrUrGrUrGrCrArGrGrUrUrUrUrArGrAmGmCmUmAmGmAmAmAmUmAmGmCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmUmGmAmAmAmAmAmGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrCrUrUrCrCrGrArGrUrCrUrUrCrCrArCrUrGrCrArCrArCrA*mG*mU*mA	30473
RNACS3674	HM_mPKU6_R20_P9	mG*mC*mC*rUrArArUrGrUrArCrUrGrUrGrUrGrCrArGrGrUrUrUrUrArGrAmGmCmUmAmGmAmAmAmUmAmGmCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmUmGmAmAmAmAmAmGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrGrCrCrUrUrCrCrGrArGrUrCrUrUrCrCrArCrUrGrCrArCrArCrA*mG*mU*mA	30474
RNACS2303	HM_mPKU6_R14_P9	mG*mC*mC*rUrArArUrGrUrArCrUrGrUrGrUrGrCrArGrGrUrUrUrUrArGrAmGmCmUmAmGmAmAmAmUmAmGmCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmUmGmAmAmAmAmAmGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrCrGrArGrUrCrUrUrCrCrArCrUrGrCrArCrArCrA*mG*mU*mA	30475
RNACS3675	HM_mPKU6_1.2	mG*mC*mC*rUrArArUrGrUrArCrUrGrUrGrUrGrCrArGrGrUrUrUrUrArGrAmGmCmUmAmGmAmAmAmUmAmGmCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmUmGmAmAmAmAmAmGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrCrUrUrCrCrGrArGrUrCrUrUrCrCrArCrUrGrCrArCrArCrArGrUrArC*mA*mU*mU	30476

Table E1A shows the sequences of E1 without chemical modifications. In some embodiments, the sequences of Table E1A may be used without chemical modifications, or with one or more chemical modifications.

Table E1A: Table E1 Sequences without Chemical Modifications

RNACS	Name	Sequence	SEQ ID NO
RNACS 1205	EM_mPKU 5_R19_P9	CCUAAUGUACUGUGUGCAGUGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUU GAAAAAGUGGCACCGAGUCGGUGCGCCUUCCGAGUCUUCCACUGCACACAGU	37166
RNACS 1256	EM_mPKU 5_R29_P8	CCUAAUGUACUGUGUGCAGUGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUU GAAAAAGUGGCACCGAGUCGGUGCGGGUGGCCUGGCCUUCCGAGUCUUCCACUGCACACAG	37167
RNACS 1184	EM_mPKU 5_R15_P10	CCUAAUGUACUGUGUGCAGUGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUU GAAAAAGUGGCACCGAGUCGGUGCUCCGAGUCUUCCACUGCACACAGUA	37168
RNACS 1216	EM_mPKU 5_R21_P8	CCUAAUGUACUGUGUGCAGUGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUU GAAAAAGUGGCACCGAGUCGGUGCUGGCCUUCCGAGUCUUCCACUGCACACAG	37169
RNACS 1215	EM_mPKU 5_R21_P9	CCUAAUGUACUGUGUGCAGUGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUU GAAAAAGUGGCACCGAGUCGGUGCUGGCCUUCCGAGUCUUCCACUGCACACAGU	37170
RNACS 1204	EM_mPKU 5_R19_P10	CCUAAUGUACUGUGUGCAGUGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUU GAAAAAGUGGCACCGAGUCGGUGCGCCUUCCGAGUCUUCCACUGCACACAGUA	37171
RNACS 1195	EM_mPKU 5_R17_P9	CCUAAUGUACUGUGUGCAGUGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUU GAAAAAGUGGCACCGAGUCGGUGCCUUCCGAGUCUUCCACUGCACACAGU	37172
RNACS 1206	EM_mPKU 5_R19_P8	CCUAAUGUACUGUGUGCAGUGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUU GAAAAAGUGGCACCGAGUCGGUGCGCCUUCCGAGUCUUCCACUGCACACAG	37173
RNACS 1166	EM_mPKU 5_R11_P8	CCUAAUGUACUGUGUGCAGUGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUU GAAAAAGUGGCACCGAGUCGGUGCAGUCUUCCACUGCACACAG	37174
RNACS 1196	EM_mPKU 5_R17_P8	CCUAAUGUACUGUGUGCAGUGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUU GAAAAAGUGGCACCGAGUCGGUGCCUUCCGAGUCUUCCACUGCACACAG	37175
RNACS 1214	EM_mPKU 5_R21_P10	CCUAAUGUACUGUGUGCAGUGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUU GAAAAAGUGGCACCGAGUCGGUGCUGGCCUUCCGAGUCUUCCACUGCACACAGUA	37176
RNACS 1186	EM_mPKU 5_R15_P8	CCUAAUGUACUGUGUGCAGUGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUU GAAAAAGUGGCACCGAGUCGGUGCUCCGAGUCUUCCACUGCACACAG	37177
RNACS 1185	EM_mPKU 5_R15_P9	CCUAAUGUACUGUGUGCAGUGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUU GAAAAAGUGGCACCGAGUCGGUGCUCCGAGUCUUCCACUGCACACAGU	37178
RNACS 1174	EM_mPKU 5_R13_P10	CCUAAUGUACUGUGUGCAGUGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUU GAAAAAGUGGCACCGAGUCGGUGCCGAGUCUUCCACUGCACACAGUA	37179
RNACS 1175	EM_mPKU 5_R13_P9	CCUAAUGUACUGUGUGCAGUGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUU GAAAAAGUGGCACCGAGUCGGUGCCGAGUCUUCCACUGCACACAGU	37180

RNACS 425	EM_mPKU 5_2.1	CCUAAUGUACUGUGUGCAGUGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUU GAAAAAGUGGCACCGAGUCGGUGCUUCCGAGUCUUCCACUGCACACAGUACAU	37181
RNACS 1375	EM_mPKU 6_R18_P9	GCCUAAUGUACUGUGUGCAGGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUU GAAAAAGUGGCACCGAGUCGGUGCCUUCCGAGUCUUCCACUGCACACAGUA	37182
RNACS 1385	EM_mPKU 6_R20_P9	GCCUAAUGUACUGUGUGCAGGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUU GAAAAAGUGGCACCGAGUCGGUGCGCCUUCCGAGUCUUCCACUGCACACAGUA	37183
RNACS 1355	EM_mPKU 6_R14_P9	GCCUAAUGUACUGUGUGCAGGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUU GAAAAAGUGGCACCGAGUCGGUGCCGAGUCUUCCACUGCACACAGUA	37184
RNACS 3664	EM_mPKU 6_1.2	GCCUAAUGUACUGUGUGCAGGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUU GAAAAAGUGGCACCGAGUCGGUGCCCUUCCGAGUCUUCCACUGCACACAGUACAUU	37185
RNACS 3665	HM_mPKU 5_R19_P9	CCUAAUGUACUGUGUGCAGUGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUU GAAAAAGUGGCACCGAGUCGGUGCGCCUUCCGAGUCUUCCACUGCACACAGU	37186
RNACS 3666	HM_mPKU 5_R29_P8	CCUAAUGUACUGUGUGCAGUGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUU GAAAAAGUGGCACCGAGUCGGUGCGGGUGGCCUGGCCUUCCGAGUCUUCCACUGCACACAG	37187
RNACS 3460	HM_mPKU 5_R15_P10	CCUAAUGUACUGUGUGCAGUGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUU GAAAAAGUGGCACCGAGUCGGUGCUCCGAGUCUUCCACUGCACACAGUA	37188
RNACS 3667	HM_mPKU 5_R21_P8	CCUAAUGUACUGUGUGCAGUGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUU GAAAAAGUGGCACCGAGUCGGUGCUGGCCUUCCGAGUCUUCCACUGCACACAG	37189
RNACS 3668	HM_mPKU 5_R21_P9	CCUAAUGUACUGUGUGCAGUGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUU GAAAAAGUGGCACCGAGUCGGUGCUGGCCUUCCGAGUCUUCCACUGCACACAGU	37190
RNACS 3669	HM_mPKU 5_R19_P10	CCUAAUGUACUGUGUGCAGUGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUU GAAAAAGUGGCACCGAGUCGGUGCGCCUUCCGAGUCUUCCACUGCACACAGUA	37191
RNACS 2302	HM_mPKU 5_R17_P9	CCUAAUGUACUGUGUGCAGUGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUU GAAAAAGUGGCACCGAGUCGGUGCCUUCCGAGUCUUCCACUGCACACAGU	37192
RNACS 3670	HM_mPKU 5_R19_P8	CCUAAUGUACUGUGUGCAGUGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUU GAAAAAGUGGCACCGAGUCGGUGCGCCUUCCGAGUCUUCCACUGCACACAG	37193
RNACS 1855	HM_mPKU 5_R11_P8	CCUAAUGUACUGUGUGCAGUGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUU GAAAAAGUGGCACCGAGUCGGUGCAGUCUUCCACUGCACACAG	37194
RNACS 3671	HM_mPKU 5_R17_P8	CCUAAUGUACUGUGUGCAGUGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUU GAAAAAGUGGCACCGAGUCGGUGCCUUCCGAGUCUUCCACUGCACACAG	37195
RNACS 3672	HM_mPKU 5_R21_P10	CCUAAUGUACUGUGUGCAGUGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUU GAAAAAGUGGCACCGAGUCGGUGCUGGCCUUCCGAGUCUUCCACUGCACACAGUA	37196
RNACS 1862	HM_mPKU 5_R15_P8	CCUAAUGUACUGUGUGCAGUGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUU GAAAAAGUGGCACCGAGUCGGUGCUCCGAGUCUUCCACUGCACACAG	37197

RNACS 2103	HM_mPKU 5_R15_P9	CCUAAUGUACUGUGUGCAGUGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUU GAAAAAGUGGCACCGAGUCGGUGCUCCGAGUCUUCCACUGCACACAGU	37198
RNACS 2104	HM_mPKU 5_R13_P10	CCUAAUGUACUGUGUGCAGUGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUU GAAAAAGUGGCACCGAGUCGGUGCCGAGUCUUCCACUGCACACAGUA	37199
RNACS 2099	HM_mPKU 5_R13_P9	CCUAAUGUACUGUGUGCAGUGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUU GAAAAAGUGGCACCGAGUCGGUGCCGAGUCUUCCACUGCACACAGU	37200
RNACS 3673	HM_mPKU 5_2.1	CCUAAUGUACUGUGUGCAGUGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUU GAAAAAGUGGCACCGAGUCGGUGCUUCCGAGUCUUCCACUGCACACAGUACAU	37201
RNACS 1869	HM_mPKU 6_R18_P9	GCCUAAUGUACUGUGUGCAGGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUU GAAAAAGUGGCACCGAGUCGGUGCCUUCCGAGUCUUCCACUGCACACAGUA	37202
RNACS 3674	HM_mPKU 6_R20_P9	GCCUAAUGUACUGUGUGCAGGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUU GAAAAAGUGGCACCGAGUCGGUGCGCCUUCCGAGUCUUCCACUGCACACAGUA	37203
RNACS 2303	HM_mPKU 6_R14_P9	GCCUAAUGUACUGUGUGCAGGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUU GAAAAAGUGGCACCGAGUCGGUGCCGAGUCUUCCACUGCACACAGUA	37204
RNACS 3675	HM_mPKU 6_1.2	GCCUAAUGUACUGUGUGCAGGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUU GAAAAAGUGGCACCGAGUCGGUGCCCUUCCGAGUCUUCCACUGCACACAGUACAUU	37205

In this example, exemplary gene modifying polypeptide RNAV209 was examined. Gene modifying polypeptide 1 (RNAV209) comprised two NLS sequences (e.g., a c-Myc NLS and an SV40 NLS), an exemplary endonuclease domain comprising nCas9 which comprised an N863A mutation relative to wildtype Cas9, an exemplary RT domain comprising a MoMLV RT sequence (comprising D200N, T306K, W313F, T330P, and L603W mutations relative to a wildtype MoMLV RT sequence), and an exemplary flexible linker connecting the RT and endonuclease domains and comprising the amino acid sequence of SEQ ID NO: 6. The amino acid sequence of RNAV209 is given by SEQ ID NO: 30477.

MPAAKRVKLDGGDKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLF
DSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRLEESFLVEEDKKHERHP
IFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDV
DKLFIQLVQTYNQLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALS
LGLTPNFKSNFDLAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVN
TEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFY
KFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNR
EKIEKILTFRIPYYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKN
LPNEKVLPKHSLLYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLK
EDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDR
EMIEERLKTYAHLFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNF
MQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPE
NIVIEMARENQTTQKGQKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRD
MYVDQELDINRLSDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQ
LLNAKLITQRKFDNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKL
IREVKVITLKSKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIKKYPKLESEFVYGDY
KVYDVRKMIAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKG
RDFATVRKVLSMPQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAY
SVLVVAKVEKGKSKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFE
LENGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEI
IEQISEFSKRVILADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDR
KRYTSTKEVLDATLIHQSITGLYETRIDLSQLGGDSGGSSGGSSGSETPGTSESATPESSGGSS
GGSSTLNIEDEYRLHETSKEPDVSLGSTWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVS
IKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVED
IHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRL
PQGFKNSPTLFNEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGY
RASAKKAQICQKQVKYLGYLLKEGQRWLTEARKETVMGQPTPKTPRQLREFLGKAGFCRLFIPG
FAEMAAPLYPLTKPGTLFNWGPDQQKAYQEIKQALLTAPALGLPDLTKPFELFVDEKQGYAKGV
LTQKLGPWRRPVAYLSKKLDPVAAGWPPCLRMVAAIAVLTKDAGKLTMGQPLVILAPHAVEALV
KQPPDRWLSNARMTHYQALLLDTDRVQFGPVVALNPATLLPLPEEGLQHNCLDILAEAHGTRPD
LTDQPLPDADHTWYTDGSSLLQEGQRKAGAAVTTETEVIWAKALPAGTSAQRAELIALTQALKM
AEGKKLNVYTDSRYAFATAHIHGEIYRRRGWLTSEGKEIKNKDEILALLKALFLPKRLSIIHCP
GHQKGHSAEARGNRMADQAARKAAITETPDTSTLLIENSSPSGGSKRTADGSEFEKRTADGSEF
ESPKKKAKVE (SEQ ID NO: 30477)

Mouse primary hepatocytes were prepared for administration of a gene modifying system as follows. The liver from animals under anesthesia were cannulated at the vena cava and perfused with 1 mg/mL Liberase digestion buffer. Upon digestion, the entire liver was dissected, cells were released into suspension in media and remaining connective tissue was eliminated by filtration with 70 µm cell strainer. Viable hepatocytes were further purified from dead cells and non-parenchymal cells by centrifugation in a 40% Percoll solution.

A gene modifying system comprising a (i) RNAV209 gene modifying polypeptide described herein, and (ii) a template RNA of any of Table E1 was nucleofected into prepared mouse primary hepatocytes in RNA format. Specifically, 4 µg of gene modifying polypeptide mRNA was combined with 10 µg of template RNAs in a total volume of 5 µL. The mRNA and template RNAs are added to 20µL P3 buffer containing 100,000 primary hepatocytes cells and cells were nucleofected. After nucleofection, cells were grown at 37˚C, 5% CO_2 for 3 days prior to cell lysis and genomic DNA extraction. To analyze gene editing activity, primers flanking the *Pah* mutation site were used to amplify across the locus. Amplicons were analyzed via short read sequencing using an Illumina MiSeq. **FIG. 13** shows a graph of the rewriting rate (the rate at which the target mutation was corrected) in primary mouse hepatocytes nucleofected with the indicated template RNA and RNAV209 gene modifying polypeptide as measured by Amp-SEQ. Rewriting was seen with a number of exemplary template RNAs.

Higher rewriting rates can increase the impact of administered gene modifying systems and could decrease the amount of a gene modifying system required to achieve a therapeutic effect. Generation of a second nick to the second strand proximal to the template RNA specified nick may increase rewriting rate, e.g., by biasing cellular DNA repair toward incorporation of the mutation correction. To test the ability of a second nick to increase rewriting, exemplary second strand-targeting gRNAs were screened by administration with the top performing template RNA from **FIG. 13** (mPKU5_R11_P8) and RNAV209 to mouse primary hepatocytes prepared as described above (**FIG. 14**).

Table E2. Exemplary second strand-targeting gRNAs (ngRNAs)

RNA CS	Description	Sequence	SEQ ID NO
RNA CS2100	mPKU_ngRNA1	UAUAAAAAGCCUUGAGUUUUGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCUUUU	30478
RNA CS2101	mPKU_ngRNA5	CUGUCGUCUCGAGAUUUCUUGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCUUUU	30479

The presence of second strand-targeting gRNAs increased the rewriting activity of the exemplary RNAV209/ mPKU5_R11_P8 gene modifying system. Two second strand-targeting gRNAs were selected for further evaluation: ngRNA1 (specifying a second strand nick more than 100 bp from the mutation to be corrected) and ngRNA5 (specifying a second strand nick less than 40 bp from the mutation to be corrected). Template RNAs from Table E1 were combined with RNAV209 and either ngRNA1 or ngRNA5 and rewrite efficiency was evaluated as above (**FIG. 15**). ngRNA5 enhanced rewrite efficiency relative to the absence of second strand-targeting gRNA when combined with a number of template RNAs.

These results demonstrate that an exemplary gene modifying system comprising RNAV209 and any of a variety of template RNAs can correct a mutation in a murine PAH gene in murine hepatocytes, and that the efficiency of rewriting can be enhanced by the addition of a second nick specified by a second strand-nicking gRNA.

Example 8: Comparing exemplary template RNAs and gene modifying polypeptides that correct an F263S mutation in a murine Pah gene in murine model animals

This example describes the use of exemplary gene modifying systems containing either of two gene modifying polypeptides and template RNAs comprising varied lengths and compositions of heterologous object sequences and PBS sequences to quantify the activity of template RNAs for correction of an F263S mutation (corresponding to a T835C base change) in the murine *Pah* gene. The enhancing effect of inclusion of a second strand-targeting gRNA was also examined. In this example, a template RNA contained:

(1) a gRNA spacer;

(2) a gRNA scaffold;

(3) a heterologous object sequence; and

(4) a primer binding site (PBS) sequence.

Exemplary template RNAs tested were template RNAs RNACS1855, RNACS1862, RNACS2103, RNACS2104, and RNACS2099, shown in Table E1. The exemplary second strand-targeting gRNA was RNACS2101, shown in Table E2.

Exemplary gene modifying polypeptide RNAV209 was compared to exemplary gene modifying polypeptide 2 (RNAIVT338). RNAIVT338 comprised two NLS sequences (e.g., a c-Myc NLS and an SV40 NLS), an exemplary endonuclease domain comprising Cas9, an exemplary RT domain comprising an AVIRE RT sequence, and an exemplary linker between the RT and endonuclease domains and comprising the amino acid sequence of SEQ ID NO: 217. The amino acid sequence of RNAIVT338 is given by SEQ ID NO: 30480.

DKKYSIGLDIGTNSVGWAVITDEYKVPSKKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLK
RTARRRYTRRKNRICYLQEIFSNEMAKVDDSFFHRLEESFLVEEDKKHERHPIFGNIVDEVAYH
EKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIEGDLNPDNSDVDKLFIQLVQTYN
QLFEENPINASGVDAKAILSARLSKSRRLENLIAQLPGEKKNGLFGNLIALSLGLTPNFKSNFD
LAEDAKLQLSKDTYDDDLDNLLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASM
IKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDG
TEELLVKLNREDLLRKQRTFDNGSIPHQIHLGELHAILRRQEDFYPFLKDNREKIEKILTFRIP
YYVGPLARGNSRFAWMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSL
LYEYFTVYNELTKVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDS
VEISGVEDRFNASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAH
LFDDKVMKQLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDGFANRNFMQLIHDDSLTFK
EDIQKAQVSGQGDSLHEHIANLAGSPAIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQT
TQKGQKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRL
SDYDVDHIVPQSFLKDDSIDNKVLTRSDKARGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKF
DNLTKAERGGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSK
LVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTALIKKYPKLESEFVYGDYKVYDVRKMIAKS
EQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSM
PQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGK
SKKLKSVKELLGITIMERSSFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLASA
GELQKGNELALPSKYVNFLYLASHYEKLKGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVI
LADANLDKVLSAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVLDA
TLIHQSITGLYETRIDLSQLGGDGGAEAAAKEAAAKEAAAKEAAAKALEAEAAAKEAAAKEAAA
KEAAAKAGGTAPLEEEYRLFLEAPIQNVTLLEQWKREIPKVWAEINPPGLASTQAPIHVQLLST
ALPVRVRQYPITLEAKRSLRETIRKFRAAGILRPVHSPWNTPLLPVRKSGTSEYRMVQDLREVN
KRVETIHPTVPNPYTLLSLLPPDRIWYSVLDLKDAFFCIPLAPESQLIFAFEWADAEEGESGQL
TWTRLPQGFKNSPTLFNEALNRDLQGFRLDHPSVSLLQYVDDLLIAADTQAACLSATRDLLMTL
AELGYRVSGKKAQLCQEEVTYLGFKIHKGSRSLSNSRTQAILQIPVPKTKRQVREFLGKIGYCR
LFIPGFAELAQPLYAATRPGNDPLVWGEKEEEAFQSLKLALTQPPALALPSLDKPFQLFVEETS
GAAKGVLTQALGPWKRPVAYLSKRLDPVAAGWPRCLRAIAAAALLTREASKLTFGQDIEITSSH
NLESLLRSPPDKWLTNARITQYQVLLLDPPRVRFKQTAALNPATLLPETDDTLPIHHCLDTLDS

LTSTRPDLTDQPLAQAEATLFTDGSSYIRDGKRYAGAAVVTLDSVIWAEPLPIGTSAQKAELIA
LTKALEWSKDKSVNIYTDSRYAFATLHVHGMIYRERGWLTAGGKAIKNAPEILALLTAVWLPKR
VAVMHCKGHQKDDAPTSTGNRRADEVAREVAIRPLSTQATISAGKRTADGSEFEKRTADGSEFE
SPKKKAKVE (SEQ ID NO: 30480)

The gene modifying system comprising either RNAV209 or RNAIVT338 gene modifying polypeptide and a template RNA described above was formulated in LNP and delivered to mice. Specifically, approximately 1.6 or 2.4 mg/kg of total RNA equivalent formulated in LNPs, combined at 1:1 (w/w) of template RNA and mRNA, were dosed intravenously in 8 to 10-week-old, mixed gender ENU2 mice (0.8 mg/kg each of template RNA and mRNA, optionally with an additional 0.8 mg/kg of ngRNA for second strand-targeting experiments) in a 10 ml/kg bolus. Mice were administered a first dose at time 0 (t = 0), and a second dose at t = 24 hours. Six hours or 7 days post-dosing (as used herein post-dosing refers to time since the first dose), animals were sacrificed, and their liver and plasma collected for analyses. To determine the expression distribution of the gene modifying polypeptide in the liver, 6-hr liver samples were subjected to immunohistochemistry using an anti-Cas9 antibody. Upon staining, quantification of Cas9-positive hepatocytes was determined by QuPath Markup. As shown in **FIG. 16**, the expression of the gene modifying polypeptide was observed in 70-80% of hepatocytes. 6-hour liver samples were further analyzed by Western blot using an anti-Cas9 antibody. As shown in **FIG. 17**, expression of the gene modifying polypeptide was observed in liver from all treated animals. These results show that both RNAV209 and RNAIVT338 gene modifying polypeptides are expressed in murine liver at 6 hours post-dosing.

7-day plasma samples were analyzed by LC/MS to determine the level of phenylalanine present. ENU2 mice harbor a mutation in the murine PAH gene that inactivates the PAH enzyme, resulting in sharply higher Phe levels in plasma than healthy wildtype mice.

Phenylalanine was extracted from mouse plasma using protein precipitation and then analyzed by a LC-MS/MS system equipped with a Shimadzu Nexera UPLC (LC-40) coupled to a Sciex API 7500 mass spectrometer. Surrogate analyte (13C2,15N-Phenylalanine) was used for phenylalanine quantitation. Equivalence of ionization for naturally occurring and surrogate compounds was established prior to and after analytical run. Data were collected in the positive ion mode with three MRM transitions, 169.1 to 123.1 (13C2,15N-Phenylalanine), 166.1 to 120.1(Phenylalanine) and 172.1 to 126.0 (13C6-Phenylalanine, internal standard). Extracted

samples were injected onto an Acquity UPLC BEH C18 column (1.7µm, 2.1x50 mm) and eluted using a gradient of 0% to 15% of mobile phase B at a flow rate of 0.8 mL/min with a total run time of 3 min per injection. Mobile phase A is 100:2:0.1 H2O:Formic acid (FA): Trifluoroacetic acid (TFA) and mobile phase B is 95:5:2:0.1 ACN:H2O:FA:TFA. Data were processed using Sciex OS software.

The results showed that Phe levels decreased in plasma from all treated mice, consistent with correction of the PAH deactivating point mutation using either gene modifying polypeptide and either of the template RNAs examined (**FIG. 18**). Treatment with LNP containing RNAIVT338 decreased Phe levels more than treatment with LNP containing RNAV209, with RNAIVT338 decreasing Phe levels by approximately 65% relative to saline compared to RNAV209 decreasing Phe levels by approximately 40%. Similarly, treatment using template RNACS1855 decreased Phe levels more than treatment with template RNACS1862, independent of which gene modifying polypeptide was administered. RNACS1855 contains a shorter reverse transcriptase binding sequence (11 nucleotides) than template RNACS1862 (15 nucleotides).

7-day liver samples were further analyzed using Amp-Seq to determine % rewriting and % INDEL in target liver cells (**FIGs. 19A** and **FIG. 19B**). To analyze gene editing activity, primers flanking the target insertion site locus were used to amplify across the locus in the genomic DNA of liver samples. Amplicons were analyzed via short read sequencing using an Illumina MiSeq. Conversion of a C nucleotide to a T nucleotide at position 835 in the PAH gene indicates successful editing. Rewriting was observed from all treated mice, demonstrating that the gene modifying systems tested successfully corrected the PAH mutation (FIG. 19A). Treatment with LNP containing RNAIVT338 resulted in a higher rewrite % than treatment with LNP containing RNAV209, with approximately twice the rewrite % observed when using RNAIVT338 relative to RNAV209. Similarly, treatment using template RNACS1855 resulted in a higher rewrite % than treatment with template RNACS1862, independent of which gene modifying polypeptide was used. Treatment with LNP containing RNAIVT338 resulted in a lower INDEL % than treatment with LNP containing RNAV209, with almost half the INDEL % observed when using RNAIVT338 relative to RNAV209 (FIG. 19B). Treatment using template RNACS1855 resulted in a lower INDEL % than treatment with template RNACS1862, independent of which gene modifying polypeptide was used.Based on RNAIVT338’s improved performance over

RNAV209, additional template RNAs were tested in combination with RNAIVT338. ENU2 mice were treated as described above using a gene modifying system comprising RNAIVT338 and one of template RNAs RNACS1855, RNACS1862, RNACS2103, RNACS2104, and RNACS2099, and liver and plasma samples were taken from sacrificed mice at 7 days post-dosing (**FIGs. 20A, 20B,** and **20C**). Rewriting was observed in all treated samples, with strong correlation between % rewriting in liver samples and Phe level reduction in plasma samples. INDEL % was much lower (approximately 25 to 35 times lower) than rewriting %, and correlated with rewriting % level (FIG. 20C). The results demonstrate that rewriting a disease-associated mutation using a gene modifying system containing RNAIVT338 can correct the disease-associated mutation and achieve the desired therapeutic effect (e.g., reduction in Phe level), and that RNAIVT338 achieves rewriting with a number of template RNAs. The results further demonstrate that the rewriting occurs with low levels of INDEL generation.

To determine whether second strand-nicking can enhance rewriting efficiency and improve Phe-reducing therapeutic effect, ENU2 mice were treated as described above with exemplary gene modifying system containing RNAIVT338, template RNA, as well as ngRNA5 which directs a second strand nick less than 40 bp from the target PAH mutation, and liver and plasma samples were analyzed as described above (**FIGs. 21A and 21B**). Administering a gene modifying system including a second strand-targeting gRNA increased % rewriting in liver and decreased plasma Phe levels relative to gene modifying systems not containing a second strand-targeting gRNA. Over 40% of the liver cells sampled contained the rewrite modification after mice were treated with a gene modifying system containing gene modifying polypeptide RNAIVT338 and an exemplary template RNA and second strand nicking gRNA (FIG. 21A), and this was accompanied by serum Phe levels of approximately 100 μM, physiologically normal for mice (FIG. 21B). Indel percent, while measurably higher when the second strand-targeting gRNA was included, remained low relative to rewriting percent. These results show adding a second strand nick proximal to the mutation to be corrected (e.g., biasing cellular DNA repair to favor correction of the mutation) can increase rewriting and substantially increase the therapeutic

effect. These results further show that unintended modifications (e.g., indels) are not significantly increased by second strand nicking.

Across *in vivo* murine samples, percent rewriting observed in liver samples should correlate inversely with Phe plasma levels if a gene modifying system is effectively correcting a PAH-inactivating, hyperphenylalaninemia (HPA)-inducing mutation. To confirm this, Phe level in plasma samples was plotted over % rewriting for all plasma and liver samples obtained from treated ENU2 mice (**FIG. 22**). The results show a clear inverse correlation; as % rewriting increases, plasma Phe levels decrease. Plotted as dotted lines are literature-recognized physiologically normal Phe levels and mild-HPA Phe levels in mice (*see, e.g.,* Ahmed et al. Mol Ther Methods Clin Dev. 2020 Mar 13;17:568-580 or Bruinenberg et al. Front Behav Neurosci. 2016; 10: 233). The results show that treatment with nearly all combinations of gene modifying polypeptides, template RNAs, and second strand-targeting gRNAs reduce Phe levels to below mild HPA levels and to normal Phe levels in many cases.

Example 9: Evaluating safety and efficacy of exemplary template RNAs and gene modifying polypeptides that insert a silent mutation in a primate PAH gene in non-human primate model animals

This example describes the use of exemplary gene modifying systems containing an exemplary gene modifying polypeptide (e.g., RNAIVT338, described above), exemplary template RNA (e.g., described in Tables 4A-4D), and optionally an exemplary second strand-nicking gRNA (e.g., described in Tables 4A-4D) to demonstrate the safety of the gene modifying systems, translation activity of the gene modifying polypeptide, and rewriting activity in a group of non-human primates (NHPs). In some embodiments, the NHPs are Cynomolgus macaques. In some embodiments, the NHPs are Rhesus macaques.

One, two, or more studies are performed. The studies treat NHPs using exemplary gene modifying systems and determine the safety of administration of the systems and/or evaluate the efficacy of the gene modifying system (e.g., percent rewriting, writing accuracy (e.g., indel and imperfect rewriting), and/or phenotypic correction (e.g., PAH protein/mRNA expression and/or plasma Phe level)).

NHPs are distributed into two treated groups, with at least 3 individuals per treated group. Pre-dosing liver biopsy samples are taken at approximately 7 days pre-dosing. Doses of gene modifying system containing mRNA encoding RNAIVT338, exemplary template RNA, and optionally exemplary second strand-nicking gRNA are formulated in LNPs, combined at 1:1 (w/w) of template RNA and mRNA (and optionally 1:1:1 w/w/w of template RNA, mRNA, and gRNA). On Day 1, a single dose is administered intravenously at 3 mg/kg. A single-dose liver biopsy sample is collected from treated individuals one week after the single dose (Day 8). One week after the single-dose liver biopsy sample is taken, the multi-dose phase of the study begins, with two or more (e.g., three) additional doses administered on an alternating day schedule (e.g., on days 15, 17, and 19). A multi-dose liver biopsy sample is collected from treated individuals one week after the last dose of the multi-dose phase (e.g., day 26).

Liver samples are analyzed by Amp-Seq to determine % rewriting, LC/MS to determine Phe levels, and/or immunohistochemistry (e.g., in situ hybridization and/or Western blot) to determine expression of the exemplary gene modifying polypeptide. Plasma samples are obtained from blood draws at each biopsy time point, as well as at shorter time points (e.g., less than 7 days post-dosing). Plasma samples are analyzed, e.g., by LC/MS, for Phe levels. Rewriting will be observed in liver cells after a single dose, with increasing rewriting % observed after multiple doses are administered. Plasma Phe levels will be observed to decrease after a single dose, with more significant decreases observed after multiple doses are administered and correlating with rewriting %.

Example 10: Demonstrating Use of Different Exemplary Template RNA Spacers to Target Macaca fascicularis PAH gene

This example describes the use of exemplary gene modifying systems containing a gene modifying polypeptide and template RNAs comprising one of four different gRNA spacer sequences combined with a variety of heterologous object sequences and PBS sequences to induce a series of phenylketonuria relevant genetic alterations in HEK293T cells modified to contain a ***Macaca fascicularis*** PAH gene. This example demonstrates gene modification to:

(1) Introduce a silent C to A mutation in the codon homologous to that encoding human R408 (CtoA)

(2) Introduce the C to A mutation of (1) and additionally a PAM/seed killing mutation that inhibits retargeting by the gene modifying polypeptide after editing (CtoA+PSkill).

(3) Introduce the C to A mutation of (1) and additional silent substitutions promoting favorable DNA repair incorporating the C to A mutation (CtoA+subs).

(4) Introduce a T to C mutation, similar to that needed to correct PKU-associated R408W in human PAH (TtoC).

In this example, a template RNA contained:

(1) a gRNA spacer;

(2) a gRNA scaffold;

(3) a heterologous object sequence; and

(4) a primer binding site (PBS) sequence.

Exemplary template RNAs contained one of the following four spacer sequences:

cPKU4: GGGUCAUAGCGAACUGAGAA (SEQ ID NO: 30481)

cPKU5.1: UAGCGAACUGAGAAGGGCCG (SEQ ID NO: 30482)

cPKU5.2: AGCGAACUGAGAAGGGCCGA (SEQ ID NO: 30483)

cPKU6: ACUUUGCUGCCACAAUCCCU (SEQ ID NO: 30484)

The exemplary gene modifying polypeptide was RNAIVT338 (described in Example 8). mRNA encoding RNAIVT338 and template RNA were transfected into HEK293T cells containing a genomic modification which inserted the ***M fascicularis*** PAH gene. After transfection, HEK293T cells were cultured for at least 4 days and then assayed for rewriting by isolating genomic DNA, conducting PCR using primers flanking the ***M fascicularis*** PAH gene, and then sequencing the amplicons using Amp-Seq.

FIG. 23 shows a graph of percent rewriting for the 4 different mutation types using the template RNAs containing the four spacer sequences under evaluation (where each dot represents that column's spacer combined with a particular of RT and PBS sequence). CtoA, CtoA+PSkill, CtoA+subs, and TtoC mutations were observed when utilizing each of the spacer sequences tested, but with different rewriting % levels. For example: a large number of template RNAs containing spacer cPKU5.2 yielded high rewriting % for CtoA+PSkill mutation and TtoC mutation; a large number of template RNAs containing spacer cPKU6 yielded high rewriting % for CtoA, CtoA+PSkill, and CtoA+subs mutations; a large number of template RNAs containing spacer cPKU5.2 yielded high rewriting % for CtoA+PSkill and CtoA+subs mutations. The

results show that gene modifying systems comprising an exemplary gene modifying polypeptide and template RNAs containing four different exemplary spacer sequences enabled 4 different PKU-relevant genetic modifications to a primate PAH gene.

Example 11: Evaluating template RNA/second strand-targeting gRNA dose response in correction of an F263S mutation in a murine Pah gene in murine model animals

This example describes the use of exemplary gene modifying systems containing a gene modifying polypeptide, either of two template RNAs (each comprising different spacers, lengths and compositions of heterologous object sequences, and PBS sequences), and a second strand-targeting gRNA to evaluate the dose response of template RNA and second strand-targeting gRNA level to rewriting activity (the correction of an F263S mutation (corresponding to a T835C base change) in the murine *Pah* gene). Two different concentrations of template RNA and second strand-targeting gRNA (1.2 milligrams per kilogram body weight (mpk) and 2.4 mpk) were evaluated. In this example, a template RNA contained:

(1) a gRNA spacer;
(2) a gRNA scaffold;
(3) a heterologous object sequence; and
(4) a primer binding site (PBS) sequence.

Exemplary template RNAs tested were template RNAs RNACS1855 and RNACS2303, shown in Table E1. The exemplary second strand-targeting gRNA was ngRNA5 (also referred to herein as RNACS2101), shown in Table E2. The exemplary gene modifying polypeptide used was RNAIVT338 (as described above and corresponding to the amino acid sequence of SEQ ID NO: 30480.

The gene modifying system was formulated in LNP and delivered to mice. Specifically, 1.2 or 2.4 mpk of total RNA equivalent formulated in LNPs, combined at 1:1 (w/w) of template RNA and mRNA or 1:1:1 (w/w/w) when including ngRNA, were dosed intravenously in 8 to 10-week-old, mixed gender ENU2 mice (0.8 mg/kg each of template RNA and mRNA, optionally with an additional 0.8 mg/kg of ngRNA for second strand-targeting experiments; or 0.4 mg/kg each of template RNA and mRNA, optionally with an additional 0.4 mg/kg of ngRNA for second strand-targeting experiments,) in a 10 ml/kg bolus. Mice were administered a first dose at

time 0 (t = 0) and a second dose 24 hours later (t = 24). 7 days post-dosing, animals were sacrificed, and their liver and plasma collected for analyses.

7-day liver samples were analyzed using Amp-Seq to determine % rewriting in target liver cells (**FIG. 24A**). To analyze gene editing activity, primers flanking the target insertion site locus were used to amplify across the locus in the genomic DNA of liver samples. Amplicons were analyzed via short read sequencing using an Illumina MiSeq. Conversion of a C nucleotide to a T nucleotide at position 835 in the PAH gene indicates successful editing. Rewriting was observed from all treated mice except for RNACS2303 without second strand-targeting gRNA. This is consistent with the interpretation that RNACS2303 is less effective at facilitating rewriting at this locus than RNACS1855 in the absence of a second strand-targeting gRNA, and that the presence of a second strand-targeting gRNA increases rewriting activity. As the dose of template RNA and second strand-targeting gRNA increased, so did the % rewriting. This suggests that the amount of template RNA and/or second strand-targeting gRNA can be adjusted to achieve a desired (e.g., sufficient) level of rewriting activity corresponding to a therapeutic outcome. Amplicon sequencing was also used to evaluate the degree to which INDELs were introduced into the liver sample DNA (**FIG. 24B**). % INDEL increased with template RNA and second strand-targeting gRNA dosage, correlating with % rewriting. The results suggest that the amount of template RNA and/or second strand-targeting gRNA can be adjusted to decrease (e.g., minimize) the % INDEL while achieving a desired (e.g., sufficient) level of rewriting activity corresponding to a therapeutic outcome.

7-day plasma samples were also analyzed by LC/MS to determine the level of phenylalanine present. ENU2 mice harbor a mutation (F263S) in the murine PAH gene that inactivates the PAH enzyme, resulting in sharply higher Phe levels in plasma than healthy wildtype mice. The ENU2 mutation is described by The Jackson Laboratory (https://www.jax.org/strain/002232) as a T835C missense mutation in the murine PAH gene, however the mutation is also described in the literature as being a T788C mutation (see, e.g., Harding, C.O. Mol Front J. 2019 Dec;3(2):110-121; or Pecimonova, M. Genes (Basel). 2019 Jun 15;10(6):459). The Examples explicitly contemplate both positions whenever reference is made to either nucleotide mutation herein.

Phenylalanine was extracted from mouse plasma using protein precipitation and then analyzed by a LC-MS/MS system equipped with a Shimadzu Nexera UPLC (LC-40) coupled to

a Sciex API 7500 mass spectrometer. Surrogate analyte (13C2,15N-Phenylalanine) was used for phenylalanine quantitation. Equivalence of ionization for naturally occurring and surrogate compounds was established prior to and after analytical run. Data were collected in the positive ion mode with three MRM transitions, 169.1 to 123.1 (13C2,15N-Phenylalanine), 166.1 to 120.1(Phenylalanine) and 172.1 to 126.0 (13C6-Phenylalanine, internal standard). Extracted samples were injected onto an Acquity UPLC BEH C18 column (1.7µm, 2.1x50 mm) and eluted using a gradient of 0% to 15% of mobile phase B at a flow rate of 0.8 mL/min with a total run time of 3 min per injection. Mobile phase A is 100:2:0.1 H2O:Formic acid (FA): Trifluoroacetic acid (TFA) and mobile phase B is 95:5:2:0.1 ACN:H2O:FA:TFA. Data were processed using Sciex OS software.

The results showed that Phe levels decreased in plasma from all treated mice except for RNACS2303 without second strand-targeting gRNA. This is consistent with the interpretation that RNACS2303 is less effective at facilitating rewriting at this locus than RNACS1855 in the absence of a second strand-targeting gRNA, and that the presence of a second strand-targeting gRNA increases rewriting activity. The results are consistent with correction of the PAH deactivating point mutation using the exemplary gene modifying polypeptide and either of the template RNAs examined (**FIG. 24C**). Treatment with LNP containing RNACS1855 decreased Phe levels more than treatment with LNP containing RNACS2303. Addition of a second strand-targeting gRNA and increasing the dosage of template RNA and second strand-targeting gRNA caused Phe levels to decrease more precipitously in RNACS2303 treated samples. The addition of a second strand-targeting gRNA and increasing the dosage of template RNA and second strand-targeting gRNA caused only small additional Phe levels decreases in RNACS1855 treated samples. These results suggest that a higher dose and/or second strand-targeting gRNA may be necessary to reduce plasma Phe levels to wild-type levels for some template RNAs, but that for highly effective template RNAs a lower dose or omission of second strand-targeting gRNA may be sufficient to reduce plasma Phe to wild-type levels. When considered together (FIGs. 24A-24C), the results show that increasing the template RNA and second strand-targeting gRNA dose increases the % rewriting, as well as % INDEL, and that for highly effective template RNAs a lower dose or omission of second strand-targeting gRNA (despite lower % rewriting) provides a nearly wild-type plasma Phe phenotype.

Example 12: Evaluating Rewriting Activity of Exemplary Human Template RNAs in hPAH Mice

This example describes the use of exemplary gene modifying systems containing a gene modifying polypeptide and template RNAs comprising varied spacers, lengths and compositions of heterologous object sequences, and PBS sequences to quantify the activity of template RNAs for correction of an R408W mutation (corresponding to a C>T base change) in a human PAH (hPAH) gene in vivo in mice modified to carry R408W hPAH.

In this example, a template RNA contained:

(1) a gRNA spacer;

(2) a gRNA scaffold;

(3) a heterologous object sequence; and

(4) a primer binding site (PBS) sequence.

Exemplary template RNAs generated are given in Table E3. Nucleotide modifications are noted as follows: phosphorothioate linkages denoted by an asterisk, 2'-O-methyl groups denoted by an 'm' preceding a nucleotide. The exemplary gene modifying polypeptide is RNAIVT338, comprising the amino acid sequence of SEQ ID NO: 30480.

Table E3 – Exemplary Template RNAs and Sequences

RNACS	Name	Sequence	SEQ ID NO
RNACS4047	hPKU3_R17_P9	mU*mG*mG*rGrUrCrGrUrArGrCrGrArArCrUrGrArGrArGrUrUrUrUrArGrAmGmCmUmAmGmAmAmAmUmAmGmCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmUmGmAmAmAmAmAmGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrArArUrArCrCrUrCrGrGrCrCrCrUrUrCrUrCrArGrUrUrC*mG*mC*mU	30485
RNACS1747	hPKU3_R19_P9	mU*mG*mG*rGrUrCrGrUrArGrCrGrArArCrUrGrArGrArGrUrUrUrUrArGrAmGmCmUmAmGmAmAmAmUmAmGmCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmUmGmAmAmAmAmAmGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrArCrArArUrArCrCrUrCrGrGrCrCrCrUrUrCrUrCrArGrUrUrC*mG*mC*mU	30486
RNACS3878	hPKU4_R16_P9	mG*mG*mG*rUrCrGrUrArGrCrGrArArCrUrGrArGrArArGrUrUrUrUrArGrAmGmCmUmAmGmAmAmAmUmAmGmCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmUmGmAmAmAmAmAmGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrArArUrArCrCrUrCrGrGrCrCrCrUrUrCrUrCrArGrUrU*mC*mG*mC	30487
RNACS3877	hPKU4_R16_P10	mG*mG*mG*rUrCrGrUrArGrCrGrArArCrUrGrArGrArArGrUrUrUrUrArGrAmGmCmUmAmGmAmAmAmUmAmGmCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmUmGmAmAmAmAmAmGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrArArUrArCrCrUrCrGrGrCrCrCrUrUrCrUrCrArGrUrUrC*mG*mC*mU	30488
RNACS4135	hPKU5_R10_P9	mU*mA*mG*rCrGrArArCrUrGrArGrArArGrGrGrCrCrArGrUrUrUrUrArGrAmGmCmUmAmGmAmAmAmUmAmGmCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmUmGmAmAmAmAmAmGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrArCrArArUrArCrCrUrCrGrGrCrCrCrUrUrCrUrCrArGrUrC*mU*mC*mA	30489
RNACS4134	hPKU5_R10_P10	mU*mA*mG*rCrGrArArCrUrGrArGrArArGrGrGrCrCrArGrUrUrUrUrArGrAmGmCmUmAmGmAmAmAmUmAmGmCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmUmGmAmAmAmAmAmGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrArCrArArUrArCrCrUrCrGrGrCrCrCrUrUrCrUrCrArGrU*mC*mA*mG	30490

RNACS2300	hPKU5_R10_P11	mU*mA*mG*rCrGrArArCrUrGrArGrArArGrGrGrCrCrArGrUrUrUrUrArGrAmGmCmUmAmGmAmAmAmUmAmGmCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmUmGmAmAmAmAmAmGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrArArUrArCrCrUrCrGrGrCrCrCrUrUrCrUrC*mA*mG*mU	30491
RNACS2299	hPKU5_R12_P10	mU*mA*mG*rCrGrArArCrUrGrArGrArArGrGrGrCrCrArGrUrUrUrUrArGrAmGmCmUmAmGmAmAmAmUmAmGmCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmUmGmAmAmAmAmAmGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrArCrArArUrArCrCrUrCrGrGrCrCrCrUrUrCrU*mC*mA*mG	30492
RNACS4142	hPKU5_R12_P11	mU*mA*mG*rCrGrArArCrUrGrArGrArArGrGrGrCrCrArGrUrUrUrUrArGrAmGmCmUmAmGmAmAmAmUmAmGmCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmUmGmAmAmAmAmAmGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrArCrArArUrArCrCrUrCrGrGrCrCrCrUrUrCrUrC*mA*mG*mU	30493
RNACS4173	hPKU5_R18_P8	mU*mA*mG*rCrGrArArCrUrGrArGrArArGrGrGrCrCrArGrUrUrUrUrArGrAmGmCmUmAmGmAmAmAmUmAmGmCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmUmGmAmAmAmAmAmGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrGrCrUrGrCrCrArCrArArUrArCrCrUrCrGrGrCrCrCrUrU*mC*mU*mC	30494
RNACS4045	hPKU3_R17_P11	mU*mG*mG*rGrUrCrGrUrArGrCrGrArArCrUrGrArGrArGrUrUrUrUrArGrAmGmCmUmAmGmAmAmAmUmAmGmCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmUmGmAmAmAmAmAmGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrArArUrArCrCrUrCrGrGrCrCrCrUrUrCrUrCrArGrUrUrCrGrC*mU*mA*mC	30495
RNACS4048	hPKU3_R17_P8	mU*mG*mG*rGrUrCrGrUrArGrCrGrArArCrUrGrArGrArGrUrUrUrUrArGrAmGmCmUmAmGmAmAmAmUmAmGmCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmUmGmAmAmAmAmAmGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrArArUrArCrCrUrCrGrGrCrCrCrUrUrCrUrCrArGrUrU*mC*mG*mC	30496
RNACS1763	hPKU4_R18_P9	mG*mG*mG*rUrCrGrUrArGrCrGrArArCrUrGrArGrArGrUrUrUrUrArGrAmGmCmUmAmGmAmAmAmUmAmGmCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmUmGmAmAmAmAmAmGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrArCrArArUrArCrCrUrCrGrGrCrCrCrUrUrCrUrCrArGrUrU*mC*mG*mC	30497

RNACS3907	hPKU4_R22_P9	mG*mG*mG*rUrCrGrUrArGrCrGrArArCrUrGrArGrArArGrUrUrUrUrArGrAmGmCmUmAmGmAmAmAmUmAmGmCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmUmGmAmAmAmAmAmGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGrCrUrCrArArUrArCrCrUrCrGrGrCrCrCrUrUrCrUrCrArGrUrU*mC*mG*mC	30498
RNACS3643	hPKU6_R11_P11	mA*mC*mU*rUrUrGrCrUrGrCrCrArCrArArUrArCrCrUrGrUrUrUrUrArGrAmGmCmUmAmGmAmAmAmUmAmGmCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmUmGmAmAmAmAmAmGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGrCrArArGrGrGrCrCrGrArGrGrUrArUrUrGrU*mC*mA*mG	30499
RNACS1792	hPKU6_R9_P11	mA*mC*mU*rUrUrGrCrUrGrCrCrArCrArArUrArCrCrUrGrUrUrUrUrArGrAmGmCmUmAmGmAmAmAmUmAmGmCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmUmGmAmAmAmAmAmGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGrCrGrGrGrCrCrGrArGrGrUrArUrUrGrU*mC*mA*mG	30500

Table E3A shows the sequences of E3 without chemical modifications. In some embodiments, the sequences of Table E3A may be used without chemical modifications, or with one or more chemical modifications.

Table E3A: Table E3 Sequences without Chemical Modifications

RNACS	Name	Sequence	SEQ ID NO
RNACS4047	hPKU3_R17_P9	UGGGUCGUAGCGAACUGAGAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCAAUACCUCGGCCCUUCUCAGUUCGCU	37206
RNACS1747	hPKU3_R19_P9	UGGGUCGUAGCGAACUGAGAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCACAAUACCUCGGCCCUUCUCAGUUCGCU	37207
RNACS3878	hPKU4_R16_P9	GGGUCGUAGCGAACUGAGAAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCAAUACCUCGGCCCUUCUCAGUUCGC	37208
RNACS3877	hPKU4_R16_P10	GGGUCGUAGCGAACUGAGAAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCAAUACCUCGGCCCUUCUCAGUUCGCU	37209
RNACS4135	hPKU5_R10_P9	UAGCGAACUGAGAAGGGCCAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCAAUACCUCGGCCCUUCUCA	37210

RNACS4134	hPKU5_R10_P10	UAGCGAACUGAGAAGGGCCAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACU UGAAAAAGUGGCACCGAGUCGGUGCAAUACCUCGGCCCUUCUCAG	37211
RNACS2300	hPKU5_R10_P11	UAGCGAACUGAGAAGGGCCAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACU UGAAAAAGUGGCACCGAGUCGGUGCAAUACCUCGGCCCUUCUCAGU	37212
RNACS2299	hPKU5_R12_P10	UAGCGAACUGAGAAGGGCCAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACU UGAAAAAGUGGCACCGAGUCGGUGCACAAUACCUCGGCCCUUCUCAG	37213
RNACS4142	hPKU5_R12_P11	UAGCGAACUGAGAAGGGCCAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACU UGAAAAAGUGGCACCGAGUCGGUGCACAAUACCUCGGCCCUUCUCAGU	37214
RNACS4173	hPKU5_R18_P8	UAGCGAACUGAGAAGGGCCAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACU UGAAAAAGUGGCACCGAGUCGGUGCGCUGCCACAAUACCUCGGCCCUUCUC	37215
RNACS4045	hPKU3_R17_P11	UGGGUCGUAGCGAACUGAGAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACU UGAAAAAGUGGCACCGAGUCGGUGCAAUACCUCGGCCCUUCUCAGUUCGCUAC	37216
RNACS4048	hPKU3_R17_P8	UGGGUCGUAGCGAACUGAGAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACU UGAAAAAGUGGCACCGAGUCGGUGCAAUACCUCGGCCCUUCUCAGUUCGC	37217
RNACS1763	hPKU4_R18_P9	GGGUCGUAGCGAACUGAGAAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACU UGAAAAAGUGGCACCGAGUCGGUGCACAAUACCUCGGCCCUUCUCAGUUCGC	37218
RNACS3907	hPKU4_R22_P9	GGGUCGUAGCGAACUGAGAAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACU UGAAAAAGUGGCACCGAGUCGGUGCUGCCACAAUACCUCGGCCCUUCUCAGUUCGC	37219
RNACS3643	hPKU6_R11_P11	ACUUUGCUGCCACAAUACCUGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACU UGAAAAAGUGGCACCGAGUCGGUGCAAGGGCCGAGGUAUUGUGGCAG	37220
RNACS1792	hPKU6_R9_P11	ACUUUGCUGCCACAAUACCUGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACU UGAAAAAGUGGCACCGAGUCGGUGCGGGCCGAGGUAUUGUGGCAG	37221

The gene modifying system comprising RNAIVT338 gene modifying polypeptide and a template RNA described above were formulated in LNP and delivered to mice. Specifically, approximately 1.6 mg/kg of total RNA equivalent formulated in LNPs (4:1 N:P ratio for mRNA, and 3:1 N:P ratio for tgRNA), combined at 1:1 (w/w) of template RNA and mRNA, were dosed intravenously in 8 to 10-week-old, mixed gender hPAH mice (0.8 mg/kg each of template RNA and mRNA) in a 10 ml/kg bolus. Mice were administered a dose at time 0 (t = 0). 7 days post-dosing (as used herein post-dosing refers to time since the first dose), animals were sacrificed, and their liver and plasma are collected for analyses.

7-day plasma samples were analyzed by LC/MS to determine the level of phenylalanine present. hPAH trangenic mice harbor a mutation in the human PAH gene that inactivates the PAH enzyme, resulting in sharply higher Phe levels in plasma than healthy wildtype mice. Successful rewriting of the hPAH transgene would be expected to result in a decrease in Phe levels in plasma.

Phenylalanine was extracted from mouse plasma using protein precipitation and was analyzed by a LC-MS/MS system equipped with a Shimadzu Nexera UPLC (LC-40) coupled to a Sciex API 7500 mass spectrometer. Surrogate analyte (13C2,15N-Phenylalanine) was used for phenylalanine quantitation. Equivalence of ionization for naturally occurring and surrogate compounds was established prior to and after analytical run. Data were collected in the positive ion mode with three MRM transitions, 169.1 to 123.1 (13C2,15N-Phenylalanine), 166.1 to 120.1(Phenylalanine) and 172.1 to 126.0 (13C6-Phenylalanine, internal standard). Extracted samples were injected onto an Acquity UPLC BEH C18 column (1.7µm, 2.1x50 mm) and eluted using a gradient of 0% to 15% of mobile phase B at a flow rate of 0.8 mL/min with a total run time of 3 min per injection. Mobile phase A was 100:2:0.1 H2O:Formic acid (FA): Trifluoroacetic acid (TFA) and mobile phase B wasa 95:5:2:0.1 ACN:H2O:FA:TFA. Data were processed using Sciex OS software.

FIG. 35 shows a graph of Phe levels in plasma from treated mice. The results show that Phe levels decreased in hPAH mice treated with exemplary gene modifying systems. The results further showed that Phe levels decreased most in mice treated with hPKU5 template RNAs, with RNACS4134 showing the steepest decrease in Phe levels. These results show that exemplary

gene modifying systems targeting mutant hPAH in vivo can achieve editing that results in clinically-relevant phenotype changes.

7-day liver samples were analyzed using Amp-Seq to determine % rewriting and % INDELs in target liver cells. To analyze gene editing activity, primers flanking the target insertion site locus were used to amplify across the locus in the genomic DNA of liver samples. Amplicons were analyzed via short read sequencing using an Illumina MiSeq. Conversion of a C nucleotide to a T nucleotide at position 1222 in exon 12 in the human PAH gene indicated successful editing.

FIG. 36A shows a graph of % rewriting level for each of the tested template RNAs. The results showed that hPKU5-spacer-containing template RNAs showed the highest rewriting activity, with RNACS4134 showing the highest rewriting activity of about 4.6%. FIG. 36B shows a graph of %INDEL activity for each of the tested template RNAs. The results showed that all tested template RNAs had very low levels of INDEL generation in hPAH in mouse liver cells, including hPKU5 template RNAs. The results show that exemplary gene modifying systems can be used to specifically correct a clinically relevant mutation in hPAH in vivo in mice.

Example 13: Evaluating Rewriting Activity of Exemplary Human Template RNAs and Second Strand-Targeting gRNAs in Several Cellular Systems

This example describes the use of exemplary gene modifying systems containing a gene modifying polypeptide, template RNAs comprising varied spacers, lengths and compositions of heterologous object sequences, and PBS sequences, and either of two second strand-targeting gRNAs to evaluate the activity of template RNAs and second strand-targeting gRNAs to: 1) produce a R408W mutation into wild-type hPAH in primary human hepatocytes, 2) produce an W408R mutation to correct the R408W mutation in hPAH in CRISPR gene-edited iPSC hepatoblast cells, and 3) produce an W408R mutation to correct the R408W mutation in hPAH transgenic mice (described in Example 12). Combinations of template RNAs and second strand-targeting gRNAs (e.g., sequences, e.g., spacer sequences) that provide high rewriting activity in one or more of (1)-(3) may also provide rewriting activity in therapeutic template RNAs and

second strand-targeting gRNAs designed for correcting pathogenic hPAH mutations in a human subject.

In this example, a template RNA contained:

(1) a gRNA spacer;

(2) a gRNA scaffold;

(3) a heterologous object sequence; and

(4) a primer binding site (PBS) sequence.

Exemplary template RNAs generated and used in iPSC hepatoblast cells and to be used in hPAH transgenic mice are given in Table E5. Exemplary template RNAs generated for use in primary human hepatocytes are given in Table E4. Nucleotide modifications are noted as follows: phosphorothioate linkages denoted by an asterisk, 2'-O-methyl groups denoted by an 'm' preceding a nucleotide. The exemplary gene modifying polypeptide is RNAIVT338, comprising the amino acid sequence of SEQ ID NO: 30480. Exemplary second strand-targeting gRNAs for use with hPKU3, hPKU4, and hPKU5 template RNAs are RNACS1809 and RNACS1810, whereas exemplary second strand-targeting gRNAs for use with hPKU6 template RNAs are RNACS1812, RNACS1834, and RNACS1831, the nucleic acid sequence and chemical modifications of which are given here.

RNACS1809:

mG*mU*mG*rCrCrCrUrUrCrArCrUrCrArArGrCrCrUrGrGrUrUrUrUrArGrAmGmCm
UmAmGmAmAmAmUmAmGmCrArArGrUrUrArArArArArUrArArGrGrCrUrArGrUrCrCrGr
UrUrArUrCrAmAmCmUmUmGmAmAmAmAmAmGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUm
GmCmU*mU*mU*mU (SEQ ID NO: 30501)

RNACS1810:

mU*mU*mC*rArCrUrCrArArGrCrCrUrGrUrGrGrUrUrUrGrUrUrUrUrArGrAmGmCm
UmAmGmAmAmAmUmAmGmCrArArGrUrUrArArArArArUrArArGrGrCrUrArGrUrCrCrGr
UrUrArUrCrAmAmCmUmUmGmAmAmAmAmAmGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUm
GmCmU*mU*mU*mU (SEQ ID NO: 30502)

RNACS1812:

mG*mU*mC*rCrArArGrArCrCrUrCrArArUrCrCrUrUrUrGrUrUrUrUrArGrAmGmCm
UmAmGmAmAmAmUmAmGmCrArArGrUrUrArArArArArUrArArGrGrCrUrArGrUrCrCrGr
UrUrArUrCrAmAmCmUmUmGmAmAmAmAmAmGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUm
GmCmU*mU*mU*mU (SEQ ID NO: 30503)

RNACS1834:

mU*mA*mG*rCrGrArArCrUrGrArGrArArArGrGrGrCrCrArGrUrUrUrUrArGrAmGmCm
UmAmGmAmAmAmUmAmGmCrArArGrUrUrArArArArArUrArArGrGrCrUrArGrUrCrCrGr
UrUrArUrCrAmAmCmUmUmGmAmAmAmAmAmGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUm
GmCmU*mU*mU*mU (SEQ ID NO: 30504)

RNACS1831:

mU*mG*mA*rGrArArGrGrGrCrCrGrArGrGrUrArUrUrGrGrUrUrUrUrArGrAmGmCm
UmAmGmAmAmAmUmAmGmCrArArGrUrUrArArArArArUrArArGrGrCrUrArGrUrCrCrGr
UrUrArUrCrAmAmCmUmUmGmAmAmAmAmAmGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUm
GmCmU*mU*mU*mU (SEQ ID NO: 30505)

Unmodified versions of these sequences are shown in Table BB below. In some embodiments, the sequences used in this table can be used without chemical modifications.

Table BB. RNACS1809, RNACS1810, RNACS1812, RNACS1834, and RNACS1831 without nucleotide modifications.

Name	Sequence	SEQ ID NO
RNACS1809	GUGCCCUUCACUCAAGCCUGGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCUUUU	37222
RNACS1810	UUCACUCAAGCCUGUGGUUUGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCUUUU	37223
RNACS1812	GUCCAAGACCUCAAUCCUUUGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCUUUU	37224
RNACS1834	UAGCGAACUGAGAAGGGCCAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCUUUU	37225
RNACS1831	UGAGAAGGGCCGAGGUAUUGGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCUUUU	37226

Table E4 – Exemplary Template RNAs and Sequences for Mutation Installation

RNACS #	Name	Sequence	SEQ ID NO
	hPKU4_R18P9	mG*mG*mG*rUrCrGrUrArGrCrGrArArCrUrGrArGrArArGrUrUrUrUrArGrAmGmCmUmAmGmAmAmAmUmAmGmCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmUmGmAmAmAmAmGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrArCrArArUrArArCrCrUrUrGrGrCrCrCrUrUrCrUrCrArGrUrU*mC*mG*mC	30506
	hPKU4_R16P9	mG*mG*mG*rUrCrGrUrArGrCrGrArArCrUrGrArGrArArGrUrUrUrUrArGrAmGmCmUmAmGmAmAmAmUmAmGmCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmUmGmAmAmAmAmGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrArArUrArCrCrUrUrGrGrCrCrCrUrUrCrUrCrArGrUrU*mC*mG*mC	30507
	hPKU4_R16P10	mG*mG*mG*rUrCrGrUrArGrCrGrArArCrUrGrArGrArArGrUrUrUrUrArGrAmGmCmUmAmGmAmAmAmUmAmGmCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmUmGmAmAmAmAmGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrArArUrArCrCrUrUrGrGrCrCrCrUrUrCrUrCrArGrUrUrC*mG*mC*mU	30508
	hPKU4_R18P10	mG*mG*mG*rUrCrGrUrArGrCrGrArArCrUrGrArGrArArGrUrUrUrUrArGrAmGmCmUmAmGmAmAmAmUmAmGmCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmUmGmAmAmAmAmGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrArCrArArUrArArCrCrUrUrGrGrCrCrCrUrUrCrUrCrArGrUrUrC*mG*mC*mU	30509
	hPKU4_R18P11	mG*mG*mG*rUrCrGrUrArGrCrGrArArCrUrGrArGrArArGrUrUrUrUrArGrAmGmCmUmAmGmAmAmAmUmAmGmCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmUmGmAmAmAmAmGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrArCrArArUrArArCrCrUrUrGrGrCrCrCrUrUrCrUrCrArGrUrUrCrG*mC*mU*mA	30510
	hPKU4_R18P8	mG*mG*mG*rUrCrGrUrArGrCrGrArArCrUrGrArGrArArGrUrUrUrUrArGrAmGmCmUmAmGmAmAmAmUmAmGmCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmUmGmAmAmAmAmGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrArCrArArUrArArCrCrUrUrGrGrCrCrCrUrUrCrUrCrArGrU*mU*mC*mG	30511
	hPKU4_R20P9	mG*mG*mG*rUrCrGrUrArGrCrGrArArCrUrGrArGrArArGrUrUrUrUrArGrAmGmCmUmAmGmAmAmAmUmAmGmCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmUmGmAmAmAmAmGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrCrCrArCrArArUrArCrCrUrUrGrGrCrCrCrUrUrCrUrCrArGrUrU*mC*mG*mC	30512

	hPKU4_R14P9	mG*mG*mG*rUrCrGrUrArGrCrGrArArCrUrGrArGrArArGrUrUrUrUrArGrAmGmCmUmAmGmAmAmAmUmAmGmCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmUmGmAmAmAmAmGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrUrArCrCrUrUrGrGrCrCrCrUrUrCrUrCrArGrUrU*mC*mG*mC	30513
	hPKU4_R24P9	mG*mG*mG*rUrCrGrUrArGrCrGrArArCrUrGrArGrArArGrUrUrUrUrArGrAmGmCmUmAmGmAmAmAmUmAmGmCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmUmGmAmAmAmAmGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrGrCrUrGrCrCrArCrArArUrArCrCrUrUrGrGrCrCrCrUrUrCrUrCrArGrUrU*mC*mG*mC	30514
	hPKU4_R22P9	mG*mG*mG*rUrCrGrUrArGrCrGrArArCrUrGrArGrArArGrUrUrUrUrArGrAmGmCmUmAmGmAmAmAmUmAmGmCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmUmGmAmAmAmAmGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrUrGrCrCrCrArCrArArUrArCrCrUrUrGrGrCrCrCrUrUrCrUrCrArGrUrU*mC*mG*mC	30515
	hPKU3_R17P8	mU*mG*mG*rGrUrCrGrUrArGrCrGrArArCrUrGrArGrArArGrUrUrUrUrArGrAmGmCmUmAmGmAmAmAmUmAmGmCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmUmGmAmAmAmAmGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrArArUrArCrCrUrUrGrGrCrCrCrUrUrCrUrCrArGrUrU*mC*mG*mC	30516
	hPKU3_R19P8	mU*mG*mG*rGrUrCrGrUrArGrCrGrArArCrUrGrArGrArArGrUrUrUrUrArGrAmGmCmUmAmGmAmAmAmUmAmGmCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmUmGmAmAmAmAmGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrArCrArArUrArCrCrUrUrGrGrCrCrCrUrUrCrUrCrArGrUrU*mC*mG*mC	30517
	hPKU3_R17P9	mU*mG*mG*rGrUrCrGrUrArGrCrGrArArCrUrGrArGrArArGrUrUrUrUrArGrAmGmCmUmAmGmAmAmAmUmAmGmCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmUmGmAmAmAmAmGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrArArUrArCrCrUrUrGrGrCrCrCrUrUrCrUrCrArGrUrUrC*mG*mC*mU	30518
	hPKU3_R17P10	mU*mG*mG*rGrUrCrGrUrArGrCrGrArArCrUrGrArGrArArGrUrUrUrUrArGrAmGmCmUmAmGmAmAmAmUmAmGmCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmUmGmAmAmAmAmGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrArArUrArCrCrUrUrGrGrCrCrCrUrUrCrUrCrArGrUrUrCrG*mC*mU*mA	30519
	hPKU3_R19P9	mU*mG*mG*rGrUrCrGrUrArGrCrGrArArCrUrGrArGrArArGrUrUrUrUrArGrAmGmCmUmAmGmAmAmAmUmAmGmCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmUmGmAmAmAmAmGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrArCrArArUrArCrCrUrUrGrGrCrCrCrUrUrCrUrCrArGrUrUrC*mG*mC*mU	30520

	hPKU3_R23P8	mU*mG*mG*rGrUrCrGrUrArGrCrGrArArCrUrGrArGrArGrUrUrUrUrArGrAmGmCmUmAmGmAmAmAmUmAmGmCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmUmGmAmAmAmAmGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrUrGrCrCrArCrArArUrArUrGrGrCrCrCrUrUrCrUrCrUrCrArGrUrU*mC*mG*mC	30521
	hPKU3_R19P10	mU*mG*mG*rGrUrCrGrUrArGrCrGrArArCrUrGrArGrArGrUrUrUrUrArGrAmGmCmUmAmGmAmAmAmUmAmGmCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmUmGmAmAmAmAmGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrArCrArArUrArCrCrUrUrGrGrCrCrCrUrUrCrUrCrUrCrArGrUrUrCrG*mC*mU*mA	30522
	hPKU3_R17P12	mU*mG*mG*rGrUrCrGrUrArGrCrGrArArCrUrGrArGrArGrUrUrUrUrArGrAmGmCmUmAmGmAmAmAmUmAmGmCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmUmGmAmAmAmAmGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrArArUrArCrCrUrUrGrrGrCrCrCrUrUrCrUrCrArGrUrUrCrGrCrU*mA*mC*mG	30523
	hPKU3_R17P11	mU*mG*mG*rGrUrCrGrUrArGrCrGrArArCrUrGrArGrArGrUrUrUrUrArGrAmGmCmUmAmGmAmAmAmUmAmGmCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmUmGmAmAmAmAmGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrArArUrArCrCrUrUrGrrGrCrCrCrUrUrCrUrCrArGrUrUrCrGrC*mU*mA*mC	30524
	hPKU3_R19P11	mU*mG*mG*rGrUrCrGrUrArGrCrGrArArCrUrGrArGrArGrUrUrUrUrArGrAmGmCmUmAmGmAmAmAmUmAmGmCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmUmGmAmAmAmAmGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrArCrArArUrArCrCrUrUrGrGrCrCrCrUrUrCrUrCrArGrUrUrCrGrC*mU*mA*mC	30525
RNACS3649	hPKU6_R9P12	mA*mC*mU*rUrUrGrCrUrGrCrCrArCrArArUrArCrCrUrGrUrUrUrUrArGrAmGmCmUmAmGmAmAmAmUmAmGmCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmUmGmAmAmAmAmGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrGrGrGrCrCrArArGrGrUrArUrUrGrUrGrGrC*mA*mG*mC	30526
RNACS3650	hPKU6_R17P11	mA*mC*mU*rUrUrGrCrUrGrCrCrArCrArArUrArCrCrUrGrUrUrUrUrArGrAmGmCmUmAmGmAmAmAmUmAmGmCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmUmGmAmAmAmAmGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrArCrUrGrArGrArArGrGrGrC*mA*mG	30527
RNACS3651	hPKU6_R13P9	mA*mC*mU*rUrUrGrCrUrGrCrCrArCrArArUrArCrCrUrGrUrUrUrUrArGrAmGmCmUmAmGmAmAmAmUmAmGmCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmUmGmAmAmAmAmGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrArGrArArGrGrGrCrCrArArArGrGrUrArUrUrGrU*mG*mG*mC	30528

RNACS 3652	hPKU6_R11P11	mA*mC*mU*rUrUrGrCrUrGrCrCrArCrArArUrArCrCrUrGrUrUrUrUrArGrAmGmCmUmAmGmAmAmAmUmAmGmCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmUmGmAmAmAmAmGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrArArGrGrGrCrCrArArGrGrUrArUrUrGrUrGrG*mC*mA*mG	30529
RNACS 3653	hPKU6_R15P11	mA*mC*mU*rUrUrGrCrUrGrCrCrArCrArArUrArCrCrUrGrUrUrUrUrArGrAmGmCmUmAmGmAmAmAmUmAmGmCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmUmGmAmAmAmAmGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrUrGrArGrArArGrGrGrCrCrArArGrGrUrArUrUrGrUrGrG*mC*mA*mG	30530
RNACS 3654	hPKU6_R13P10	mA*mC*mU*rUrUrGrCrUrGrCrCrArCrArArUrArCrCrUrGrUrUrUrUrArGrAmGmCmUmAmGmAmAmAmUmAmGmCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmUmGmAmAmAmAmGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrArGrArArGrGrGrCrCrArArGrGrUrArUrUrGrUrG*mG*mC*mA	30531
RNACS 3655	hPKU6_R11P13	mA*mC*mU*rUrUrGrCrUrGrCrCrArCrArArUrArCrCrUrGrUrUrUrUrArGrAmGmCmUmAmGmAmAmAmUmAmGmCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmUmGmAmAmAmAmGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrArArGrGrGrCrCrArArGrGrUrArUrUrGrUrGrGrCrA*mG*mC*mA	30532
RNACS 1799	hPKU6_R9P11	mA*mC*mU*rUrUrGrCrUrGrCrCrArCrArArUrArCrCrUrGrUrUrUrUrArGrAmGmCmUmAmGmAmAmAmUmAmGmCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmUmGmAmAmAmAmGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrGrGrGrCrCrArArGrGrUrArUrUrGrUrGrG*mC*mA*mG	30533
RNACS 3656	hPKU6_R13P13	mA*mC*mU*rUrUrGrCrUrGrCrCrArCrArArUrArCrCrUrGrUrUrUrUrArGrAmGmCmUmAmGmAmAmAmUmAmGmCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmUmGmAmAmAmAmGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrArGrArArGrGrGrCrCrArArGrGrUrArUrUrGrUrGrGrCrA*mG*mC*mA	30534
RNACS 3657	hPKU6_R11P9	mA*mC*mU*rUrUrGrCrUrGrCrCrArCrArArUrArCrCrUrGrUrUrUrUrArGrAmGmCmUmAmGmAmAmAmUmAmGmCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmUmGmAmAmAmAmGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrArArGrGrGrCrCrArArGrGrUrArUrUrGrU*mG*mG*mC	30535

Table E5 – Further Exemplary Template RNAs and Sequences for Mutation Correction

RNACS#	Name	Sequence	SEQ ID NO
RNACS4947	hPKU5_R12P10	mU*mA*mG*rCrGrArArCrUrGrArGrArArGrGrGrCrCrArGrUrUrUrUrArGrAmGmCmUmAmGmAmAmAmUmAmGmCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmUmGmAmAmAmAmGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrArCrArArUrArCrCrUrCrGrGrCrCrCrUrUrCrUrC*mC*mA*mG	30536
RNACS2300	hPKU5_R10P11	mU*mA*mG*rCrGrArArCrUrGrArGrArArGrGrGrCrCrArGrUrUrUrUrArGrAmGmCmUmAmGmAmAmAmUmAmGmCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmUmGmAmAmAmAmGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrArCrArArUrArCrCrUrCrGrGrCrCrCrUrUrCrUrC*mA*mG*mU	30537
RNACS2301	hPKU5_R12P12	mU*mA*mG*rCrGrArArCrUrGrArGrArArGrGrGrCrCrArGrUrUrUrUrArGrAmGmCmUmAmGmAmAmAmUmAmGmCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmUmGmAmAmAmAmGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrArCrArArUrArCrCrUrCrGrGrCrCrCrUrUrCrUrCrA*mG*mU*mU	30538
RNACS4134	hPKU5_R10P10	mU*mA*mG*rCrGrArArCrUrGrArGrArArGrGrGrCrCrArGrUrUrUrUrArGrAmGmCmUmAmGmAmAmAmUmAmGmCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmUmGmAmAmAmAmGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrArCrArArUrArCrCrUrCrGrGrCrCrCrUrUrCrUrC*mC*mA*mG	30539
RNACS4172	hPKU5_R18P10	mU*mA*mG*rCrGrArArCrUrGrArGrArArGrGrGrCrCrArGrUrUrUrUrArGrAmGmCmUmAmGmAmAmAmUmAmGmCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmUmGmAmAmAmAmGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrArCrArArUrArCrCrUrCrGrGrCrCrCrUrUrCrUrCrU*mC*mA*mG	30540
RNACS4142	hPKU5_R12P11	mU*mA*mG*rCrGrArArCrUrGrArGrArArGrGrGrCrCrArGrUrUrUrUrArGrAmGmCmUmAmGmAmAmAmUmAmGmCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmUmGmAmAmAmAmGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrArCrArArUrArCrCrUrCrGrGrCrCrCrUrUrCrUrC*mA*mG*mU	30541
RNACS4163	hPKU5_R16P9	mU*mA*mG*rCrGrArArCrUrGrArGrArArGrGrGrCrCrArGrUrUrUrUrArGrAmGmCmUmAmGmAmAmAmUmAmGmCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmUmGmAmAmAmAmGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrUrGrCrCrArCrArArUrArCrC*mU*mC*mA	30542

RNAC S4173	hPKU 5_R18 P8	mU*mA*mG*rCrGrArArCrUrGrArGrArArGrGrGrCrCrArGrUrUrUrUrArGrAmGmCmUmAmGmAmAmAmUmAmGmCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmUmGmAmAmAmAmGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrGrCrUrGrCrCrArCrArArUrArCrCrUrCrGrGrCrCrCrUrU*mC*mU*mC	30543
RNAC S4181	hPKU 5_R20 P10	mU*mA*mG*rCrGrArArCrUrGrArGrArArGrGrGrCrCrArGrUrUrUrUrArGrAmGmCmUmAmGmAmAmAmUmAmGmCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmUmGmAmAmAmAmGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrUrUrGrCrUrGrCrCrArCrArArUrArCrCrUrCrGrGrCrCrCrUrUrCrU*mC*mA*mG	30544
RNAC S4135	hPKU 5_R10 P9	mU*mA*mG*rCrGrArArCrUrGrArGrArArGrGrGrCrCrArGrUrUrUrUrArGrAmGmCmUmAmGmAmAmAmUmAmGmCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmUmGmAmAmAmAmGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrArArUrArCrCrUrCrGrGrCrCrCrUrUrC*mU*mC*mA	30545
RNAC S1763	hPKU 4_R18 P9	mG*mG*mG*rUrCrGrUrArGrCrGrArArCrUrGrArGrArArGrUrUrUrUrArGrAmGmCmUmAmGmAmAmAmUmAmGmCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmUmGmAmAmAmAmGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrArCrArArUrArCrCrUrCrGrGrCrCrCrUrUrCrUrCrArGrUrU*mC*mG*mC	30546
RNAC S3878	hPKU 4_R16 P9	mG*mG*mG*rUrCrGrUrArGrCrGrArArCrUrGrArGrArArGrUrUrUrUrArGrAmGmCmUmAmGmAmAmAmUmAmGmCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmUmGmAmAmAmAmGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrArArUrArCrCrUrCrGrGrCrCrCrUrUrCrUrCrArGrUrU*mC*mG*mC	30547
RNAC S3877	hPKU 4_R16 P10	mG*mG*mG*rUrCrGrUrArGrCrGrArArCrUrGrArGrArArGrUrUrUrUrArGrAmGmCmUmAmGmAmAmAmUmAmGmCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmUmGmAmAmAmAmGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrArArUrArCrCrUrCrGrGrCrCrCrUrUrCrUrCrArGrUrUrC*mG*mC*mU	30548
RNAC S3887	hPKU 4_R18 P10	mG*mG*mG*rUrCrGrUrArGrCrGrArArCrUrGrArGrArArGrUrUrUrUrArGrAmGmCmUmAmGmAmAmAmUmAmGmCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmUmGmAmAmAmAmGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrArCrArArUrArCrCrUrCrGrGrCrCrCrUrUrCrUrCrArGrUrUrC*mG*mC*mU	30549
RNAC S3886	hPKU 4_R18 P11	mG*mG*mG*rUrCrGrUrArGrCrGrArArCrUrGrArGrArArGrUrUrUrUrArGrAmGmCmUmAmGmAmAmAmUmAmGmCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmUmGmAmAmAmAmGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrArCrArArUrArCrCrUrCrGrGrCrCrCrUrUrCrUrCrArGrUrUrCrG*mC*mU*mA	30550

RNAC S3888	hPKU 4_R18 P8	mG*mG*mG*rUrCrGrUrArGrCrGrArArCrUrGrArGrArArGrUrUrUrUrArGrAmGmCmUmAmGmAmAmAmUmAmGmCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmUmGmAmAmAmAmGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrArCrArArUrArCrCrUrCrGrGrCrCrCrUrUrCrUrCrArGrU*mU*mC*mG	30551
RNAC S3897	hPKU 4_R20 P9	mG*mG*mG*rUrCrGrUrArGrCrGrArArCrUrGrArGrArArGrUrUrUrUrArGrAmGmCmUmAmGmAmAmAmUmAmGmCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmUmGmAmAmAmAmGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrCrCrArCrArArUrArCrCrUrCrGrGrCrCrCrUrUrCrUrCrArGrU*mC*mG*mC	30552
RNAC S3868	hPKU 4_R14 P9	mG*mG*mG*rUrCrGrUrArGrCrGrArArCrUrGrArGrArArGrUrUrUrUrArGrAmGmCmUmAmGmAmAmAmUmAmGmCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmUmGmAmAmAmAmGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrUrArCrCrUrCrGrGrCrCrCrUrUrCrUrCrArGrU*mC*mG*mC	30553
RNAC S3917	hPKU 4_R24 P9	mG*mG*mG*rUrCrGrUrArGrCrGrArArCrUrGrArGrArArGrUrUrUrUrArGrAmGmCmUmAmGmAmAmAmUmAmGmCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmUmGmAmAmAmAmGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrGrCrUrGrCrCrArCrArArUrArCrCrUrCrGrGrCrCrCrUrUrCrUrCrArGrU*mC*mG*mC	30554
RNAC S3907	hPKU 4_R22 P9	mG*mG*mG*rUrCrGrUrArGrCrGrArArCrUrGrArGrArArGrUrUrUrUrArGrAmGmCmUmAmGmAmAmAmUmAmGmCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmUmGmAmAmAmAmGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrUrGrCrCrArCrArArUrArCrCrUrCrGrGrCrCrCrUrUrCrUrCrArGrU*mC*mG*mC	30555
RNAC S4048	hPKU 3_R17 P8	mU*mG*mG*rGrUrCrGrUrArGrCrGrArArCrUrGrArGrArArGrUrUrUrUrArGrAmGmCmUmAmGmAmAmAmUmAmGmCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmUmGmAmAmAmAmGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrArArUrArCrCrUrCrGrGrCrCrCrUrUrCrUrCrArGrU*mC*mG*mC	30556
RNAC S4057	hPKU 3_R19 P8	mU*mG*mG*rGrUrCrGrUrArGrCrGrArArCrUrGrArGrArArGrUrUrUrUrArGrAmGmCmUmAmGmAmAmAmUmAmGmCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmUmGmAmAmAmAmGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrArCrArArUrArCrCrUrCrGrGrCrCrCrUrUrCrUrCrArGrU*mC*mG*mC	30557
RNAC S4047	hPKU 3_R17 P9	mU*mG*mG*rGrUrCrGrUrArGrCrGrArArCrUrGrArGrArArGrUrUrUrUrArGrAmGmCmUmAmGmAmAmAmUmAmGmCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmUmGmAmAmAmAmGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrArArUrArCrCrUrCrGrGrCrCrCrUrUrCrUrCrArGrUrUrC*mG*mC*mU	30558

RNAC S4046	hPKU 3_R17 P10	mU*mG*mG*rGrUrCrGrUrArGrCrGrArArCrUrGrArGrArGrUrUrUrUrArGrAmGmCmUmAmGmAmAmAmUmAmGmCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmUmGmAmAmAmAmGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrArArUrArCrCrUrCrGrGrCrCrCrUrUrCrUrCrArGrUrUrCrG*mC*mU*mA	30559
RNAC S1747	hPKU 3_R19 P9	mU*mG*mG*rGrUrCrGrUrArGrCrGrArArCrUrGrArGrArGrUrUrUrUrArGrAmGmCmUmAmGmAmAmAmUmAmGmCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmUmGmAmAmAmAmGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrArCrArArUrArCrCrUrCrGrGrCrCrCrUrUrCrUrCrArGrUrUrC*mG*mC*mU	30560
RNAC S4077	hPKU 3_R23 P8	mU*mG*mG*rGrUrCrGrUrArGrCrGrArArCrUrGrArGrArGrUrUrUrUrArGrAmGmCmUmAmGmAmAmAmUmAmGmCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmUmGmAmAmAmAmGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrUrGrCrCrArCrArArUrArCrCrUrCrGrGrCrCrCrUrUrCrUrCrArGrUrU*mC*mG*mC	30561
RNAC S4056	hPKU 3_R19 P10	mU*mG*mG*rGrUrCrGrUrArGrCrGrArArCrUrGrArGrArGrUrUrUrUrArGrAmGmCmUmAmGmAmAmAmUmAmGmCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmUmGmAmAmAmAmGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrArCrArArUrArCrCrUrCrGrGrCrCrCrUrUrCrUrCrArGrUrUrCrG*mC*mU*mA	30562
RNAC S4044	hPKU 3_R17 P12	mU*mG*mG*rGrUrCrGrUrArGrCrGrArArCrUrGrArGrArGrUrUrUrUrArGrAmGmCmUmAmGmAmAmAmUmAmGmCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmUmGmAmAmAmAmGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrArArUrArCrCrUrCrGrGrCrCrCrUrUrCrUrCrArGrUrUrCrGrCrU*mA*mC*mG	30563
RNAC S4045	hPKU 3_R17 P11	mU*mG*mG*rGrUrCrGrUrArGrCrGrArArCrUrGrArGrArGrUrUrUrUrArGrAmGmCmUmAmGmAmAmAmUmAmGmCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmUmGmAmAmAmAmGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrArArUrArCrCrUrCrGrGrCrCrCrUrUrCrUrCrArGrUrUrCrGrC*mU*mA*mC	30564
RNAC S4055	hPKU 3_R19 P11	mU*mG*mG*rGrUrCrGrUrArGrCrGrArArCrUrGrArGrArGrUrUrUrUrArGrAmGmCmUmAmGmAmAmAmUmAmGmCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmUmGmAmAmAmAmGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrArCrArArUrArCrCrUrCrGrGrCrCrCrUrUrCrUrCrArGrUrUrCrGrC*mU*mA*mC	30565
RNAC S3640	hPKU 6_R9P 12	mA*mC*mU*rUrUrGrCrUrGrCrCrArCrArArUrArCrCrUrGrUrUrUrUrArGrAmGmCmUmAmGmAmAmAmUmAmGmCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmUmGmAmAmAmAmGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrGrGrGrCrCrGrArGrGrUrArUrUrGrUrGrC*mA*mG*mC	30566

RNAC S3641	hPKU 6_R17 P11	mA*mC*mU*rUrUrGrCrUrGrCrCrArCrArArUrArCrCrUrGrUrUrUrUrArGrAmGmCmUmAmGmAmAmAmUmAmGmCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmUmGmAmAmAmAmGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrArCrUrGrArGrArArGrGrGrCrCrGrArGrGrUrArUrUrGrUrGrG*mC*mA*mG	30567
RNAC S3642	hPKU 6_R13 P9	mA*mC*mU*rUrUrGrCrUrGrCrCrArCrArArUrArCrCrUrGrUrUrUrUrArGrAmGmCmUmAmGmAmAmAmUmAmGmCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmUmGmAmAmAmAmGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrArGrArArGrGrGrCrCrGrArGrGrUrArUrUrGrU*mG*mG*mC	30568
RNAC S3643	hPKU 6_R11 P11	mA*mC*mU*rUrUrGrCrUrGrCrCrArCrArArUrArCrCrUrGrUrUrUrUrArGrAmGmCmUmAmGmAmAmAmUmAmGmCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmUmGmAmAmAmAmGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrArArGrGrGrCrCrGrArGrGrUrArUrUrGrG*mC*mA*mG	30569
RNAC S3644	hPKU 6_R15 P11	mA*mC*mU*rUrUrGrCrUrGrCrCrArCrArArUrArCrCrUrGrUrUrUrUrArGrAmGmCmUmAmGmAmAmAmUmAmGmCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmUmGmAmAmAmAmGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrUrGrArGrArArGrGrGrCrCrGrArGrGrUrArUrUrGrUrGrG*mC*mA*mG	30570
RNAC S3645	hPKU 6_R13 P10	mA*mC*mU*rUrUrGrCrUrGrCrCrArCrArArUrArCrCrUrGrUrUrUrUrArGrAmGmCmUmAmGmAmAmAmUmAmGmCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmUmGmAmAmAmAmGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrArGrArArGrGrGrCrCrGrArGrGrUrArUrUrGrU*mG*mC*mA	30571
RNAC S3646	hPKU 6_R11 P13	mA*mC*mU*rUrUrGrCrUrGrCrCrArCrArArUrArCrCrUrGrUrUrUrUrArGrAmGmCmUmAmGmAmAmAmUmAmGmCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmUmGmAmAmAmAmGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrArArGrGrGrCrCrGrArGrGrUrArUrUrGrGrCrA*mG*mC*mA	30572
RNAC S1792	hPKU 6_R9P 11	mA*mC*mU*rUrUrGrCrUrGrCrCrArCrArArUrArCrCrUrGrUrUrUrUrArGrAmGmCmUmAmGmAmAmAmUmAmGmCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmUmGmAmAmAmAmGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrGrGrGrCrCrGrArGrGrUrArUrUrGrG*mC*mA*mG	30573
RNAC S3647	hPKU 6_R13 P13	mA*mC*mU*rUrUrGrCrUrGrCrCrArCrArArUrArCrCrUrGrUrUrUrUrArGrAmGmCmUmAmGmAmAmAmUmAmGmCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmUmGmAmAmAmAmGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrArGrArArGrGrGrCrCrGrArGrGrUrArUrUrGrUrGrCrA*mG*mC*mA	30574

RNAC S3648	hPKU 6_R11 P9	mA*mC*mU*rUrUrGrCrUrGrCrCrArCrArArUrArCrCrUrGrUrUrUrUrArGrAmGmCmUmAmGmAm AmAmUmAmGmCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCm UmUmGmAmAmAmAmGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrArArGrGrGrCrCrGrArGr GrUrArUrUrGrU*mG*mG*mC	30575

Table E5A shows the sequences of E5 without chemical modifications. In some embodiments, the sequences of Table E5 may be used without chemical modifications, or with one or more chemical modifications.

Table E5A: Table E5 Sequences without Chemical Modifications

RNAC S#	Name	Sequence	SEQ ID NO
RNAC S4947	hPKU5_ R12P10	UAGCGAACUGAGAAGGGCCAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAAC UUGAAAAAGUGGCACCGAGUCGGUGCACAAUACCUCGGCCCUUCUCAG	37227
RNAC S2300	hPKU5_ R10P11	UAGCGAACUGAGAAGGGCCAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAAC UUGAAAAAGUGGCACCGAGUCGGUGCAAUACCUCGGCCCUUCUCAGU	37228
RNAC S2301	hPKU5_ R12P12	UAGCGAACUGAGAAGGGCCAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAAC UUGAAAAAGUGGCACCGAGUCGGUGCACAAUACCUCGGCCCUUCUCAGUU	37229
RNAC S4134	hPKU5_ R10P10	UAGCGAACUGAGAAGGGCCAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAAC UUGAAAAAGUGGCACCGAGUCGGUGCAAUACCUCGGCCCUUCUCAG	37230
RNAC S4172	hPKU5_ R18P10	UAGCGAACUGAGAAGGGCCAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAAC UUGAAAAAGUGGCACCGAGUCGGUGCGCUGCCACAAUACCUCGGCCCUUCUCAG	37231
RNAC S4142	hPKU5_ R12P11	UAGCGAACUGAGAAGGGCCAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAAC UUGAAAAAGUGGCACCGAGUCGGUGCACAAUACCUCGGCCCUUCUCAGU	37232
RNAC S4163	hPKU5_ R16P9	UAGCGAACUGAGAAGGGCCAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAAC UUGAAAAAGUGGCACCGAGUCGGUGCUGCCACAAUACCUCGGCCCUUCUCA	37233
RNAC S4173	hPKU5_ R18P8	UAGCGAACUGAGAAGGGCCAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAAC UUGAAAAAGUGGCACCGAGUCGGUGCGCUGCCACAAUACCUCGGCCCUUCUC	37234
RNAC S4181	hPKU5_ R20P10	UAGCGAACUGAGAAGGGCCAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAAC UUGAAAAAGUGGCACCGAGUCGGUGCUUGCUGCCACAAUACCUCGGCCCUUCUCAG	37235

RNAC S4135	hPKU5_ R10P9	UAGCGAACUGAGAAGGGCCAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAAC UUGAAAAAGUGGCACCGAGUCGGUGCAAUACCUCGGCCCUUCUCA	37236
RNAC S1763	hPKU4_ R18P9	GGGUCGUAGCGAACUGAGAAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAAC UUGAAAAAGUGGCACCGAGUCGGUGCACAAUACCUCGGCCCUUCUCAGUUCGC	37237
RNAC S3878	hPKU4_ R16P9	GGGUCGUAGCGAACUGAGAAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAAC UUGAAAAAGUGGCACCGAGUCGGUGCAAUACCUCGGCCCUUCUCAGUUCGC	37238
RNAC S3877	hPKU4_ R16P10	GGGUCGUAGCGAACUGAGAAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAAC UUGAAAAAGUGGCACCGAGUCGGUGCAAUACCUCGGCCCUUCUCAGUUCGCU	37239
RNAC S3887	hPKU4_ R18P10	GGGUCGUAGCGAACUGAGAAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAAC UUGAAAAAGUGGCACCGAGUCGGUGCACAAUACCUCGGCCCUUCUCAGUUCGCU	37240
RNAC S3886	hPKU4_ R18P11	GGGUCGUAGCGAACUGAGAAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAAC UUGAAAAAGUGGCACCGAGUCGGUGCACAAUACCUCGGCCCUUCUCAGUUCGCUA	37241
RNAC S3888	hPKU4_ R18P8	GGGUCGUAGCGAACUGAGAAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAAC UUGAAAAAGUGGCACCGAGUCGGUGCACAAUACCUCGGCCCUUCUCAGUUCG	37242
RNAC S3897	hPKU4_ R20P9	GGGUCGUAGCGAACUGAGAAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAAC UUGAAAAAGUGGCACCGAGUCGGUGCCCACAAUACCUCGGCCCUUCUCAGUUCGC	37243
RNAC S3868	hPKU4_ R14P9	GGGUCGUAGCGAACUGAGAAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAAC UUGAAAAAGUGGCACCGAGUCGGUGCUACCUCGGCCCUUCUCAGUUCGC	37244
RNAC S3917	hPKU4_ R24P9	GGGUCGUAGCGAACUGAGAAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAAC UUGAAAAAGUGGCACCGAGUCGGUGCGCUGCCACAAUACCUCGGCCCUUCUCAGUUCGC	37245
RNAC S3907	hPKU4_ R22P9	GGGUCGUAGCGAACUGAGAAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAAC UUGAAAAAGUGGCACCGAGUCGGUGCUGCCACAAUACCUCGGCCCUUCUCAGUUCGC	37246
RNAC S4048	hPKU3_ R17P8	UGGGUCGUAGCGAACUGAGAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAAC UUGAAAAAGUGGCACCGAGUCGGUGCAAUACCUCGGCCCUUCUCAGUUCGC	37247
RNAC S4057	hPKU3_ R19P8	UGGGUCGUAGCGAACUGAGAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAAC UUGAAAAAGUGGCACCGAGUCGGUGCACAAUACCUCGGCCCUUCUCAGUUCGC	37248
RNAC S4047	hPKU3_ R17P9	UGGGUCGUAGCGAACUGAGAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAAC UUGAAAAAGUGGCACCGAGUCGGUGCAAUACCUCGGCCCUUCUCAGUUCGCU	37249
RNAC S4046	hPKU3_ R17P10	UGGGUCGUAGCGAACUGAGAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAAC UUGAAAAAGUGGCACCGAGUCGGUGCAAUACCUCGGCCCUUCUCAGUUCGCUA	37250
RNAC S1747	hPKU3_ R19P9	UGGGUCGUAGCGAACUGAGAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAAC UUGAAAAAGUGGCACCGAGUCGGUGCACAAUACCUCGGCCCUUCUCAGUUCGCU	37251

RNAC S4077	hPKU3_ R23P8	UGGGUCGUAGCGAACUGAGAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAAC UUGAAAAAGUGGCACCGAGUCGGUGCUGCCACAAUACCUCGGCCCUUCUCAGUUCGC	37252
RNAC S4056	hPKU3_ R19P10	UGGGUCGUAGCGAACUGAGAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAAC UUGAAAAAGUGGCACCGAGUCGGUGCACAAUACCUCGGCCCUUCUCAGUUCGCUA	37253
RNAC S4044	hPKU3_ R17P12	UGGGUCGUAGCGAACUGAGAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAAC UUGAAAAAGUGGCACCGAGUCGGUGCAAUACCUCGGCCCUUCUCAGUUCGCUACG	37254
RNAC S4045	hPKU3_ R17P11	UGGGUCGUAGCGAACUGAGAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAAC UUGAAAAAGUGGCACCGAGUCGGUGCAAUACCUCGGCCCUUCUCAGUUCGCUAC	37255
RNAC S4055	hPKU3_ R19P11	UGGGUCGUAGCGAACUGAGAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAAC UUGAAAAAGUGGCACCGAGUCGGUGCACAAUACCUCGGCCCUUCUCAGUUCGCUAC	37256
RNAC S3640	hPKU6_ R9P12	ACUUUGCUGCCACAAUACCUGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAAC UUGAAAAAGUGGCACCGAGUCGGUGCGGGCCGAGGUAUUGUGGCAGC	37257
RNAC S3641	hPKU6_ R17P11	ACUUUGCUGCCACAAUACCUGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAAC UUGAAAAAGUGGCACCGAGUCGGUGCACUGAGAAGGGCCGAGGUAUUGUGGCAG	37258
RNAC S3642	hPKU6_ R13P9	ACUUUGCUGCCACAAUACCUGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAAC UUGAAAAAGUGGCACCGAGUCGGUGCAGAAGGGCCGAGGUAUUGUGGC	37259
RNAC S3643	hPKU6_ R11P11	ACUUUGCUGCCACAAUACCUGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAAC UUGAAAAAGUGGCACCGAGUCGGUGCAAGGGCCGAGGUAUUGUGGCAG	37260
RNAC S3644	hPKU6_ R15P11	ACUUUGCUGCCACAAUACCUGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAAC UUGAAAAAGUGGCACCGAGUCGGUGCUGAGAAGGGCCGAGGUAUUGUGGCAG	37261
RNAC S3645	hPKU6_ R13P10	ACUUUGCUGCCACAAUACCUGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAAC UUGAAAAAGUGGCACCGAGUCGGUGCAGAAGGGCCGAGGUAUUGUGGCA	37262
RNAC S3646	hPKU6_ R11P13	ACUUUGCUGCCACAAUACCUGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAAC UUGAAAAAGUGGCACCGAGUCGGUGCAAGGGCCGAGGUAUUGUGGCAGCA	37263
RNAC S1792	hPKU6_ R9P11	ACUUUGCUGCCACAAUACCUGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAAC UUGAAAAAGUGGCACCGAGUCGGUGCGGGCCGAGGUAUUGUGGCAG	37264
RNAC S3647	hPKU6_ R13P13	ACUUUGCUGCCACAAUACCUGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAAC UUGAAAAAGUGGCACCGAGUCGGUGCAGAAGGGCCGAGGUAUUGUGGCAGCA	37265
RNAC S3648	hPKU6_ R11P9	ACUUUGCUGCCACAAUACCUGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAAC UUGAAAAAGUGGCACCGAGUCGGUGCAAGGGCCGAGGUAUUGUGGC	37266

The gene modifying system comprising mRNA encoding the gene modifying polypeptide listed above, a template RNA listed above, and a second strand-targeting gRNA described above were transfected into primary human hepatocytes. The gene modifying polypeptide, template RNA, and second strand-targeting gRNA were delivered by nucleofection in the RNA format. Specifically, 4 µg of gene modifying polypeptide mRNA were combined with 10 µg of chemically synthesized template RNA in 5 µL of water. The transfection mix was added to 100,000 primary hepatocytes in Buffer P3 [Lonza], and cells were nucleofected using program DG-138. After nucleofection, cells were grown at 37˚C, 5% CO_2 for 3 days prior to cell lysis and genomic DNA extraction. To analyze gene editing activity, primers flanking the target insertion site locus were used to amplify across the locus. Amplicons were analyzed via short read sequencing using an Illumina MiSeq. Conversion of C nucleotide to T nucleotide indicates successful editing.

FIG. 25A shows a heatmap of % rewriting for each combination of template RNA and second strand-targeting RNA. The results show that many combinations of exemplary template RNAs and exemplary second strand-targeting gRNAs facilitated installation of the R408W mutation into hPAH gene of primary human hepatocytes.

The gene modifying system comprising mRNA encoding the gene modifying polypeptide listed above, a template RNA listed above, and a second strand-targeting gRNA described above were transfected into hepatoblasts differentiated from CRISPR-edited iPSCs containing the R408W mutation in the human PAH gene. Briefly PAH iPSCs are dissociated into single cells and then replated onto Geltex-coated plates. The iPSCs were then differentiated into definitive endoderm cells by treatment with Activin A, FGF2, and ChIR for 7 days. Definitive endoderm cells are then further patterned into foregut endoderm cells by activation of the BMP4 and FGF2 signaling pathway for an additional 6 days. Lastly, foregut endoderm cells were patterned into hepatoblast cells by treatment with oncostamin M, dexamethasone, hepatocyte growth factors, and ChIR for 12 days. Hepatoblasts were then sub-cultured onto collagen1-coated plates and expanded in media containing FGF19, Dexamethazone, ChIR, and SB431542 prior to transfection. The gene modifying polypeptide, template RNA, and second strand-targeting gRNA were delivered by nucleofection in the RNA format. Specifically, 4 µg of gene modifying polypeptide mRNA were combined with 10 µg of chemically synthesized template RNA, with or

without 10 µg of second strand-targeting gRNA, in 5 µL of water. The transfection mix was added to 100,000 iPSCs in Buffer P3 [Lonza], and cells were nucleofected using program DG-138. After nucleofection, cells were grown at 37˚C, 5% CO_2 for 3 days prior to cell lysis and genomic DNA extraction. To analyze gene editing activity, primers flanking the target insertion site locus were used to amplify across the locus. Amplicons were analyzed via short read sequencing using an Illumina MiSeq. Conversion of T>C indicates successful editing.

FIG. 25B shows a heatmap of % rewriting for each combination of template RNA and second strand-targeting RNA. The results show that many combinations of exemplary template RNAs and exemplary second strand-targeting gRNAs facilitated a corrective W408R mutation in the mutant hPAH gene of iPSC hepatoblasts. In particular, template RNAs RNACS1747, RNACS3877, RNACS4135, RNACS4134, RNACS2300, RNACS2299, RNACS4142, RNACS4173, RNACS4045, RNACS4048, and RNACS1763 showed the highest rewriting activity in this experiment.

The gene modifying system comprising mRNA encoding the gene modifying polypeptide listed above, a template RNA listed above, and a second strand-targeting gRNA described above were nucleofected in primary mouse hepatocytes from transgenic animals harboring the humanized region of exon 12 of the human PAH gene and contain the R408W PAH mutation. The gene modifying polypeptide, template RNA, and second strand-targeting gRNA were delivered by nucleofection in the RNA format. Specifically, 4 µg of gene modifying polypeptide mRNA were combined with 10 µg of chemically synthesized template RNA in 5 µL of water. The transfection mix was added to 100,000 primary hepatocytes in Buffer P3 [Lonza], and cells were nucleofected using program DG-138. After nucleofection, cells were grown at 37˚C, 5% CO_2 for 3 days prior to cell lysis and genomic DNA extraction. To analyze gene editing activity, primers flanking the target insertion site locus were used to amplify across the locus. Amplicons were analyzed via short read sequencing using an Illumina MiSeq. Conversion of C nucleotide to T nucleotide indicates successful editing.

FIG. 25C shows a heatmap of % rewriting for each combination of template RNA and second strand-targeting RNA. The results show that many combinations of exemplary template RNAs and exemplary second strand-targeting gRNAs facilitated a corrective W408R mutation in the mutant hPAH gene of primary mouse hepatocytes. In particular, template RNAs RNACS4134 and RNACS1792 showed the highest rewriting activity in this experiment. In particular, template RNAs RNACS4134 and RNACS1792 showed high rewriting activity in combination with second strand-targeting gRNA RNACS1812 (about 17% and about 14% editing, respectively).

The gene modifying system comprising the gene modifying polypeptide listed above, a template RNA listed above, and a second strand-targeting gRNA listed above is formulated in LNP and delivered to mice. Specifically, approximately 2.4 mg/kg of total RNA equivalent formulated in LNPs (4:1 N:P ratio for mRNA, and 3:1 N:P ratio for tgRNA/gRNA), combined at 1:1:1 (w/w) of template RNA:mRNA:gRNA, are dosed intravenously in 8 to 10-week-old, mixed gender hPAH mice (0.8 mg/kg each of template RNA, mRNA, and gRNA) in a 10 ml/kg bolus. Mice are administered a dose at time 0 (t = 0). 7 days post-dosing (as used herein post-dosing refers to time since the first dose), animals are sacrificed, and their liver and plasma are collected for analyses.

7-day plasma samples are analyzed by LC/MS to determine the level of phenylalanine present. Using CRISPR, hPAH transgenic mice were generated with a humanized region of exon 12 of the human PAH gene and contain the R408W PAH mutation that inactivates the PAH enzyme, resulting in sharply higher Phe levels in plasma than healthy wildtype mice. Successful rewriting of the hPAH transgene is expected to result in a decrease in Phe levels in plasma.]]

Phenylalanine is extracted from mouse plasma using protein precipitation and is analyzed by a LC-MS/MS system equipped with a Shimadzu Nexera UPLC (LC-40) coupled to a Sciex API 7500 mass spectrometer. Surrogate analyte (13C2,15N-Phenylalanine) is used for phenylalanine quantitation. Equivalence of ionization for naturally occurring and surrogate compounds is established prior to and after analytical run. Data are collected in the positive ion mode with three MRM transitions, 169.1 to 123.1 (13C2,15N-Phenylalanine), 166.1 to 120.1(Phenylalanine) and 172.1 to 126.0 (13C6-Phenylalanine, internal standard). Extracted samples are injected onto an Acquity UPLC BEH C18 column (1.7µm, 2.1x50 mm) and eluted

using a gradient of 0% to 15% of mobile phase B at a flow rate of 0.8 mL/min with a total run time of 3 min per injection. Mobile phase A is 100:2:0.1 H2O:Formic acid (FA): Trifluoroacetic acid (TFA) and mobile phase B is 95:5:2:0.1 ACN:H2O:FA:TFA. Data are processed using Sciex OS software.

The results will show that Phe levels decreased in plasma from mice with exemplary gene modifying systems targeting hPAH.

7-day liver samples are analyzed using Amp-Seq to determine % rewriting in target liver cells. To analyze gene editing activity, primers flanking the target insertion site locus are used to amplify across the locus in the genomic DNA of liver samples. Amplicons are analyzed via short read sequencing using an Illumina MiSeq. Conversion of a T nucleotide to a C nucleotide at position 1222 in the PAH gene indicates successful editing. The results will show that rewriting is observed in mice treated with exemplary gene modifying systems targeting hPAH.

Example 14: Evaluating the Rewriting Activity Over Time and Short-Term Safety of Exemplary Murine Template RNAs and Second Strand-Targeting gRNAs in an ENU2 Mouse Model

This example describes the use of exemplary gene modifying systems containing a gene modifying polypeptide, an exemplary template RNA, and exemplary second strand-targeting gRNA to evaluate the stability of rewriting over time and the short term safety of gene modifying systems used to correct the F263S mutation in ENU2 mice.

In this example, a template RNA contained:

(1) a gRNA spacer;

(2) a gRNA scaffold;

(3) a heterologous object sequence; and

(4) a primer binding site (PBS) sequence.

The exemplary template RNA tested was template RNA RNACS1855 shown in Table E1. The exemplary second strand-targeting gRNA was ngRNA5 (also referred to herein as RNACS2101), shown in Table E2. The exemplary gene modifying polypeptide used was RNAIVT338 (as described above and corresponding to the amino acid sequence of SEQ ID NO: 30480).

The gene modifying system was formulated in LNP and delivered to mice. [[Specifically, 2.4 mpk of total RNA equivalent formulated in LNPs, combined at 1:1 (w/w) of template RNA and mRNA, were dosed intravenously in 8 to 10-week-old, mixed gender ENU2 mice (0.8 mg/kg each of template RNA and mRNA with an additional 0.8 mg/kg of ngRNA in a 10 ml/kg bolus. Mice were administered a dose at time 0 (t = 0). 7 days and 28 days post-dosing, animals were sacrificed, and their liver, brain, plasma collected for analyses.

7-day and 28-day liver samples were analyzed using Amp-Seq to determine % rewriting in target liver cells (**FIG. 26A**). To analyze gene editing activity, primers flanking the target insertion site locus were used to amplify across the locus in the genomic DNA of liver samples. Amplicons were analyzed via short read sequencing using an Illumina MiSeq. Conversion of a C nucleotide to a T nucleotide at position 835 in the PAH gene indicated successful editing. Rewriting was observed from all treated mice at the 7d and 28d timepoints, and the % rewriting at the 7d and 28d timepoints were very similar. Amplicon sequencing was also used to evaluate the degree to which INDELs were introduced into the liver sample DNA (**FIG. 26B**). As seen in other data described herein, the % INDEL was significantly lower than the % rewriting, and the % INDEL at the 7d and 28d timepoints were very similar.

7-day and 28-day plasma and brain samples were also analyzed by LC/MS to determine the level of phenylalanine present. ENU2 mice harbor a mutation in the murine PAH gene that inactivates the PAH enzyme, resulting in sharply higher Phe levels in plasma and brain than healthy wildtype mice.

Phenylalanine was extracted from mouse plasma and brain using protein precipitation and then analyzed by a LC-MS/MS system equipped with a Shimadzu Nexera UPLC (LC-40) coupled to a Sciex API 7500 mass spectrometer. Surrogate analyte (13C2,15N-Phenylalanine) was used for phenylalanine quantitation. Equivalence of ionization for naturally occurring and surrogate compounds was established prior to and after analytical run. Data were collected in the positive ion mode with three MRM transitions, 169.1 to 123.1 (13C2,15N-Phenylalanine), 166.1 to 120.1(Phenylalanine) and 172.1 to 126.0 (13C6-Phenylalanine, internal standard). Extracted samples were injected onto an Acquity UPLC BEH C18 column (1.7µm, 2.1x50 mm) and eluted using a gradient of 0% to 15% of mobile phase B at a flow rate of 0.8 mL/min with a total run time of 3 min per injection. Mobile phase A is 100:2:0.1 H2O:Formic acid (FA): Trifluoroacetic

acid (TFA) and mobile phase B is 95:5:2:0.1 ACN:H2O:FA:TFA. Data were processed using Sciex OS software.

The results showed that Phe levels decreased in plasma from all treated mice, consistent with correction of the PAH deactivating point mutation using the gene modifying polypeptide and template RNAs examined (**FIG. 27**). The plasma Phe levels were consistently low at the 7d and 28d timepoints, showing that treated mice achieved stable Phe levels comparable to strain-matched wildtype mice at least out to 28d. When considered together (FIGs. 26A-27), the results show that the exemplary gene modifying systems can be used to specifically rewrite the mPAH gene of ENU2 mice, resulting in stable genetic modification and stable therapeutic phenotypic change.

The results showed that Phe levels decreased in brain from all treated mice, consistent with correction of the PAH deactivating point mutation using the gene modifying polypeptide and template RNAs examined (**FIG. 28**). The brain Phe levels were consistently low at the 7d and 28d timepoints, showing that treated mice achieved stable Phe levels comparable to strain-matched wildtype mice at least out to 28d. When considered together (FIGs. 26A-26B and 28), the results show that the exemplary gene modifying systems can be used to specifically rewrite the mPAH gene of ENU2 mice, resulting in stable genetic modification and stable therapeutic phenotypic change.

FIG. 29 shows a graph plotting correlation of plasma and brain Phe levels from samples used to generate FIGs. 27 and 28. The results show that plasma Phe level and brain Phe levels strongly correlate, with samples derived from saline treated ENU2 mice having higher Phe levels in plasma and in brain and samples derived from ENU2 mice treated with exemplary gene modifying systems as described herein having much lower Phe levels in plasma and in brain, similar to samples from saline treated wildtype mice.

At 90 days post dosing, animals are sacrificed, and their liver, brain, and plasma collected for analyses. The above analyses of % rewriting, % INDEL, and plasma Phe level are repeated with 90d liver, brain, and plasma samples. The results will show comparable rewriting and INDEL

levels to 7d and 28d samples from treated mice, and comparable Phe plasma and brain levels to 7d and 28d samples from treated mice.

Example 15: Evaluating Rewriting Activity of Exemplary Template RNAs and Second Strand-Targeting gRNAs in Cynomolgus macaque hepatocytes

This example describes the use of exemplary gene modifying systems containing a gene modifying polypeptide, template RNAs comprising varied spacers, lengths and compositions of heterologous object sequences, and PBS sequences, and either of two second strand-targeting gRNAs to evaluate the activity of template RNAs and second strand-targeting gRNAs to produce a R408 silent mutation (C to A) or P407 silent mutation (T to C) mutation into wild-type PAH in primary cyno hepatocytes. Sequences (e.g., spacer sequences) of template RNAs or combinations of sequences of template RNAs and second strand-targeting gRNAs that provide high rewriting activity in a comparable model system may also provide rewriting activity in therapeutic template RNAs and second strand-targeting gRNAs designed for correcting pathogenic hPAH mutations in a human subject.

In this example, a template RNA contained:

(1) a gRNA spacer;
(2) a gRNA scaffold;
(3) a heterologous object sequence; and
(4) a primer binding site (PBS) sequence.

Exemplary template RNAs generated and used are given in Table EX. Nucleotide modifications are noted as follows: phosphorothioate linkages denoted by an asterisk, 2'-O-methyl groups denoted by an 'm' preceding a nucleotide. The exemplary gene modifying polypeptide is RNAIVT338, comprising the amino acid sequence of SEQ ID NO: 30480. Exemplary second strand-targeting gRNAs for use with cPKU4, cPKU5.1, and cPKU5.2 template RNAs are RNACS1809 and RNACS1810, whereas exemplary second strand-targeting gRNAs for use with cPKU6 template RNAs are RNACS1906, RNACS1812, and RNACS1813, the nucleic acid sequence and chemical modifications of which are given here.

RNACS1809:

mG*mU*mG*rCrCrCrUrUrCrArCrUrCrArArGrCrCrUrGrGrUrUrUrUrArGrAmGmCm
UmAmGmAmAmAmUmAmGmCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGr
UrUrArUrCrAmAmCmUmUmGmAmAmAmAmAmGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUm
GmCmU*mU*mU*mU (SEQ ID NO: 30576)

RNACS1810:

mU*mU*mC*rArCrUrCrArArGrCrCrUrGrUrGrGrUrUrUrGrUrUrUrUrArGrAmGmCm
UmAmGmAmAmAmUmAmGmCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGr
UrUrArUrCrAmAmCmUmUmGmAmAmAmAmAmGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUm
GmCmU*mU*mU*mU (SEQ ID NO: 30577)

RNACS1812:

mG*mU*mC*rCrArArGrArCrCrUrCrArArUrCrCrUrUrUrGrUrUrUrUrArGrAmGmCm
UmAmGmAmAmAmUmAmGmCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGr
UrUrArUrCrAmAmCmUmUmGmAmAmAmAmAmGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUm
GmCmU*mU*mU*mU (SEQ ID NO: 30578)

RNACS1813:

mU*mG*mU*rCrCrArArGrArCrCrUrCrArArUrCrCrUrUrGrUrUrUrUrArGrAmGmCm
UmAmGmAmAmAmUmAmGmCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGr
UrUrArUrCrAmAmCmUmUmGmAmAmAmAmAmGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUm
GmCmU*mU*mU*mU (SEQ ID NO: 30579)

RNACS1906:

mC*mC*mU*rCrArArUrCrCrUrUrUrGrGrGrUrGrUrArUrGrUrUrUrUrArGrAmGmCm
UmAmGmAmAmAmUmAmGmCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGr
UrUrArUrCrAmAmCmUmUmGmAmAmAmAmAmGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUm
GmCmU*mU*mU*mU (SEQ ID NO: 30580)

Table EX – Further Exemplary Template RNAs and Sequences for use in C. macaques

RNAC S#	Name	Sequence	SEQ ID NO
RNAC S2611	cPKU4_P9R16_CtoA-PSkill	mG*mG*mG*rUrCrArUrArGrCrGrArArCrUrGrArGrArArGrUrUrUrUrArGrAmGmCmUmAmGmAmA mAmUmAmGmCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmU mGmAmAmAmAmAmGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrArArUrCrCrCr UrArGrGrCrCrCrUrUrUrUrCrArGrUrU*mC*mG*mC	30581
RNAC S2620	cPKU4_P9R18_CtoA-PSkill	mG*mG*mG*rUrCrArUrArGrCrGrArArCrUrGrArGrArArGrUrUrUrUrArGrAmGmCmUmAmGmAmA mAmUmAmGmCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmU mGmAmAmAmAmAmGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrArCrArArUrCr CrCrUrArGrGrCrCrCrUrUrUrUrCrArGrUrU*mC*mG*mC	30582
RNAC S2610	cPKU4_P10R16_CtoA-PSkill	mG*mG*mG*rUrCrArUrArGrCrGrArArCrUrGrArGrArArGrUrUrUrUrArGrAmGmCmUmAmGmAmA mAmUmAmGmCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmU mGmAmAmAmAmAmGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrArArUrCrCrCr UrArGrGrCrCrCrUrUrUrUrCrArGrUrUrC*mG*mC*mU	30583
RNAC S2602	cPKU4_P9R14_CtoA-PSkill	mG*mG*mG*rUrCrArUrArGrCrGrArArCrUrGrArGrArArGrUrUrUrUrArGrAmGmCmUmAmGmAmA mAmUmAmGmCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmU mGmAmAmAmAmAmGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrUrCrCrCrUrAr GrGrCrCrCrUrUrUrUrCrArGrUrU*mC*mG*mC	30584
RNAC S2618	cPKU4_P11R18_CtoA-PSkill	mG*mG*mG*rUrCrArUrArGrCrGrArArCrUrGrArGrArArGrUrUrUrUrArGrAmGmCmUmAmGmAmA mAmUmAmGmCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmU mGmAmAmAmAmAmGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrArCrArArUrCr CrCrUrArGrGrCrCrCrUrUrUrUrCrArGrUrUrCrG*mC*mU*mA	30585
RNAC S2609	cPKU4_P11R16_CtoA-PSkill	mG*mG*mG*rUrCrArUrArGrCrGrArArCrUrGrArGrArArGrUrUrUrUrArGrAmGmCmUmAmGmAmA mAmUmAmGmCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmU mGmAmAmAmAmAmGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrArArUrCrCrCr UrArGrGrCrCrCrUrUrUrUrCrArGrUrUrCrG*mC*mU*mA	30586
RNAC	cPKU4_P10R1	mG*mG*mG*rUrCrArUrArGrCrGrArArCrUrGrArGrArArGrUrUrUrUrArGrAmGmCmUmAmGmAmA mAmUmAmGmCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmU	30587

S2619	8_CtoA-PSkill	mGmAmAmAmAmAmGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrArCrArArUrCrCrCrUrArGrGrCrCrCrUrUrUrUrCrArGrUrUrC*mG*mC*mU	
RNACS2606	cPKU4_P14R16_CtoA-PSkill	mG*mG*mG*rUrCrArUrArGrCrGrArArCrUrGrArGrArArGrUrUrUrUrArGrAmGmCmUmAmGmAmAmAmUmAmGmCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmUmGmAmAmAmAmAmGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrArArUrCrCrCrUrArGrGrCrCrCrUrUrUrUrCrArGrUrUrCrGrCrUrA*mU*mG*mA	30588
RNACS2638	cPKU4_P9R22_CtoA-PSkill	mG*mG*mG*rUrCrArUrArGrCrGrArArCrUrGrArGrArArGrUrUrUrUrArGrAmGmCmUmAmGmAmAmAmUmAmGmCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmUmGmAmAmAmAmAmGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrUrGrCrCrArCrArArUrCrCrCrUrArGrGrCrCrCrUrUrUrUrCrArGrUrU*mC*mG*mC	30589
RNACS2607	cPKU4_P13R16_CtoA-PSkill	mG*mG*mG*rUrCrArUrArGrCrGrArArCrUrGrArGrArArGrUrUrUrUrArGrAmGmCmUmAmGmAmAmAmUmAmGmCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmUmGmAmAmAmAmAmGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrArArUrCrCrCrUrArGrGrCrCrCrUrUrUrUrCrArGrUrUrCrGrCrU*mA*mU*mG	30590
RNACS2648	cPKU4_P8R24_CtoA-PSkill	mG*mG*mG*rUrCrArUrArGrCrGrArArCrUrGrArGrArArGrUrUrUrUrArGrAmGmCmUmAmGmAmAmAmUmAmGmCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmUmGmAmAmAmAmAmGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrGrCrUrGrCrCrArCrArArUrCrCrCrUrArGrGrCrCrCrUrUrUrUrCrArGrU*mU*mC*mG	30591
RNACS2689	cPKU5.1_P12R12_CtoA-PSkill	mU*mA*mG*rCrGrArArCrUrGrArGrArArGrGrGrCrCrGrGrUrUrUrUrArGrAmGmCmUmAmGmAmAmAmUmAmGmCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmUmGmAmAmAmAmAmGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrArCrArArUrCrCrCrUrArGrGrCrCrCrUrUrUrUrCrArGrArCrCrCrUrUrCrUrCrA*mG*mU*mU	30592
RNACS2718	cPKU5.1_P10R18_CtoA-PSkill	mU*mA*mG*rCrGrArArCrUrGrArGrArArGrGrGrCrCrGrGrUrUrUrUrArGrAmGmCmUmAmGmAmAmAmUmAmGmCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmUmGmAmAmAmAmAmGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrArCrArArUrCrCrCrUrArGrArCrCrCrUrUrCrU*mC*mA*mG	30593
RNACS2691	cPKU5.1_P10R12_CtoA-PSkill	mU*mA*mG*rCrGrArArCrUrGrArGrArArGrGrGrCrCrGrGrUrUrUrUrArGrAmGmCmUmAmGmAmAmAmUmAmGmCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmUmGmAmAmAmAmAmGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrArCrArArUrCrCrCrUrArGrArCrCrCrUrUrCrU*mC*mA*mG	30594

RNAC S2690	cPKU5.1_P11R12_CtoA-PSkill	mU*mA*mG*rCrGrArArCrUrGrArGrArArGrGrGrCrCrGrGrUrUrUrUrArGrAmGmCmUmAmGmAmAmAmUmAmGmCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmUmGmAmAmAmAmAmGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrArCrArArUrCrCrCrUrArGrArCrCrCrUrUrCrUrC*mA*mG*mU	30595
RNAC S2717	cPKU5.1_P11R18_CtoA-PSkill	mU*mA*mG*rCrGrArArCrUrGrArGrArArGrGrGrCrCrGrGrUrUrUrUrArGrAmGmCmUmAmGmAmAmAmUmAmGmCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmUmGmAmAmAmAmAmGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrGrCrUrGrCrCrArCrArArUrCrCrCrUrArGrArCrCrCrUrUrCrUrC*mA*mG*mU	30596
RNAC S2681	cPKU5.1_P11R10_CtoA-PSkill	mU*mA*mG*rCrGrArArCrUrGrArGrArArGrGrGrCrCrGrGrUrUrUrUrArGrAmGmCmUmAmGmAmAmAmUmAmGmCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmUmGmAmAmAmAmAmGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrArArUrCrCrCrUrArGrArCrCrCrUrUrCrUrC*mA*mG*mU	30597
RNAC S2679	cPKU5.1_P13R10_CtoA-PSkill	mU*mA*mG*rCrGrArArCrUrGrArGrArArGrGrGrCrCrGrGrUrUrUrUrArGrAmGmCmUmAmGmAmAmAmUmAmGmCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmUmGmAmAmAmAmAmGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrArArUrCrCrCrUrArGrArCrCrCrUrUrCrUrC*mA*mG*mU	30598
RNAC S2680	cPKU5.1_P12R10_CtoA-PSkill	mU*mA*mG*rCrGrArArCrUrGrArGrArArGrGrGrCrCrGrGrUrUrUrUrArGrAmGmCmUmAmGmAmAmAmUmAmGmCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmUmGmAmAmAmAmAmGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrArArUrCrCrCrUrArGrArCrCrCrUrUrCrUrC*mA*mG*mU	30599
RNAC S2709	cPKU5.1_P10R16_CtoA-PSkill	mU*mA*mG*rCrGrArArCrUrGrArGrArArGrGrGrCrCrGrGrUrUrUrUrArGrAmGmCmUmAmGmAmAmAmUmAmGmCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmUmGmAmAmAmAmAmGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrUrGrCrCrArCrArArUrCrCrCrUrArGrArCrCrCrUrUrCrU*mC*mA*mG	30600
RNAC	cPKU5.1_P9R1	mU*mA*mG*rCrGrArArCrUrGrArGrArArGrGrGrCrCrGrGrUrUrUrUrArGrAmGmCmUmAmGmAmAmAmUmAmGmCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmU	30601

S2692	2_CtoA-PSkill	mGmAmAmAmAmAmGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrArCrArArUrCrCrCrUrArGrArCrCrCrUrUrC*mU*mC*mA	
RNAC S2736	cPKU5.1_P10R22_CtoA-PSkill	mU*mA*mG*rCrGrArArCrUrGrArGrArArGrGrGrCrCrGrGrUrUrUrUrArGrAmGmCmUmAmGmAmA mAmUmAmGmCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmU mGmAmAmAmAmAmGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrCrUrUrUrUrGrCr UrGrCrCrArCrArArUrCrCrCrUrArGrArCrCrCrUrUrCrU*mC*mA*mG	30602
RNAC S2738	cPKU5.1_P8R22_CtoA-PSkill	mU*mA*mG*rCrGrArArCrUrGrArGrArArGrGrGrCrCrGrGrUrUrUrUrArGrAmGmCmUmAmGmAmA mAmUmAmGmCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmU mGmAmAmAmAmAmGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrCrUrUrUrUrGrCr UrGrCrCrArCrArArUrCrCrCrUrArGrArCrCrCrUrU*mC*mU*mC	30603
RNAC S2782	cPKU5.2_P9R19_CtoA-PSkill	mA*mG*mC*rGrArArCrUrGrArGrArArGrGrGrCrCrGrArGrUrUrUrUrArGrAmGmCmUmAmGmAmA mAmUmAmGmCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmU mGmAmAmAmAmAmGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrUrUrGrCrUrGr CrCrArCrArArUrArCrCrUrArGrGrCrCrCrUrU*mC*mU*mC	30604
RNAC S2773	cPKU5.2_P9R17_CtoA-PSkill	mA*mG*mC*rGrArArCrUrGrArGrArArGrGrGrCrCrGrArGrUrUrUrUrArGrAmGmCmUmAmGmAmA mAmUmAmGmCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmU mGmAmAmAmAmAmGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrGrCrUrGrCrCr ArCrArArUrArCrCrUrArGrGrCrCrCrUrU*mC*mU*mC	30605
RNAC S2764	cPKU5.2_P9R15_CtoA-PSkill	mA*mG*mC*rGrArArCrUrGrArGrArArGrGrGrCrCrGrArGrUrUrUrUrArGrAmGmCmUmAmGmAmA mAmUmAmGmCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmU mGmAmAmAmAmAmGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrUrGrCrCrArCr ArArUrArCrCrUrArGrGrCrCrCrUrU*mC*mU*mC	30606
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RNAC S2765	cPKU5.2_P8R15_CtoA-PSkill	mA*mG*mC*rGrArArCrUrGrArGrArArGrGrGrCrCrGrArGrUrUrUrUrArGrAmGmCmUmAmGmAmA mAmUmAmGmCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmU mGmAmAmAmAmAmGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrUrGrCrCrArCr ArArUrArCrCrUrArGrGrCrCrCrU*mU*mC*mU	30608

RNAC S2763	cPKU5.2_P10R15_CtoA-PSkill	mA*mG*mC*rGrArArCrUrGrArGrArArGrGrGrCrCrGrArGrUrUrUrUrArGrAmGmCmUmAmGmAmA mAmUmAmGmCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmU mGmAmAmAmAmAmGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrUrGrCrCrArCr ArArUrArCrCrUrArGrGrCrCrCrUrUrC*mU*mC*mA	30609
RNAC S2762	cPKU5.2_P11R15_CtoA-PSkill	mA*mG*mC*rGrArArCrUrGrArGrArArGrGrGrCrCrGrArGrUrUrUrUrArGrAmGmCmUmAmGmAmA mAmUmAmGmCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmU mGmAmAmAmAmAmGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrUrGrCrCrArCr ArArUrArCrCrUrArGrGrCrCrCrUrUrCrU*mC*mA*mG	30610
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RNAC S2800	cPKU5.2_P9R23_CtoA-PSkill	mA*mG*mC*rGrArArCrUrGrArGrArArGrGrGrCrCrGrArGrUrUrUrUrArGrAmGmCmUmAmGmAmA mAmUmAmGmCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmU mGmAmAmAmAmAmGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrArArCrUrUrUr GrCrUrGrCrCrArCrArArUrArCrCrUrArGrGrCrCrCrUrU*mC*mU*mC	30613
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RNAC S2817	cPKU6_P10R11_CtoA-PSkill	mA*mC*mU*rUrUrGrCrUrGrCrCrArCrArArUrCrCrCrUrGrUrUrUrUrArGrAmGmCmUmAmGmAmA mAmUmAmGmCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmU mGmAmAmAmAmAmGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrArArGrGrGrUr CrUrArGrGrGrArUrUrGrUrG*mG*mC*mA	30616
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RNAC S3277	cPKU5.1_P9R15_TtoC	mU*mA*mG*rCrGrArArCrUrGrArGrArArGrGrGrCrCrGrGrUrUrUrUrArGrAmGmCmUmAmGmAmA mAmUmAmGmCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmU mGmAmAmAmAmAmGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrGrCrCrArCrAr ArUrCrCrCrCrCrGrGrCrCrCrUrUrC*mU*mC*mA	30640
RNAC S3278	cPKU5.1_P8R15_TtoC	mU*mA*mG*rCrGrArArCrUrGrArGrArArGrGrGrCrCrGrGrUrUrUrUrArGrAmGmCmUmAmGmAmA mAmUmAmGmCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmU mGmAmAmAmAmAmGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrGrCrCrArCrAr ArUrCrCrCrCrCrGrGrCrCrCrUrU*mC*mU*mC	30641
RNAC S3249	cPKU5.1_P10R9_TtoC	mU*mA*mG*rCrGrArArCrUrGrArGrArArGrGrGrCrCrGrGrUrUrUrUrArGrAmGmCmUmAmGmAmA mAmUmAmGmCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmU mGmAmAmAmAmAmGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrArUrCrCrCrCrC rGrGrCrCrCrUrUrCrU*mC*mA*mG	30642
RNAC S3275	cPKU5.1_P11R15_TtoC	mU*mA*mG*rCrGrArArCrUrGrArGrArArGrGrGrCrCrGrGrUrUrUrUrArGrAmGmCmUmAmGmAmA mAmUmAmGmCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmU mGmAmAmAmAmAmGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrGrCrCrArCrAr ArUrCrCrCrCrCrGrGrCrCrCrUrUrCrUrC*mA*mG*mU	30643
RNAC S3303	cPKU5.1_P10R21_TtoC	mU*mA*mG*rCrGrArArCrUrGrArGrArArGrGrGrCrCrGrGrUrUrUrUrArGrAmGmCmUmAmGmAmA mAmUmAmGmCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmU mGmAmAmAmAmAmGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrUrUrUrGrCrUr GrCrCrArCrArArUrCrCrCrCrGrGrCrCrCrUrUrCrU*mC*mA*mG	30644
RNAC S3250	cPKU5.1_P9R9_TtoC	mU*mA*mG*rCrGrArArCrUrGrArGrArArGrGrGrCrCrGrGrUrUrUrUrArGrAmGmCmUmAmGmAmA mAmUmAmGmCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmU mGmAmAmAmAmAmGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrArUrCrCrCrCrC rGrGrCrCrCrUrUrC*mU*mC*mA	30645
RNAC S3304	cPKU5.1_P9R21_TtoC	mU*mA*mG*rCrGrArArCrUrGrArGrArArGrGrGrCrCrGrGrUrUrUrUrArGrAmGmCmUmAmGmAmA mAmUmAmGmCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmU mGmAmAmAmAmAmGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrUrUrUrGrCrUr GrCrCrArCrArArUrCrCrCrCrGrGrCrCrCrUrUrC*mU*mC*mA	30646
RNAC S3248	cPKU5.1_P11R9_TtoC	mU*mA*mG*rCrGrArArCrUrGrArGrArArGrGrGrCrCrGrGrUrUrUrUrArGrAmGmCmUmAmGmAmA mAmUmAmGmCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmU mGmAmAmAmAmAmGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrArUrCrCrCrCrC rGrGrCrCrCrUrUrCrUrC*mA*mG*mU	30647

RNAC S3274	cPKU5.1_P12R15_TtoC	mU*mA*mG*rCrGrArArCrUrGrArGrArArGrGrGrCrCrGrGrUrUrUrUrArGrAmGmCmUmAmGmAmA mAmUmAmGmCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmU mGmAmAmAmAmAmGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrGrCrCrArCrAr ArUrCrCrCrCrCrGrGrCrCrCrUrUrCrUrCrA*mG*mU*mU	30648
RNAC S3295	cPKU5.1_P9R19_TtoC	mU*mA*mG*rCrGrArArCrUrGrArGrArArGrGrGrCrCrGrGrUrUrUrUrArGrAmGmCmUmAmGmAmA mAmUmAmGmCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmU mGmAmAmAmAmAmGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrUrGrCrUrGrCr CrArCrArArUrCrCrCrCrCrGrGrCrCrCrUrUrC*mU*mC*mA	30649
RNAC S3294	cPKU5.1_P10R19_TtoC	mU*mA*mG*rCrGrArArCrUrGrArGrArArGrGrGrCrCrGrGrUrUrUrUrArGrAmGmCmUmAmGmAmA mAmUmAmGmCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmU mGmAmAmAmAmAmGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrUrGrCrUrGrCr CrArCrArArUrCrCrCrCrCrGrGrCrCrCrUrUrCrU*mC*mA*mG	30650
RNAC S3349	cPKU5.2_P9R14_TtoC	mA*mG*mC*rGrArArCrUrGrArGrArArGrGrGrCrCrGrArGrUrUrUrUrArGrAmGmCmUmAmGmAmA mAmUmAmGmCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmU mGmAmAmAmAmAmGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrGrCrCrArCrAr ArUrCrCrCrCrCrGrGrCrCrCrUrU*mC*mU*mC	30651
RNAC S3347	cPKU5.2_P11R14_TtoC	mA*mG*mC*rGrArArCrUrGrArGrArArGrGrGrCrCrGrArGrUrUrUrUrArGrAmGmCmUmAmGmAmA mAmUmAmGmCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmU mGmAmAmAmAmAmGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrGrCrCrArCrAr ArUrCrCrCrCrCrGrGrCrCrCrUrUrCrU*mC*mA*mG	30652
RNAC S3385	cPKU5.2_P9R22_TtoC	mA*mG*mC*rGrArArCrUrGrArGrArArGrGrGrCrCrGrArGrUrUrUrUrArGrAmGmCmUmAmGmAmA mAmUmAmGmCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmU mGmAmAmAmAmAmGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrArCrUrUrUrGr CrUrGrCrCrArCrArArUrCrCrCrCrCrGrGrCrCrCrUrU*mC*mU*mC	30653
RNAC S3384	cPKU5.2_P10R22_TtoC	mA*mG*mC*rGrArArCrUrGrArGrArArGrGrGrCrCrGrArGrUrUrUrUrArGrAmGmCmUmAmGmAmA mAmUmAmGmCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmU mGmAmAmAmAmAmGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrArCrUrUrUrGr CrUrGrCrCrArCrArArUrCrCrCrCrCrGrGrCrCrCrUrUrC*mU*mC*mA	30654
RNAC S3377	cPKU5.2_P8R20_TtoC	mA*mG*mC*rGrArArCrUrGrArGrArArGrGrGrCrCrGrArGrUrUrUrUrArGrAmGmCmUmAmGmAmA mAmUmAmGmCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmU mGmAmAmAmAmAmGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrUrUrUrGrCrUr GrCrCrArCrArArUrCrCrCrCrCrGrGrCrCrCrU*mU*mC*mU	30655

RNAC S3350	cPKU5.2_P8R14_TtoC	mA*mG*mC*rGrArArCrUrGrArGrArArGrGrGrCrCrGrArGrUrUrUrUrArGrAmGmCmUmAmGmAmA mAmUmAmGmCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmU mGmAmAmAmAmAmGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrGrCrCrArCrAr ArUrCrCrCrCrCrGrGrCrCrCrU*mU*mC*mU	30656
RNAC S3378	cPKU5.2_P7R20_TtoC	mA*mG*mC*rGrArArCrUrGrArGrArArGrGrGrCrCrGrArGrUrUrUrUrArGrAmGmCmUmAmGmAmA mAmUmAmGmCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmU mGmAmAmAmAmAmGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrUrUrUrGrCrUr GrCrCrArCrArArUrCrCrCrCrCrGrGrCrCrC*mU*mU*mC	30657
RNAC S3320	cPKU5.2_P11R8_TtoC	mA*mG*mC*rGrArArCrUrGrArGrArArGrGrGrCrCrGrArGrUrUrUrUrArGrAmGmCmUmAmGmAmA mAmUmAmGmCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmU mGmAmAmAmAmAmGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrArUrCrCrCrCrC rGrGrCrCrCrUrUrCrU*mC*mA*mG	30658
RNAC S3348	cPKU5.2_P10R14_TtoC	mA*mG*mC*rGrArArCrUrGrArGrArArGrGrGrCrCrGrArGrUrUrUrUrArGrAmGmCmUmAmGmAmA mAmUmAmGmCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmU mGmAmAmAmAmAmGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrGrCrCrArCrAr ArUrCrCrCrCrCrGrGrCrCrCrUrUrC*mU*mC*mA	30659
RNAC S3360	cPKU5.2_P7R16_TtoC	mA*mG*mC*rGrArArCrUrGrArGrArArGrGrGrCrCrGrArGrUrUrUrUrArGrAmGmCmUmAmGmAmA mAmUmAmGmCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmU mGmAmAmAmAmAmGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrCrUrGrCrCrArC rArArUrCrCrCrCrCrGrGrCrCrC*mU*mU*mC	30660
RNAC S3331	cPKU5.2_P9R10_TtoC	mA*mG*mC*rGrArArCrUrGrArGrArArGrGrGrCrCrGrArGrUrUrUrUrArGrAmGmCmUmAmGmAmA mAmUmAmGmCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmU mGmAmAmAmAmAmGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrCrArArUrCrCrC rCrCrGrGrCrCrCrUrU*mC*mU*mC	30661
RNAC S3328	cPKU5.2_P12R10_TtoC	mA*mG*mC*rGrArArCrUrGrArGrArArGrGrGrCrCrGrArGrUrUrUrUrArGrAmGmCmUmAmGmAmA mAmUmAmGmCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmU mGmAmAmAmAmAmGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrCrArArUrCrCrC rCrCrGrGrCrCrCrUrUrCrUrC*mA*mG*mU	30662
RNAC S3392	cPKU6_P11R8_TtoC	mA*mC*mU*rUrUrGrCrUrGrCrCrArCrArArUrCrCrCrUrGrUrUrUrUrArGrAmGmCmUmAmGmAmA mAmUmAmGmCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmU mGmAmAmAmAmAmGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrGrGrCrCrGrGr GrGrGrArUrUrGrUrGrG*mC*mA*mG	30663

RNAC S3391	cPKU6_P12R8_TtoC	mA*mC*mU*rUrUrGrCrUrGrCrCrArCrArArUrCrCrCrUrGrUrUrUrUrArGrAmGmCmUmAmGmAmA mAmUmAmGmCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmU mGmAmAmAmAmAmGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrGrGrCrCrGrGr GrGrGrArUrUrGrUrGrGrC*mA*mG*mC	30664
RNAC S3390	cPKU6_P13R8_TtoC	mA*mC*mU*rUrUrGrCrUrGrCrCrArCrArArUrCrCrCrUrGrUrUrUrUrArGrAmGmCmUmAmGmAmA mAmUmAmGmCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmU mGmAmAmAmAmAmGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrGrGrCrCrGrGr GrGrGrArUrUrGrUrGrGrCrA*mG*mC*mA	30665
RNAC S3401	cPKU6_P11R10_TtoC	mA*mC*mU*rUrUrGrCrUrGrCrCrArCrArArUrCrCrCrUrGrUrUrUrUrArGrAmGmCmUmAmGmAmA mAmUmAmGmCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmU mGmAmAmAmAmAmGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrArGrGrGrCrCr GrGrGrGrGrArUrUrGrUrGrG*mC*mA*mG	30666
RNAC S3393	cPKU6_P10R8_TtoC	mA*mC*mU*rUrUrGrCrUrGrCrCrArCrArArUrCrCrCrUrGrUrUrUrUrArGrAmGmCmUmAmGmAmA mAmUmAmGmCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmU mGmAmAmAmAmAmGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrGrGrCrCrGrGr GrGrGrArUrUrGrUrG*mG*mC*mA	30667
RNAC S3402	cPKU6_P10R10_TtoC	mA*mC*mU*rUrUrGrCrUrGrCrCrArCrArArUrCrCrCrUrGrUrUrUrUrArGrAmGmCmUmAmGmAmA mAmUmAmGmCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmU mGmAmAmAmAmAmGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrArGrGrGrCrCr GrGrGrGrGrArUrUrGrUrG*mG*mC*mA	30668
RNAC S3400	cPKU6_P12R10_TtoC	mA*mC*mU*rUrUrGrCrUrGrCrCrArCrArArUrCrCrCrUrGrUrUrUrUrArGrAmGmCmUmAmGmAmA mAmUmAmGmCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmU mGmAmAmAmAmAmGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrArGrGrGrCrCr GrGrGrGrGrArUrUrGrUrGrC*mA*mG*mC	30669
RNAC S3389	cPKU6_P14R8_TtoC	mA*mC*mU*rUrUrGrCrUrGrCrCrArCrArArUrCrCrCrUrGrUrUrUrUrArGrAmGmCmUmAmGmAmA mAmUmAmGmCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmU mGmAmAmAmAmAmGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrGrGrCrCrGrGr GrGrGrArUrUrGrUrGrGrCrArG*mC*mA*mA	30670
RNAC S3403	cPKU6_P9R10_TtoC	mA*mC*mU*rUrUrGrCrUrGrCrCrArCrArArUrCrCrCrUrGrUrUrUrUrArGrAmGmCmUmAmGmAmA mAmUmAmGmCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmU mGmAmAmAmAmAmGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrArGrGrGrCrCr GrGrGrGrGrArUrUrGrU*mG*mG*mC	30671

RNAC S3394	cPKU6_P9R8_TtoC	mA*mC*mU*rUrUrGrCrUrGrCrCrArCrArArUrCrCrCrUrGrUrUrUrUrArGrAmGmCmUmAmGmAmA mAmUmAmGmCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmU mGmAmAmAmAmAmGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrGrGrCrCrGrGr GrGrGrArUrUrGrU*mG*mG*mC	30672
RNAC S3410	cPKU6_P11R12_TtoC	mA*mC*mU*rUrUrGrCrUrGrCrCrArCrArArUrCrCrCrUrGrUrUrUrUrArGrAmGmCmUmAmGmAmA mAmUmAmGmCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmU mGmAmAmAmAmAmGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrGrArArGrGrGr CrCrGrGrGrGrGrArUrUrGrUrGrG*mC*mA*mG	30673

The gene modifying system comprising mRNA encoding the gene modifying polypeptide listed above, a template RNA listed above, and a second strand-targeting gRNA described above were transfected into primary cyno hepatocytes. The gene modifying polypeptide, template RNA, and second strand-targeting gRNA were delivered by nucleofection in the RNA format. Specifically, 4 µg of gene modifying polypeptide mRNA were combined with 4 µg of chemically synthesized template RNA and 4 ug of nicking gRNA in 5 µL of water. The transfection mix was added to 100,000 primary hepatocytes in Buffer P3 [Lonza], and cells were nucleofected using program DG-138. After nucleofection, cells were grown at 37˚C, 5% CO_2 for 3 days prior to cell lysis and genomic DNA extraction. To analyze gene editing activity, primers flanking the target insertion site locus were used to amplify across the locus. Amplicons were analyzed via short read sequencing using an Illumina MiSeq. Conversion of T to C or C to A nucleotide indicated successful editing.

FIGS. 30A-30H show heatmaps of % rewriting for each combination of template RNA and second strand-targeting RNA, with FIGs. 30A-30D showing C to A rewriting and FIGs. 30E-30H showing T to C rewriting and grouped by the spacer of the template RNA. The results show that many combinations of exemplary template RNAs and exemplary second strand-targeting gRNAs facilitated installation of the silent mutations at R408 or P407 positions into cPAH gene of primary cyno hepatocytes. The results showed that for C to A editing, cPKU6 template RNAs showed the highest % rewriting compared to other spacers. For this edit, the second strand-targeting gRNA RNACS1906 showed the highest % rewriting combined with cPKU6 template RNAs (e.g., RNACS2827 template RNA combined with RNACS1906 showed 43% rewriting). The results showed that for T to C editing, cPKU5.2 template RNAs showed the highest % rewriting compared to other spacers, followed by cPKU6 template RNAs. For this edit, the second strand-targeting gRNA RNACS1810 showed the highest % rewriting combined with cPKU5.2 template RNAs (e.g., RNACS3349 template RNA combined with RNACS1810 showed 57% rewriting), whereas the second strand-targeting gRNA RNACS1906 showed the highest % rewriting combined with cPKU6 template RNAs.

Example 16: Evaluating Impact of Different Silent Substitutions on Rewriting Activity in human iPSC-derived hepatoblasts

This example describes the use of exemplary gene modifying systems containing a gene modifying polypeptide and template RNAs comprising four different spacers (hPKU3, hPKU4, hPKU5, and hPKU6), five lengths of heterologous object sequences, and three lengths of PBS sequences, wherein the template RNAs comprised one of five different silent substitutions. The example describes evaluation of the activity of template RNAs containing said silent substitutions to produce an W408R mutation to correct the R408W mutation in hPAH in CRISPR gene-edited iPSC-derived hepatoblast cells.

In this example, a template RNA contained:

(1) a gRNA spacer;

(2) a gRNA scaffold;

(3) a heterologous object sequence; and

(4) a primer binding site (PBS) sequence.

Exemplary template RNAs generated and used are given in Table E6. Nucleotide modifications are noted as follows: phosphorothioate linkages denoted by an asterisk, 2'-O-methyl groups denoted by an 'm' preceding a nucleotide. The exemplary gene modifying polypeptide is RNAIVT338, comprising the amino acid sequence of SEQ ID NO: 30480.

Table E6 – Exemplary Template RNAs with Various Silent Substitutions

RNACS #	Name	IDT Notation	SEQ ID NO
RNACS 4741	hPKU3_R25_P10_sub0	mU*mG*mG*rGrUrCrGrUrArGrCrGrArArCrUrGrArGrArGrUrUrUrUrArGrAmGmCmUmAmGmAmAmAmUmAmGmCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmUmGmAmAmAmAmAmGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrGrCrUrGrCrCrArCrArArUrArCrCrUrCrGrGrCrCrCrUrUrCrUrCrArGrUrUrCrG*mC*mU*mA	30674
RNACS 4742	hPKU3_R25_P10_sub1	mU*mG*mG*rGrUrCrGrUrArGrCrGrArArCrUrGrArGrArGrUrUrUrUrArGrAmGmCmUmAmGmAmAmAmUmAmGmCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmUmGmAmAmAmAmAmGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrGrCrUrGrCrCrArCrArArUrArCrCrGrCrGrCrGrCrCrCrUrUrCrUrCrArGrUrUrCrG*mC*mU*mA	30675
RNACS 4743	hPKU3_R25_P10_sub2	mU*mG*mG*rGrUrCrGrUrArGrCrGrArArCrUrGrArGrArGrUrUrUrUrArGrAmGmCmUmAmGmAmAmAmUmAmGmCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmUmGmAmAmAmAmAmGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrGrCrUrGrCrCrArCrArArUrArCrCrUrCrGrGrCrCrCrUrUrCrUrCrArGrUrUrCrG*mC*mU*mA	30676
RNACS 4744	hPKU3_R25_P10_sub4	mU*mG*mG*rGrUrCrGrUrArGrCrGrArArCrUrGrArGrArGrUrUrUrUrArGrAmGmCmUmAmGmAmAmAmUmAmGmCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmUmGmAmAmAmAmAmGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrGrCrUrGrCrCrArCrArArUrArCrCrUrCrGrGrCrCrCrUrUrCrUrCrArGrUrUrCrG*mC*mU*mA	30677
RNACS 4745	hPKU3_R25_P10_sub7	mU*mG*mG*rGrUrCrGrUrArGrCrGrArArCrUrGrArGrArGrUrUrUrUrArGrAmGmCmUmAmGmAmAmAmUmAmGmCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmUmGmAmAmAmAmAmGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrGrCrUrGrCrCrArCrArArUrArCrCrUrCrGrGrCrCrCrUrUrCrUrCrArGrUrUrCrG*mC*mU*mA	30678
RNACS 4746	hPKU3_R25_P10_sub8	mU*mG*mG*rGrUrCrGrUrArGrCrGrArArCrUrGrArGrArGrUrUrUrUrArGrAmGmCmUmAmGmAmAmAmUmAmGmCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmUmGmAmAmAmAmAmGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrGrCrUrGrCrCrArCrArArUrArCrCrUrCrGrGrCrCrCrUrUrCrUrCrArGrUrUrCrG*mC*mU*mA	30679
RNACS 4747	hPKU3_R23_P10_sub0	mU*mG*mG*rGrUrCrGrUrArGrCrGrArArCrUrGrArGrArGrUrUrUrUrArGrAmGmCmUmAmGmAmAmAmUmAmGmCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmUmGmAmAmAmAmAmGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrUrGrCrCrArCrArArUrArCrCrUrCrGrGrCrCrCrUrUrCrUrCrArGrUrUrCrG*mC*mU*mA	30680

RNACS 4748	hPKU3_R23_P10_sub1	mU*mG*mG*rGrUrCrGrUrArGrCrGrArArCrUrGrArGrArGrUrUrUrUrArGrAmGmCmUmAmGmAmAmAmUmAmGmCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmUmGmAmAmAmAmAmGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrUrGrCrCrArCrArArUrArCrCrGrCrGrGrCrCrCrUrUrCrUrCrArGrUrUrCrG*mC*mU*mA	30681
RNACS 4749	hPKU3_R23_P10_sub2	mU*mG*mG*rGrUrCrGrUrArGrCrGrArArCrUrGrArGrArGrUrUrUrUrArGrAmGmCmUmAmGmAmAmAmUmAmGmCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmUmGmAmAmAmAmAmGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrUrGrCrCrArCrArArUrArCrCrGrCrGrGrCrCrCrUrUrCrUrCrArGrUrUrCrG*mC*mU*mA	30682
RNACS 4750	hPKU3_R23_P10_sub4	mU*mG*mG*rGrUrCrGrUrArGrCrGrArArCrUrGrArGrArGrUrUrUrUrArGrAmGmCmUmAmGmAmAmAmUmAmGmCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmUmGmAmAmAmAmAmGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrUrGrCrCrArCrArArUrArCrCrGrCrGrGrCrCrCrUrUrCrUrCrArGrUrUrCrG*mC*mU*mA	30683
RNACS 4751	hPKU3_R23_P10_sub7	mU*mG*mG*rGrUrCrGrUrArGrCrGrArArCrUrGrArGrArGrUrUrUrUrArGrAmGmCmUmAmGmAmAmAmUmAmGmCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmUmGmAmAmAmAmAmGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrUrGrCrCrArCrArArUrArCrCrGrCrGrGrCrCrCrUrUrCrUrCrArGrUrUrCrG*mC*mU*mA	30684
RNACS 4752	hPKU3_R23_P10_sub8	mU*mG*mG*rGrUrCrGrUrArGrCrGrArArCrUrGrArGrArGrUrUrUrUrArGrAmGmCmUmAmGmAmAmAmUmAmGmCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmUmGmAmAmAmAmAmGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrUrGrCrCrArCrArArUrArCrCrGrCrGrGrCrCrCrArUrUrCrUrCrArGrUrUrCrG*mC*mU*mA	30685
RNACS 4753	hPKU3_R21_P10_sub0	mU*mG*mG*rGrUrCrGrUrArGrCrGrArArCrUrGrArGrArGrUrUrUrUrArGrAmGmCmUmAmGmAmAmAmUmAmGmCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmUmGmAmAmAmAmAmGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrCrCrArCrArArUrArCrCrGrCrGrGrCrCrCrUrUrCrUrCrArGrUrUrCrG*mC*mU*mA	30686
RNACS 4754	hPKU3_R21_P10_sub1	mU*mG*mG*rGrUrCrGrUrArGrCrGrArArCrUrGrArGrArGrUrUrUrUrArGrAmGmCmUmAmGmAmAmAmUmAmGmCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmUmGmAmAmAmAmAmGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrCrCrArCrArArUrArCrCrGrCrGrGrCrCrCrUrUrCrUrCrArGrUrUrCrG*mC*mU*mA	30687
RNACS 4755	hPKU3_R21_P10_sub2	mU*mG*mG*rGrUrCrGrUrArGrCrGrArArCrUrGrArGrArGrUrUrUrUrArGrAmGmCmUmAmGmAmAmAmUmAmGmCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmUmGmAmAmAmAmAmGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrCrCrArCrArArUrArCrCrGrCrGrGrCrCrCrUrUrCrUrCrArGrUrUrCrG*mC*mU*mA	30688

RNACS 4756	hPKU3_R21_P10_sub4	mU*mG*mG*rGrUrCrGrUrArGrCrGrArArCrUrGrArGrArGrUrUrUrUrArGrAmGmCmUmAmGmAmAmAmUmAmGmCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmUmGmAmAmAmAmAmGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrCrCrArCrArArUrArCrCrUrCrGrCrCrCrCrUrUrCrUrCrArGrUrUrCrG*mC*mU*mA	30689
RNACS 4757	hPKU3_R21_P10_sub7	mU*mG*mG*rGrUrCrGrUrArGrCrGrArArCrUrGrArGrArGrUrUrUrUrArGrAmGmCmUmAmGmAmAmAmUmAmGmCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmUmGmAmAmAmAmAmGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrCrCrArCrArArUrArCrCrGrCrGrCrCrCrCrUrUrCrUrCrArGrUrUrCrG*mC*mU*mA	30690
RNACS 4758	hPKU3_R21_P10_sub8	mU*mG*mG*rGrUrCrGrUrArGrCrGrArArCrUrGrArGrArGrUrUrUrUrArGrAmGmCmUmAmGmAmAmAmUmAmGmCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmUmGmAmAmAmAmAmGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrCrCrArCrArArUrArCrCrGrCrGrCrCrCrArUrUrCrUrCrArGrUrUrCrG*mC*mU*mA	30691
RNACS 4759	hPKU3_R19_P10_sub0	mU*mG*mG*rGrUrCrGrUrArGrCrGrArArCrUrGrArGrArGrUrUrUrUrArGrAmGmCmUmAmGmAmAmAmUmAmGmCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmUmGmAmAmAmAmAmGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrArCrArArUrArCrCrUrCrGrCrCrCrUrUrCrUrCrArGrUrUrCrG*mC*mU*mA	30692
RNACS 4760	hPKU3_R19_P10_sub1	mU*mG*mG*rGrUrCrGrUrArGrCrGrArArCrUrGrArGrArGrUrUrUrUrArGrAmGmCmUmAmGmAmAmAmUmAmGmCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmUmGmAmAmAmAmAmGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrArCrArArUrArCrCrGrCrGrCrCrCrUrUrCrUrCrArGrUrUrCrG*mC*mU*mA	30693
RNACS 4761	hPKU3_R19_P10_sub2	mU*mG*mG*rGrUrCrGrUrArGrCrGrArArCrUrGrArGrArGrUrUrUrUrArGrAmGmCmUmAmGmAmAmAmUmAmGmCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmUmGmAmAmAmAmAmGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrArCrArArUrCrCrCrUrCrGrGrCrCrCrUrUrCrUrCrArGrUrUrCrG*mC*mU*mA	30694
RNACS 4762	hPKU3_R19_P10_sub4	mU*mG*mG*rGrUrCrGrUrArGrCrGrArArCrUrGrArGrArGrUrUrUrUrArGrAmGmCmUmAmGmAmAmAmUmAmGmCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmUmGmAmAmAmAmAmGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrArCrArArUrArCrCrUrCrGrCrCrCrCrUrUrCrUrCrArGrUrUrCrG*mC*mU*mA	30695
RNACS 4763	hPKU3_R19_P10_sub7	mU*mG*mG*rGrUrCrGrUrArGrCrGrArArCrUrGrArGrArGrUrUrUrUrArGrAmGmCmUmAmGmAmAmAmUmAmGmCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmUmGmAmAmAmAmAmGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrArCrArArUrArCrCrGrCrGrCrCrCrUrUrCrUrCrArGrUrUrCrG*mC*mU*mA	30696

RNACS 4764	hPKU3_R19_P10_sub8	mU*mG*mG*rGrUrCrGrUrArGrCrGrArArCrUrGrArGrArGrUrUrUrUrArGrAmGmCmUmAmGmAmAmAmUmAmGmCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmUmGmAmAmAmAmAmGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrArCrArArUrArCrCrGrCrGrCrCrCrArUrUrCrUrCrArGrUrUrCrG*mC*mU*mA	30697
RNACS 4765	hPKU3_R17_P10_sub0	mU*mG*mG*rGrUrCrGrUrArGrCrGrArArCrUrGrArGrArGrUrUrUrUrArGrAmGmCmUmAmGmAmAmAmUmAmGmCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmUmGmAmAmAmAmAmGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrArArGrUrCrUrCrGrGrCrCrCrUrUrCrUrCrArGrUrUrCrG*mC*mU*mA	30698
RNACS 4766	hPKU3_R17_P10_sub1	mU*mG*mG*rGrUrCrGrUrArGrCrGrArArCrUrGrArGrArGrUrUrUrUrArGrAmGmCmUmAmGmAmAmAmUmAmGmCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmUmGmAmAmAmAmAmGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrArArGrCrCrUrCrGrGrCrCrCrUrUrCrUrCrArGrUrUrCrG*mC*mU*mA	30699
RNACS 4767	hPKU3_R17_P10_sub2	mU*mG*mG*rGrUrCrGrUrArGrCrGrArArCrUrGrArGrArGrUrUrUrUrArGrAmGmCmUmAmGmAmAmAmUmAmGmCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmUmGmAmAmAmAmAmGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrArArUrCrCrUrCrGrGrCrCrCrUrUrCrUrCrArGrUrUrCrG*mC*mU*mA	30700
RNACS 4768	hPKU3_R17_P10_sub4	mU*mG*mG*rGrUrCrGrUrArGrCrGrArArCrUrGrArGrArGrUrUrUrUrArGrAmGmCmUmAmGmAmAmAmUmAmGmCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmUmGmAmAmAmAmAmGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrArArUrCrCrUrCrGrGrCrCrCrUrUrCrUrCrArGrUrUrCrG*mC*mU*mA	30701
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RNACS 4773	hPKU3_R25_P9_sub2	mU*mG*mG*rGrUrCrGrUrArGrCrGrArArCrUrGrArGrArGrUrUrUrUrArGrAmGmCmUmAmGmAmAmAmUmAmGmCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmUmGmAmAmAmAmAmGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrGrCrUrGrCrCrArCrArArUrCrCrCrUrCrGrGrCrCrCrUrUrCrUrCrArGrUrUrC*mG*mC*mU	30706

RNACS 4774	hPKU3_R25_P9_sub4	mU*mG*mG*rGrUrCrGrUrArGrCrGrArArCrUrGrArGrArGrUrUrUrUrArGrAmGmCmUmAmGmAmAmAmUmAmGmCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmUmGmAmAmAmAmAmGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrGrCrUrGrCrCrArCrArArUrArCrCrUrCrGrCrCrCrCrUrUrCrUrCrArGrUrUrC*mG*mC*mU	30707
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RNACS 4781	hPKU3_R23_P9_sub7	mU*mG*mG*rGrUrCrGrUrArGrCrGrArArCrUrGrArGrArGrUrUrUrUrArGrAmGmCmUmAmGmAmAmAmUmAmGmCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmUmGmAmAmAmAmAmGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrGrCrUrGrCrCrArCrArArUrArCrCrGrCrGrCrCrCrUrUrCrUrCrArGrUrUrC*mG*mC*mU	30714

RNACS 4782	hPKU3_R23_P9_sub8	mU*mG*mG*rGrUrCrGrUrArGrCrGrArArCrUrGrArGrArGrUrUrUrUrArGrAmGmCmUmAmGmAmAmAmUmAmGmCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmUmGmAmAmAmAmAmGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrUrGrCrCrArCrArArUrArCrCrGrCrGrCrCrCrArUrUrCrUrCrArGrUrUrC*mG*mC*mU	30715
RNACS 4783	hPKU3_R21_P9_sub0	mU*mG*mG*rGrUrCrGrUrArGrCrGrArArCrUrGrArGrArGrUrUrUrUrArGrAmGmCmUmAmGmAmAmAmUmAmGmCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmUmGmAmAmAmAmAmGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrCrCrArCrArArUrArCrCrUrCrGrGrCrCrCrUrUrCrUrCrArGrUrUrC*mG*mC*mU	30716
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RNACS 4789	hPKU3_R19_P9_sub0	mU*mG*mG*rGrUrCrGrUrArGrCrGrArArCrUrGrArGrArGrUrUrUrUrArGrAmGmCmUmAmGmAmAmAmUmAmGmCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmUmGmAmAmAmAmAmGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrArCrArArUrArCrCrUrCrGrGrCrCrCrUrUrCrUrCrArGrUrUrC*mG*mC*mU	30722
RNACS 4790	hPKU3_R19_P9_sub1	mU*mG*mG*rGrUrCrGrUrArGrCrGrArArCrUrGrArGrArGrUrUrUrUrArGrAmGmCmUmAmGmAmAmAmUmAmGmCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmUmGmAmAmAmAmAmGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrArCrArArUrArCrCrGrCrGrGrCrCrCrUrUrCrUrCrArGrUrUrC*mG*mC*mU	30723

RNACS 4791	hPKU3_R19_P9_sub2	mU*mG*mG*rGrUrCrGrUrArGrCrGrArArCrUrGrArGrArGrUrUrUrUrArGrAmGmCmUmAmGmAmAmAmUmAmGmCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmUmGmAmAmAmAmAmGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrArCrArArUrCrCrCrUrCrGrGrCrCrCrUrUrCrUrCrArGrUrUrC*mG*mC*mU	30724
RNACS 4792	hPKU3_R19_P9_sub4	mU*mG*mG*rGrUrCrGrUrArGrCrGrArArCrUrGrArGrArGrUrUrUrUrArGrAmGmCmUmAmGmAmAmAmUmAmGmCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmUmGmAmAmAmAmAmGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrArCrArArUrArCrCrUrCrGrGrCrCrCrUrUrCrUrCrArGrUrUrC*mG*mC*mU	30725
RNACS 4793	hPKU3_R19_P9_sub7	mU*mG*mG*rGrUrCrGrUrArGrCrGrArArCrUrGrArGrArGrUrUrUrUrArGrAmGmCmUmAmGmAmAmAmUmAmGmCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmUmGmAmAmAmAmAmGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrArCrArArUrArCrCrGrCrGrCrCrCrUrUrCrUrCrArGrUrUrC*mG*mC*mU	30726
RNACS 4794	hPKU3_R19_P9_sub8	mU*mG*mG*rGrUrCrGrUrArGrCrGrArArCrUrGrArGrArGrUrUrUrUrArGrAmGmCmUmAmGmAmAmAmUmAmGmCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmUmGmAmAmAmAmAmGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrArCrArArUrArCrCrGrCrGrCrCrCrArUrUrCrUrCrArGrUrUrC*mG*mC*mU	30727
RNACS 4795	hPKU3_R17_P9_sub0	mU*mG*mG*rGrUrCrGrUrArGrCrGrArArCrUrGrArGrArGrUrUrUrUrArGrAmGmCmUmAmGmAmAmAmUmAmGmCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmUmGmAmAmAmAmAmGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrArArGrUrUrCrCrGrCrGrCrCrCrUrUrCrUrCrArGrUrUrC*mG*mC*mU	30728
RNACS 4796	hPKU3_R17_P9_sub1	mU*mG*mG*rGrUrCrGrUrArGrCrGrArArCrUrGrArGrArGrUrUrUrUrArGrAmGmCmUmAmGmAmAmAmUmAmGmCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmUmGmAmAmAmAmAmGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrArArGrUrUrCrCrGrCrGrCrCrCrUrUrCrUrCrArGrUrUrC*mG*mC*mU	30729
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RNACS 4798	hPKU3_R17_P9_sub4	mU*mG*mG*rGrUrCrGrUrArGrCrGrArArCrUrGrArGrArGrUrUrUrUrArGrAmGmCmUmAmGmAmAmAmUmAmGmCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmUmGmAmAmAmAmAmGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrArArGrUrUrCrCrGrCrGrCrCrCrUrUrCrUrCrArGrUrUrC*mG*mC*mU	30731
RNACS 4799	hPKU3_R17_P9_sub7	mU*mG*mG*rGrUrCrGrUrArGrCrGrArArCrUrGrArGrArGrUrUrUrUrArGrAmGmCmUmAmGmAmAmAmUmAmGmCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmUmGmAmAmAmAmAmGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrArArGrUrUrCrCrGrCrGrCrCrCrUrUrCrUrCrArGrUrUrC*mG*mC*mU	30732
RNACS 4800	hPKU3_R17_P9_sub8	mU*mG*mG*rGrUrCrGrUrArGrCrGrArArCrUrGrArGrArGrUrUrUrUrArGrAmGmCmUmAmGmAmAmAmUmAmGmCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmUmGmAmAmAmAmAmGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrArArGrUrUrCrCrGrCrGrCrCrCrArUrUrCrUrCrArGrUrUrC*mG*mC*mU	30733
RNACS 4801	hPKU3_R25_P8_sub0	mU*mG*mG*rGrUrCrGrUrArGrCrGrArArCrUrGrArGrArGrUrUrUrUrArGrAmGmCmUmAmGmAmAmAmUmAmGmCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmUmGmAmAmAmAmAmGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrGrCrUrGrCrCrArCrArArUrArCrCrUrCrGrGrCrCrCrUrUrCrUrCrArGrUrU*mC*mG*mC	30734

RNACS 4802	hPKU3_R25_P8_sub1	mU*mG*mG*rGrUrCrGrUrArGrCrGrArArCrUrGrArGrArGrUrUrUrUrArGrAmGmCmUmAmGmAmAmAmUmAmGmCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmUmGmAmAmAmAmAmGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrGrCrUrGrCrCrArCrArArUrArCrCrGrCrGrGrCrCrCrUrUrCrUrCrArGrUrU*mC*mG*mC	30735
RNACS 4803	hPKU3_R25_P8_sub2	mU*mG*mG*rGrUrCrGrUrArGrCrGrArArCrUrGrArGrArGrUrUrUrUrArGrAmGmCmUmAmGmAmAmAmUmAmGmCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmUmGmAmAmAmAmAmGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrGrCrUrGrCrCrArCrArArUrArCrCrGrCrGrGrCrCrCrUrUrCrUrCrArGrUrU*mC*mG*mC	30736
RNACS 4804	hPKU3_R25_P8_sub4	mU*mG*mG*rGrUrCrGrUrArGrCrGrArArCrUrGrArGrArGrUrUrUrUrArGrAmGmCmUmAmGmAmAmAmUmAmGmCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmUmGmAmAmAmAmAmGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrGrCrUrGrCrCrArCrArArUrArCrCrGrCrGrGrCrCrCrUrUrCrUrCrArGrUrU*mC*mG*mC	30737
RNACS 4805	hPKU3_R25_P8_sub7	mU*mG*mG*rGrUrCrGrUrArGrCrGrArArCrUrGrArGrArGrUrUrUrUrArGrAmGmCmUmAmGmAmAmAmUmAmGmCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmUmGmAmAmAmAmAmGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrGrCrUrGrCrCrArCrArArUrArCrCrGrCrGrGrCrCrCrUrUrCrUrCrArGrUrU*mC*mG*mC	30738
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RNACS 4810	hPKU3_R23_P8_sub4	mU*mG*mG*rGrUrCrGrUrArGrCrGrArArCrUrGrArGrArGrUrUrUrUrArGrAmGmCmUmAmGmAmAmAmUmAmGmCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmUmGmAmAmAmAmAmGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrUrGrCrCrArCrArArUrArCrCrUrCrGrCrCrCrCrUrUrCrUrCrArGrUrU*mC*mG*mC	30743
RNACS 4811	hPKU3_R23_P8_sub7	mU*mG*mG*rGrUrCrGrUrArGrCrGrArArCrUrGrArGrArGrUrUrUrUrArGrAmGmCmUmAmGmAmAmAmUmAmGmCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmUmGmAmAmAmAmAmGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrUrGrCrCrArCrArArUrArCrCrGrCrGrCrCrCrCrUrUrCrUrCrArGrUrU*mC*mG*mC	30744
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RNACS 4815	hPKU3_R21_P8_sub2	mU*mG*mG*rGrUrCrGrUrArGrCrGrArArCrUrGrArGrArGrUrUrUrUrArGrAmGmCmUmAmGmAmAmAmUmAmGmCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmUmGmAmAmAmAmAmGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrCrCrArCrArArUrCrCrCrUrCrGrGrCrCrCrUrUrCrUrCrArGrUrU*mC*mG*mC	30748
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RNACS 4818	hPKU3_R21_P8_sub8	mU*mG*mG*rGrUrCrGrUrArGrCrGrArArCrUrGrArGrArGrUrUrUrUrArGrAmGmCmUmAmGmAmAmAmUmAmGmCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmUmGmAmAmAmAmAmGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrCrCrArCrArArUrArCrCrGrCrGrCrCrCrArUrUrCrUrCrArGrUrU*mC*mG*mC	30751
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RNACS 4829	hPKU3_R17_P8_sub7	mU*mG*mG*rGrUrCrGrUrArGrCrGrArArCrUrGrArGrArGrUrUrUrUrArGrAmGmCmUmAmGmAmAmAmUmAmGmCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmUmGmAmAmAmAmAmGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrArArUrArCrCrGrCrGrCrCrCrCrUrUrCrUrCrArGrUrU*mC*mG*mC	30762
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RNACS 4832	hPKU4_R24_P10_sub1	mG*mG*mG*rUrCrGrUrArGrCrGrArArCrUrGrArGrArGrUrUrUrUrArGrAmGmCmUmAmGmAmAmAmUmAmGmCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmUmGmAmAmAmAmAmGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrGrCrUrGrCrCrArCrArArUrArCrCrUrCrGrGrGrCrCrCrUrUrCrUrCrArGrUrUrC*mG*mC*mU	30765
RNACS 4833	hPKU4_R24_P10_sub4	mG*mG*mG*rUrCrGrUrArGrCrGrArArCrUrGrArGrArGrUrUrUrUrArGrAmGmCmUmAmGmAmAmAmUmAmGmCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmUmGmAmAmAmAmAmGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrGrCrUrGrCrCrArCrArArUrArCrCrUrCrGrGrGrCrCrCrUrUrCrUrCrArGrUrUrC*mG*mC*mU	30766
RNACS 4834	hPKU4_R24_P10_sub5	mG*mG*mG*rUrCrGrUrArGrCrGrArArCrUrGrArGrArGrUrUrUrUrArGrAmGmCmUmAmGmAmAmAmUmAmGmCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmUmGmAmAmAmAmAmGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrGrCrUrGrCrCrArCrArArUrArCrCrUrCrGrGrGrCrCrCrArUrUrCrUrCrArGrUrUrC*mG*mC*mU	30767
RNACS 4835	hPKU4_R24_P10_sub7	mG*mG*mG*rUrCrGrUrArGrCrGrArArCrUrGrArGrArGrUrUrUrUrArGrAmGmCmUmAmGmAmAmAmUmAmGmCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmUmGmAmAmAmAmAmGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrGrCrUrGrCrCrArCrArArUrArCrCrUrCrGrGrGrCrCrCrUrUrCrUrCrArGrUrUrC*mG*mC*mU	30768
RNACS 4836	hPKU4_R24_P10_sub8	mG*mG*mG*rUrCrGrUrArGrCrGrArArCrUrGrArGrArGrUrUrUrUrArGrAmGmCmUmAmGmAmAmAmUmAmGmCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmUmGmAmAmAmAmAmGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrGrCrUrGrCrCrArCrArArUrArCrCrUrCrGrGrGrCrCrCrArUrUrCrUrCrArGrUrUrC*mG*mC*mU	30769
RNACS 4837	hPKU4_R22_P10_sub0	mG*mG*mG*rUrCrGrUrArGrCrGrArArCrUrGrArGrArGrUrUrUrUrArGrAmGmCmUmAmGmAmAmAmUmAmGmCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmUmGmAmAmAmAmAmGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrUrGrCrCrArCrArArUrArCrCrUrCrGrGrGrCrCrCrUrUrCrUrCrArGrUrUrC*mG*mC*mU	30770

RNACS 4838	hPKU4_R22_P10_sub1	mG*mG*mG*rUrCrGrUrArGrCrGrArArCrUrGrArGrArArGrUrUrUrUrArGrAmGmCmUmAmGmAmAmAmUmAmGmCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmUmGmAmAmAmAmAmGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrUrGrCrCrArCrArArUrArCrCrGrCrGrCrCrCrUrUrCrUrCrArGrUrUrC*mG*mC*mU	30771
RNACS 4839	hPKU4_R22_P10_sub4	mG*mG*mG*rUrCrGrUrArGrCrGrArArCrUrGrArGrArArGrUrUrUrUrArGrAmGmCmUmAmGmAmAmAmUmAmGmCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmUmGmAmAmAmAmAmGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrUrGrCrCrArCrArArUrArCrCrUrCrGrCrCrCrUrUrCrUrCrArGrUrUrC*mG*mC*mU	30772
RNACS 4840	hPKU4_R22_P10_sub5	mG*mG*mG*rUrCrGrUrArGrCrGrArArCrUrGrArGrArArGrUrUrUrUrArGrAmGmCmUmAmGmAmAmAmUmAmGmCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmUmGmAmAmAmAmAmGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrUrGrCrCrArCrArArUrArCrCrUrCrGrCrCrCrArUrUrCrUrCrArGrUrUrC*mG*mC*mU	30773
RNACS 4841	hPKU4_R22_P10_sub7	mG*mG*mG*rUrCrGrUrArGrCrGrArArCrUrGrArGrArArGrUrUrUrUrArGrAmGmCmUmAmGmAmAmAmUmAmGmCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmUmGmAmAmAmAmAmGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrUrGrCrCrArCrArArUrArCrCrGrCrGrCrCrCrUrUrCrUrCrArGrUrUrC*mG*mC*mU	30774
RNACS 4842	hPKU4_R22_P10_sub8	mG*mG*mG*rUrCrGrUrArGrCrGrArArCrUrGrArGrArArGrUrUrUrUrArGrAmGmCmUmAmGmAmAmAmUmAmGmCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmUmGmAmAmAmAmAmGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrUrGrCrCrArCrArArUrArCrCrGrCrGrCrCrCrArUrUrCrUrCrArGrUrUrC*mG*mC*mU	30775
RNACS 4843	hPKU4_R20_P10_sub0	mG*mG*mG*rUrCrGrUrArGrCrGrArArCrUrGrArGrArArGrUrUrUrUrArGrAmGmCmUmAmGmAmAmAmUmAmGmCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmUmGmAmAmAmAmAmGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrCrCrArCrArArUrArCrCrUrCrGrGrCrCrCrUrUrCrUrCrArGrUrUrC*mG*mC*mU	30776
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RNACS 4845	hPKU4_R20_P10_sub4	mG*mG*mG*rUrCrGrUrArGrCrGrArArCrUrGrArGrArArGrUrUrUrUrArGrAmGmCmUmAmGmAmAmAmUmAmGmCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmUmGmAmAmAmAmAmGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrCrCrArCrArArUrArCrCrUrCrGrCrCrCrUrUrCrUrCrArGrUrUrC*mG*mC*mU	30778

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RNACS 4847	hPKU4_R20_P10_sub7	mG*mG*mG*rUrCrGrUrArGrCrGrArArCrUrGrArGrArArGrUrUrUrUrArGrAmGmCmUmAmGmAmAmAmUmAmGmCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmUmGmAmAmAmAmAmGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrCrCrArCrArArUrArCrCrGrCrGrCrCrCrArUrUrCrUrCrArGrUrUrC*mG*mC*mU	30780
RNACS 4848	hPKU4_R20_P10_sub8	mG*mG*mG*rUrCrGrUrArGrCrGrArArCrUrGrArGrArArGrUrUrUrUrArGrAmGmCmUmAmGmAmAmAmUmAmGmCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmUmGmAmAmAmAmAmGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrCrCrArCrArArUrArCrCrGrCrGrCrCrCrArUrUrCrUrCrArGrUrUrC*mG*mC*mU	30781
RNACS 4849	hPKU4_R18_P10_sub0	mG*mG*mG*rUrCrGrUrArGrCrGrArArCrUrGrArGrArArGrUrUrUrUrArGrAmGmCmUmAmGmAmAmAmUmAmGmCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmUmGmAmAmAmAmAmGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrArCrArArUrArCrCrGrCrGrCrCrCrArUrUrCrUrCrArGrUrUrC*mG*mC*mU	30782
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RNACS 4851	hPKU4_R18_P10_sub4	mG*mG*mG*rUrCrGrUrArGrCrGrArArCrUrGrArGrArArGrUrUrUrUrArGrAmGmCmUmAmGmAmAmAmUmAmGmCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmUmGmAmAmAmAmAmGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrArCrArArUrArCrCrGrCrGrCrCrCrArUrUrCrUrCrArGrUrUrC*mG*mC*mU	30784
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RNACS 4855	hPKU4_R16_P10_sub0	mG*mG*mG*rUrCrGrUrArGrCrGrArArCrUrGrArGrArArGrUrUrUrUrArGrAmGmCmUmAmGmAmAmAmUmAmGmCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmUmGmAmAmAmAmAmGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmUmGmAmAmAmAmAmGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrCrCrArCrArArUrArCrCrUrCrGrCrCrCrArUrUrCrUrCrArGrUrUrC*mG*mC*mU	30788

RNACS 4856	hPKU4_R16_P10_sub1	mG*mG*mG*rUrCrGrUrArGrCrGrArArCrUrGrArGrArArGrUrUrUrUrArGrAmGmCmUmAmGmAmAmAmUmAmGmCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmUmGmAmAmAmAmAmGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrArArUrArCrCrGrCrGrGrCrCrCrUrUrCrUrCrArGrUrUrC*mG*mC*mU	30789
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RNACS 4865	hPKU4_R24_P9_sub7	mG*mG*mG*rUrCrGrUrArGrCrGrArArCrUrGrArGrArArGrUrUrUrUrArGrAmGmCmUmAmGmAmAmAmUmAmGmCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmUmGmAmAmAmAmAmGmUmGmGmC	30798

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RNACS4866	hPKU4_R24_P9_sub8	mG*mG*mG*rUrCrGrUrArGrCrGrArArCrUrGrArGrArArGrUrUrUrUrArGrAmGmCmUmAmGmAmAmAmUmAmGmCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmUmGmAmAmAmAmAmGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrGrCrUrGrCrCrArCrArArUrArCrCrGrCrGrCrCrCrArUrUrCrUrCrArGrUrU*mC*mG*mC	30799
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RNACS4873	hPKU4_R20_P9_sub0	mG*mG*mG*rUrCrGrUrArGrCrGrArArCrUrGrArGrArArGrUrUrUrUrArGrAmGmCmUmAmGmAmAmAmUmAmGmCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmUmGmAmAmAmAmAmGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrCrCrArCrArArUrArCrCrUrCrGrGrCrCrCrUrUrCrUrCrArGrUrU*mC*mG*mC	30806

RNACS 4874	hPKU4_R20_P9_sub1	mG*mG*mG*rUrCrGrUrArGrCrGrArArCrUrGrArGrArArGrUrUrUrUrArGrAmGmCmUmAmGmAmAmAmUmAmGmCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmUmGmAmAmAmAmAmGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrCrCrArCrArArUrArCrCrUrGrCrCrCrCrUrUrCrUrCrArGrUrU*mC*mG*mC	30807
RNACS 4875	hPKU4_R20_P9_sub4	mG*mG*mG*rUrCrGrUrArGrCrGrArArCrUrGrArGrArArGrUrUrUrUrArGrAmGmCmUmAmGmAmAmAmUmAmGmCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmUmGmAmAmAmAmAmGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrCrCrArCrArArUrArCrCrUrGrCrCrCrCrUrUrCrUrCrArGrUrU*mC*mG*mC	30808
RNACS 4876	hPKU4_R20_P9_sub5	mG*mG*mG*rUrCrGrUrArGrCrGrArArCrUrGrArGrArArGrUrUrUrUrArGrAmGmCmUmAmGmAmAmAmUmAmGmCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmUmGmAmAmAmAmAmGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrCrCrArCrArArUrArCrCrUrGrCrCrCrCrUrUrCrUrCrArGrUrU*mC*mG*mC	30809
RNACS 4877	hPKU4_R20_P9_sub7	mG*mG*mG*rUrCrGrUrArGrCrGrArArCrUrGrArGrArArGrUrUrUrUrArGrAmGmCmUmAmGmAmAmAmUmAmGmCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmUmGmAmAmAmAmAmGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrCrCrArCrArArUrArCrCrUrGrCrCrCrCrUrUrCrUrCrArGrUrU*mC*mG*mC	30810
RNACS 4878	hPKU4_R20_P9_sub8	mG*mG*mG*rUrCrGrUrArGrCrGrArArCrUrGrArGrArArGrUrUrUrUrArGrAmGmCmUmAmGmAmAmAmUmAmGmCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmUmGmAmAmAmAmAmGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrCrCrArCrArArUrArCrCrUrGrCrCrCrCrUrUrCrUrCrArGrUrU*mC*mG*mC	30811
RNACS 4879	hPKU4_R18_P9_sub0	mG*mG*mG*rUrCrGrUrArGrCrGrArArCrUrGrArGrArArGrUrUrUrUrArGrAmGmCmUmAmGmAmAmAmUmAmGmCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmUmGmAmAmAmAmAmGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrCrCrArCrArArUrArCrCrUrGrCrCrCrCrUrUrCrUrCrArGrUrU*mC*mG*mC	30812
RNACS 4880	hPKU4_R18_P9_sub1	mG*mG*mG*rUrCrGrUrArGrCrGrArArCrUrGrArGrArArGrUrUrUrUrArGrAmGmCmUmAmGmAmAmAmUmAmGmCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmUmGmAmAmAmAmAmGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrCrCrArCrArArUrArCrCrUrGrCrCrCrCrUrUrCrUrCrArGrUrU*mC*mG*mC	30813
RNACS 4881	hPKU4_R18_P9_sub4	mG*mG*mG*rUrCrGrUrArGrCrGrArArCrUrGrArGrArArGrUrUrUrUrArGrAmGmCmUmAmGmAmAmAmUmAmGmCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmUmGmAmAmAmAmAmGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrCrCrArCrArArUrArCrCrUrGrCrCrCrCrUrUrCrUrCrArGrUrU*mC*mG*mC	30814
RNACS 4882	hPKU4_R18_P9_sub5	mG*mG*mG*rUrCrGrUrArGrCrGrArArCrUrGrArGrArArGrUrUrUrUrArGrAmGmCmUmAmGmAmAmAmUmAmGmCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmUmGmAmAmAmAmAmGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrCrCrArCrArArUrArCrCrUrGrCrCrCrCrUrUrCrUrCrArGrUrU*mC*mG*mC	30815

RNACS 4883	hPKU4_R18_P9_sub7	mG*mG*mG*rUrCrGrUrArGrCrGrArArCrUrGrArGrArArGrUrUrUrUrArGrAmGmCmUmAmGmAmAmAmUmAmGmCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmUmGmAmAmAmAmAmGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrArCrArUrArCrCrGrCrGrCrCrCrCrUrUrCrUrCrArGrUrU*mC*mG*mC	30816
RNACS 4884	hPKU4_R18_P9_sub8	mG*mG*mG*rUrCrGrUrArGrCrGrArArCrUrGrArGrArArGrUrUrUrUrArGrAmGmCmUmAmGmAmAmAmUmAmGmCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmUmGmAmAmAmAmAmGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrArCrArUrArCrCrGrCrGrCrCrCrCrArUrUrCrUrCrArGrUrU*mC*mG*mC	30817
RNACS 4885	hPKU4_R16_P9_sub0	mG*mG*mG*rUrCrGrUrArGrCrGrArArCrUrGrArGrArArGrUrUrUrUrArGrAmGmCmUmAmGmAmAmAmUmAmGmCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmUmGmAmAmAmAmAmGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrArArUrArCrCrUrCrGrGrCrCrCrCrUrUrCrUrCrArGrUrU*mC*mG*mC	30818
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RNACS 4888	hPKU4_R16_P9_sub5	mG*mG*mG*rUrCrGrUrArGrCrGrArArCrUrGrArGrArArGrUrUrUrUrArGrAmGmCmUmAmGmAmAmAmUmAmGmCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmUmGmAmAmAmAmAmGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrArArUrArCrCrUrCrGrGrCrCrCrArUrUrCrUrCrArGrUrU*mC*mG*mC	30821
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RNACS 4893	hPKU4_R24_P8_sub4	mG*mG*mG*rUrCrGrUrArGrCrGrArArCrUrGrArGrArArGrUrUrUrUrArGrAmGmCmUmAmGmAmAmAmUmAmGmCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmUmGmAmAmAmAmAmGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrGrCrUrGrCrCrArCrArArUrArCrCrUrCrGrCrCrCrCrUrUrCrUrCrArGrU*mU*mC*mG	30826
RNACS 4894	hPKU4_R24_P8_sub5	mG*mG*mG*rUrCrGrUrArGrCrGrArArCrUrGrArGrArArGrUrUrUrUrArGrAmGmCmUmAmGmAmAmAmUmAmGmCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmUmGmAmAmAmAmAmGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrGrCrUrGrCrCrArCrArArUrArCrCrUrCrGrCrCrCrCrArUrUrCrUrCrArGrU*mU*mC*mG	30827
RNACS 4895	hPKU4_R24_P8_sub7	mG*mG*mG*rUrCrGrUrArGrCrGrArArCrUrGrArGrArArGrUrUrUrUrArGrAmGmCmUmAmGmAmAmAmUmAmGmCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmUmGmAmAmAmAmAmGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrGrCrUrGrCrCrArCrArArUrArCrCrGrCrGrCrCrCrUrUrCrUrCrArGrU*mU*mC*mG	30828
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RNACS 4897	hPKU4_R22_P8_sub0	mG*mG*mG*rUrCrGrUrArGrCrGrArArCrUrGrArGrArArGrUrUrUrUrArGrAmGmCmUmAmGmAmAmAmUmAmGmCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmUmGmAmAmAmAmAmGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrUrGrCrCrArCrArArUrArCrCrUrCrGrCrCrCrArUrUrCrUrCrArGrU*mU*mC*mG	30830
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RNACS 4900	hPKU4_R22_P8_sub5	mG*mG*mG*rUrCrGrUrArGrCrGrArArCrUrGrArGrArArGrUrUrUrUrArGrAmGmCmUmAmGmAmAmAmUmAmGmCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmUmGmAmAmAmAmAmGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrUrGrCrCrArCrArArUrArCrCrGrCrCrCrCrArUrUrCrUrCrArGrU*mU*mC*mG	30833

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RNACS 4902	hPKU4_R22_P8_sub8	mG*mG*mG*rUrCrGrUrArGrCrGrArArCrUrGrArGrArArGrUrUrUrUrArGrAmGmCmUmAmGmAmAmAmUmAmGmCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmUmGmAmAmAmAmAmGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrUrGrCrCrArCrArArUrArCrCrGrCrGrCrCrCrArUrUrCrUrCrArGrU*mU*mC*mG	30835
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RNACS 4911	hPKU4_R18_P8_sub4	mG*mG*mG*rUrCrGrUrArGrCrGrArArCrUrGrArGrArArGrUrUrUrUrArGrAmGmCmUmAmGmAmAmAmUmAmGmCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmUmGmAmAmAmAmAmGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrArCrArArUrArCrCrUrCrGrCrCrCrCrUrUrCrUrCrArGrU*mU*mC*mG	30844
RNACS 4912	hPKU4_R18_P8_sub5	mG*mG*mG*rUrCrGrUrArGrCrGrArArCrUrGrArGrArArGrUrUrUrUrArGrAmGmCmUmAmGmAmAmAmUmAmGmCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmUmGmAmAmAmAmAmGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrArCrArArUrArCrCrUrCrGrCrCrCrCrArUrUrCrUrCrArGrU*mU*mC*mG	30845
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RNACS 4917	hPKU4_R16_P8_sub4	mG*mG*mG*rUrCrGrUrArGrCrGrArArCrUrGrArGrArArGrUrUrUrUrArGrAmGmCmUmAmGmAmAmAmUmAmGmCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmUmGmAmAmAmAmAmGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrArArUrArCrCrGrCrGrCrCrCrUrUrCrUrCrArGrU*mU*mC*mG	30850
RNACS 4918	hPKU4_R16_P8_sub5	mG*mG*mG*rUrCrGrUrArGrCrGrArArCrUrGrArGrArArGrUrUrUrUrArGrAmGmCmUmAmGmAmAmAmUmAmGmCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmUmGmAmAmAmAmAmGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrArArUrArCrCrGrCrGrCrCrCrArUrUrCrUrCrArGrU*mU*mC*mG	30851
RNACS 4919	hPKU4_R16_P8_sub7	mG*mG*mG*rUrCrGrUrArGrCrGrArArCrUrGrArGrArArGrUrUrUrUrArGrAmGmCmUmAmGmAmAmAmUmAmGmCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmUmGmAmAmAmAmAmGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrArArUrArCrCrGrCrGrCrCrCrCrUrUrCrUrCrArGrU*mU*mC*mG	30852
RNACS 4920	hPKU4_R16_P8_sub8	mG*mG*mG*rUrCrGrUrArGrCrGrArArCrUrGrArGrArArGrUrUrUrUrArGrAmGmCmUmAmGmAmAmAmUmAmGmCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmUmGmAmAmAmAmAmGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrArCrArArUrArCrCrGrCrGrCrCrCrArUrUrCrUrCrArGrU*mU*mC*mG	30853
RNACS 4923	hPKU5_R20_P10_sub0	mU*mA*mG*rCrGrArArCrUrGrArGrArArGrGrGrCrCrArGrUrUrUrUrArGrAmGmCmUmAmGmAmAmAmAmUmAmGmCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmUmGmAmAmAmAmAmGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrUrUrGrCrUrGrCrCrArCrArArUrArCrCrUrCrGrGrCrCrCrUrUrCrU*mC*mA*mG	30854

RNACS 4924	hPKU5_R20_P10_sub1	mU*mA*mG*rCrGrArArCrUrGrArGrArArGrGrGrCrCrArGrUrUrUrUrArGrAmGmCmUmAmGmAmAmAmUmAmGmCrA rArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmUmGmAmAmAmAmAmGmUmGmGmC mAmCmCmGmAmGmUmCmGmGmUmGmCrUrUrGrCrUrGrCrCrArCrArArUrArCrCrGrCrGrGrCrCrCrUrUrCrU*mC*mA *mG	30855
RNACS 4925	hPKU5_R20_P10_sub2	mU*mA*mG*rCrGrArArCrUrGrArGrArArGrGrGrCrCrArGrUrUrUrUrArGrAmGmCmUmAmGmAmAmAmUmAmGmCrA rArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmUmGmAmAmAmAmAmGmUmGmGmC mAmCmCmGmAmGmUmCmGmGmUmGmCrUrUrGrCrUrGrCrCrArCrArArUrCrCrCrUrCrGrGrCrCrCrUrUrCrU*mC*mA *mG	30856
RNACS 4926	hPKU5_R20_P10_sub3	mU*mA*mG*rCrGrArArCrUrGrArGrArArGrGrGrCrCrArGrUrUrUrUrArGrAmGmCmUmAmGmAmAmAmUmAmGmCrA rArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmUmGmAmAmAmAmAmGmUmGmGmC mAmCmCmGmAmGmUmCmGmGmUmGmCrUrUrGrCrUrGrCrCrArCrArArUrCrCrCrGrCrGrGrCrCrCrUrUrCrU*mC*mA *mG	30857
RNACS 4927	hPKU5_R20_P10_sub4	mU*mA*mG*rCrGrArArCrUrGrArGrArArGrGrGrCrCrArGrUrUrUrUrArGrAmGmCmUmAmGmAmAmAmUmAmGmCrA rArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmUmGmAmAmAmAmAmGmUmGmGmC mAmCmCmGmAmGmUmCmGmGmUmGmCrUrUrGrCrUrGrCrCrArCrArArUrArCrCrUrCrGrCrCrCrUrUrCrU*mC*mA *mG	30858
RNACS 4928	hPKU5_R20_P10_sub7	mU*mA*mG*rCrGrArArCrUrGrArGrArArGrGrGrCrCrArGrUrUrUrUrArGrAmGmCmUmAmGmAmAmAmUmAmGmCrA rArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmUmGmAmAmAmAmAmGmUmGmGmC mAmCmCmGmAmGmUmCmGmGmUmGmCrUrUrGrCrUrGrCrCrArCrGrArUrArCrCrUrCrGrGrCrCrCrUrUrCrU*mC*mA *mG	30859
RNACS 4929	hPKU5_R18_P10_sub0	mU*mA*mG*rCrGrArArCrUrGrArGrArArGrGrGrCrCrArGrUrUrUrUrArGrAmGmCmUmAmGmAmAmAmUmAmGmCrA rArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmUmGmAmAmAmAmAmGmUmGmGmC mAmCmCmGmAmGmUmCmGmGmUmGmCrGrCrUrGrCrCrArCrArArUrArCrCrUrCrGrCrCrCrUrUrCrU*mC*mA*mG	30860
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RNACS 4934	hPKU5_R18_P10_sub7	mU*mA*mG*rCrGrArArCrUrGrArGrArArGrGrGrCrCrArGrUrUrUrUrArGrAmGmCmUmAmGmAmAmAmUmAmGmCrA rArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmUmGmAmAmAmAmAmGmUmGmGmC mAmCmCmGmAmGmUmCmGmGmUmGmCrGrCrUrGrCrCrArCrGrArUrArCrCrUrCrGrCrCrCrCrUrUrCrU*mC*mA*mG	30865
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RNACS4963	hPKU5_R18_P9_sub4	mU*mA*mG*rCrGrArArCrUrGrArGrArArGrGrGrCrCrArGrUrUrUrUrArGrAmGmCmUmAmGmAmAmAmUmAmGmCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmUmGmAmAmAmAmAmGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrUrUrGrCrUrGrCrCrArCrArArUrCrCrCrGrCrGrGrCrCrCrUrUrC*mU*mC*mA	30894

RNACS 4964	hPKU5_R18_P9_sub7	mU*mA*mG*rCrGrArArCrUrGrArGrArArGrGrGrCrCrArGrUrUrUrUrArGrAmGmCmUmAmGmAmAmAmUmAmGmCrA rArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmUmGmAmAmAmAmAmGmUmGmGmC mAmCmCmGmAmGmUmCmGmGmUmGmCrGrCrUrGrCrCrArCrGrArUrArCrCrUrCrGrGrCrCrCrUrUrC*mU*mC*mA	30895
RNACS 4965	hPKU5_R16_P9_sub0	mU*mA*mG*rCrGrArArCrUrGrArGrArArGrGrGrCrCrArGrUrUrUrUrArGrAmGmCmUmAmGmAmAmAmUmAmGmCrA rArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmUmGmAmAmAmAmAmGmUmGmGmC mAmCmCmGmAmGmUmCmGmGmUmGmCrUrGrCrCrArCrArArUrArCrCrUrCrGrGrCrCrCrUrUrC*mU*mC*mA	30896
RNACS 4966	hPKU5_R16_P9_sub1	mU*mA*mG*rCrGrArArCrUrGrArGrArArGrGrGrCrCrArGrUrUrUrUrArGrAmGmCmUmAmGmAmAmAmUmAmGmCrA rArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmUmGmAmAmAmAmAmGmUmGmGmC mAmCmCmGmAmGmUmCmGmGmUmGmCrUrGrCrCrArCrArArUrArCrCrGrCrGrGrCrCrCrUrUrC*mU*mC*mA	30897
RNACS 4967	hPKU5_R16_P9_sub2	mU*mA*mG*rCrGrArArCrUrGrArGrArArGrGrGrCrCrArGrUrUrUrUrArGrAmGmCmUmAmGmAmAmAmUmAmGmCrA rArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmUmGmAmAmAmAmAmGmUmGmGmC mAmCmCmGmAmGmUmCmGmGmUmGmCrUrGrCrCrArCrArArUrCrCrCrUrCrGrGrCrCrCrUrUrC*mU*mC*mA	30898
RNACS 4968	hPKU5_R16_P9_sub3	mU*mA*mG*rCrGrArArCrUrGrArGrArArGrGrGrCrCrArGrUrUrUrUrArGrAmGmCmUmAmGmAmAmAmUmAmGmCrA rArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmUmGmAmAmAmAmAmGmUmGmGmC mAmCmCmGmAmGmUmCmGmGmUmGmCrUrGrCrCrArCrArArUrCrCrGrCrGrGrCrCrCrUrUrC*mU*mC*mA	30899
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RNACS 4970	hPKU5_R16_P9_sub7	mU*mA*mG*rCrGrArArCrUrGrArGrArArGrGrGrCrCrArGrUrUrUrUrArGrAmGmCmUmAmGmAmAmAmUmAmGmCrA rArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmUmGmAmAmAmAmAmGmUmGmGmC mAmCmCmGmAmGmUmCmGmGmUmGmCrUrGrCrCrArCrGrArUrArCrCrUrCrGrGrCrCrCrUrUrC*mU*mC*mA	30901
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RNACS 4976	hPKU5_R14_P9_sub7	mU*mA*mG*rCrGrArArCrUrGrArGrArArGrGrGrCrCrArGrUrUrUrUrArGrAmGmCmUmAmGmAmAmAmUmAmGmCrA rArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmUmGmAmAmAmAmAmGmUmGmGmC mAmCmCmGmAmGmUmCmGmGmUmGmCrCrCrArCrGrArUrArCrCrUrCrGrGrCrCrCrUrUrC*mU*mC*mA	30907
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RNACS 5006	hPKU5_R14_P8_sub7	mU*mA*mG*rCrGrArArCrUrGrArGrArArGrGrGrCrCrArGrUrUrUrUrArGrAmGmCmUmAmGmAmAmAmUmAmGmCrA rArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmUmGmAmAmAmAmAmGmUmGmGmC mAmCmCmGmAmGmUmCmGmGmUmGmCrCrCrArCrGrArUrArCrCrUrCrGrGrCrCrCrUrU*mC*mU*mC	30937
RNACS 5007	hPKU5_R12_P8_sub0	mU*mA*mG*rCrGrArArCrUrGrArGrArArGrGrGrCrCrArGrUrUrUrUrArGrAmGmCmUmAmGmAmAmAmUmAmGmCrA rArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmUmGmAmAmAmAmAmGmUmGmGmC mAmCmCmGmAmGmUmCmGmGmUmGmCrArCrArArUrArCrCrUrCrGrGrCrCrCrUrU*mC*mU*mC	30938

RNACS 5008	hPKU5_R12_P8_sub1	mU*mA*mG*rCrGrArArCrUrGrArGrArArGrGrGrCrCrArGrUrUrUrUrArGrAmGmCmUmAmGmAmAmAmUmAmGmCrA rArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmUmGmAmAmAmAmAmGmUmGmGmC mAmCmCmGmAmGmUmCmGmGmUmGmCrArCrArArUrArCrCrGrCrGrGrCrCrCrUrU*mC*mU*mC	30939
RNACS 5009	hPKU5_R12_P8_sub2	mU*mA*mG*rCrGrArArCrUrGrArGrArArGrGrGrCrCrArGrUrUrUrUrArGrAmGmCmUmAmGmAmAmAmUmAmGmCrA rArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmUmGmAmAmAmAmAmGmUmGmGmC mAmCmCmGmAmGmUmCmGmGmUmGmCrArCrArArUrCrCrCrUrCrGrGrCrCrCrUrU*mC*mU*mC	30940
RNACS 5010	hPKU5_R12_P8_sub3	mU*mA*mG*rCrGrArArCrUrGrArGrArArGrGrGrCrCrArGrUrUrUrUrArGrAmGmCmUmAmGmAmAmAmUmAmGmCrA rArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmUmGmAmAmAmAmAmGmUmGmGmC mAmCmCmGmAmGmUmCmGmGmUmGmCrArCrArArUrCrCrCrGrCrGrGrCrCrCrUrU*mC*mU*mC	30941
RNACS 5011	hPKU5_R12_P8_sub4	mU*mA*mG*rCrGrArArCrUrGrArGrArArGrGrGrCrCrArGrUrUrUrUrArGrAmGmCmUmAmGmAmAmAmUmAmGmCrA rArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmUmGmAmAmAmAmAmGmUmGmGmC mAmCmCmGmAmGmUmCmGmGmUmGmCrArCrArArUrArCrCrUrCrGrCrCrCrUrU*mC*mU*mC	30942
RNACS 5012	hPKU5_R12_P8_sub7	mU*mA*mG*rCrGrArArCrUrGrArGrArArGrGrGrCrCrArGrUrUrUrUrArGrAmGmCmUmAmGmAmAmAmUmAmGmCrA rArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmUmGmAmAmAmAmAmGmUmGmGmC mAmCmCmGmAmGmUmCmGmGmUmGmCrArCrGrArUrArCrCrUrCrGrGrCrCrCrUrU*mC*mU*mC	30943
RNACS 5013	hPKU6_R20_P11_sub0	mA*mC*mU*rUrUrGrCrUrGrCrCrArCrArArUrArCrCrUrGrUrUrUrUrArGrAmGmCmUmAmGmAmAmAmUmAmGmCrA rArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmUmGmAmAmAmAmAmGmUmGmGmC mAmCmCmGmAmGmUmCmGmGmUmGmCrCrGrArArCrUrGrArGrGrArArGrGrCrCrGrGrUrArUrUrGrUrGrG*mC* mA*mG	30944
RNACS 5014	hPKU6_R20_P11_sub1	mA*mC*mU*rUrUrGrCrUrGrCrCrArCrArArUrArCrCrUrGrUrUrUrUrArGrAmGmCmUmAmGmAmAmAmUmAmGmCrA rArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmUmGmAmAmAmAmAmGmUmGmGmC mAmCmCmGmAmGmUmCmGmGmUmGmCrCrGrArArCrUrGrArGrGrArArGrGrCrCrGrGrUrArUrUrGrUrGrG*mC *mA*mG	30945
RNACS 5015	hPKU6_R20_P11_sub4	mA*mC*mU*rUrUrGrCrUrGrCrCrArCrArArUrArCrCrUrGrUrUrUrUrArGrAmGmCmUmAmGmAmAmAmUmAmGmCrA rArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmUmGmAmAmAmAmAmGmUmGmGmC mAmCmCmGmAmGmUmCmGmGmUmGmCrCrGrArArCrUrGrArGrArArCrGrGrCrCrGrGrGrUrArUrUrGrUrGrG*mC* mA*mG	30946
RNACS 5016	hPKU6_R20_P11_sub5	mA*mC*mU*rUrUrGrCrUrGrCrCrArCrArArUrArCrCrUrGrUrUrUrUrArGrAmGmCmUmAmGmAmAmAmUmAmGmCrA rArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmUmGmAmAmAmAmAmGmUmGmGmC mAmCmCmGmAmGmUmCmGmGmUmGmCrCrGrArArCrUrGrArGrArArCrGrGrArCrGrGrGrGrUrArUrUrGrUrGrG*mC* mA*mG	30947
RNACS 5017	hPKU6_R20_P11_sub6	mA*mC*mU*rUrUrGrCrUrGrCrCrArCrArArUrArCrCrUrGrUrUrUrUrArGrAmGmCmUmAmGmAmAmAmUmAmGmCrA rArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmUmGmAmAmAmAmAmGmUmGmGmC	30948

		mAmCmCmGmAmGmUmCmGmGmUmGmCrCrGrArArCrUrGrArGrArArGrGrGrCrCrGrCrGrGrUrArUrUrGrUrGrG*mC*mA*mG	
RNACS5018	hPKU6_R20_P11_sub7	mA*mC*mU*rUrUrGrCrUrGrCrCrArCrArArUrArCrCrUrGrUrUrUrUrArGrAmGmCmUmAmGmAmAmAmUmAmGmCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmUmGmAmAmAmAmAmGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrCrGrArArCrUrGrArGrArArGrGrGrArCrGrCrGrGrUrArUrUrGrUrGrG*mC*mA*mG	30949
RNACS5019	hPKU6_R18_P11_sub0	mA*mC*mU*rUrUrGrCrUrGrCrCrArCrArArUrArCrCrUrGrUrUrUrUrArGrAmGmCmUmAmGmAmAmAmUmAmGmCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmUmGmAmAmAmAmAmGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrArArCrUrGrArGrArArGrGrGrCrCrGrArGrGrUrArUrUrGrUrGrG*mC*mA*mG	30950
RNACS5020	hPKU6_R18_P11_sub1	mA*mC*mU*rUrUrGrCrUrGrCrCrArCrArArUrArCrCrUrGrUrUrUrUrArGrAmGmCmUmAmGmAmAmAmUmAmGmCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmUmGmAmAmAmAmAmGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrArArCrUrGrArGrArArGrGrGrCrCrGrGrGrUrArUrUrGrUrGrG*mC*mA*mG	30951
RNACS5021	hPKU6_R18_P11_sub4	mA*mC*mU*rUrUrGrCrUrGrCrCrArCrArArUrArCrCrUrGrUrUrUrUrArGrAmGmCmUmAmGmAmAmAmUmAmGmCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmUmGmAmAmAmAmAmGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrArArCrUrGrArGrArArCrGrGrCrCrGrGrGrUrArUrUrGrUrGrG*mC*mA*mG	30952
RNACS5022	hPKU6_R18_P11_sub5	mA*mC*mU*rUrUrGrCrUrGrCrCrArCrArArUrArCrCrUrGrUrUrUrUrArGrAmGmCmUmAmGmAmAmAmUmAmGmCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmUmGmAmAmAmAmAmGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrArArCrUrGrArGrArArCrGrGrArCrGrGrGrUrArUrUrGrUrGrG*mC*mA*mG	30953
RNACS5023	hPKU6_R18_P11_sub6	mA*mC*mU*rUrUrGrCrUrGrCrCrArCrArArUrArCrCrUrGrUrUrUrUrArGrAmGmCmUmAmGmAmAmAmUmAmGmCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmUmGmAmAmAmAmAmGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrArArCrUrGrArGrArArCrGrGrArCrGrCrGrUrArUrUrGrUrGrG*mC*mA*mG	30954
RNACS5024	hPKU6_R18_P11_sub7	mA*mC*mU*rUrUrGrCrUrGrCrCrArCrArArUrArCrCrUrGrUrUrUrUrArGrAmGmCmUmAmGmAmAmAmUmAmGmCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmUmGmAmAmAmAmAmGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrArArCrUrGrArGrArArCrGrGrArCrGrCrGrUrArUrUrGrUrGrG*mC*mA*mG	30955
RNACS5025	hPKU6_R16_P11_sub0	mA*mC*mU*rUrUrGrCrUrGrCrCrArCrArArUrArCrCrUrGrUrUrUrUrArGrAmGmCmUmAmGmAmAmAmUmAmGmCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmUmGmAmAmAmAmAmGmUmGmGmCmAmCmCmGmAmGmUmCrCrUrGrArGrGrArArGrGrGrCrCrGrArGrGrUrArUrUrGrUrGrG*mC*mA*mG	30956

RNACS 5026	hPKU6_R16_P11_sub1	mA*mC*mU*rUrUrGrCrUrGrCrCrArCrArArUrArCrCrUrGrUrUrUrUrArGrAmGmCmUmAmGmAmAmAmUmAmGmCrA rArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmUmGmAmAmAmAmAmGmUmGmGmC mAmCmCmGmAmGmUmCmGmGmUmGmCrCrUrGrArGrArArGrGrGrCrCrGrGrGrGrUrArUrUrGrUrGrG*mC*mA*mG	30957
RNACS 5027	hPKU6_R16_P11_sub4	mA*mC*mU*rUrUrGrCrUrGrCrCrArCrArArUrArCrCrUrGrUrUrUrUrArGrAmGmCmUmAmGmAmAmAmUmAmGmCrA rArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmUmGmAmAmAmAmAmGmUmGmGmC mAmCmCmGmAmGmUmCmGmGmUmGmCrCrUrGrArGrArArCrGrGrCrCrGrGrGrGrUrArUrUrGrUrGrG*mC*mA*mG	30958
RNACS 5028	hPKU6_R16_P11_sub5	mA*mC*mU*rUrUrGrCrUrGrCrCrArCrArArUrArCrCrUrGrUrUrUrUrArGrAmGmCmUmAmGmAmAmAmUmAmGmCrA rArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmUmGmAmAmAmAmAmGmUmGmGmC mAmCmCmGmAmGmUmCmGmGmUmGmCrCrUrGrArGrArArCrGrGrArCrGrGrGrGrUrArUrUrGrUrGrG*mC*mA*mG	30959
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RNACS 5030	hPKU6_R16_P11_sub7	mA*mC*mU*rUrUrGrCrUrGrCrCrArCrArArUrArCrCrUrGrUrUrUrUrArGrAmGmCmUmAmGmAmAmAmUmAmGmCrA rArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmUmGmAmAmAmAmAmGmUmGmGmC mAmCmCmGmAmGmUmCmGmGmUmGmCrCrUrGrArGrArArGrGrGrArCrCrGrCrGrGrGrUrArUrUrGrUrGrG*mC*mA*mG	30961
RNACS 5031	hPKU6_R14_P11_sub0	mA*mC*mU*rUrUrGrCrUrGrCrCrArCrArArUrArCrCrUrGrUrUrUrUrArGrAmGmCmUmAmGmAmAmAmUmAmGmCrA rArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmUmGmAmAmAmAmAmGmUmGmGmC mAmCmCmGmAmGmUmCmGmGmUmGmCrGrArGrArArGrGrGrCrCrGrArGrGrUrArUrUrGrUrGrG*mC*mA*mG	30962
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RNACS 5047	hPKU6_R20_P10_sub6	mA*mC*mU*rUrUrGrCrUrGrCrCrArCrArArUrArCrCrUrGrUrUrUrUrArGrAmGmCmUmAmGmAmAmAmUmAmGmCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmUmGmAmAmAmAmAmGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrCrGrArArCrUrGrArGrArArGrGrGrCrCrGrCrGrUrArUrUrGrUrG*mG*mC*mA	30978
RNACS 5048	hPKU6_R20_P10_sub7	mA*mC*mU*rUrUrGrCrUrGrCrCrArCrArArUrArCrCrUrGrUrUrUrUrArGrAmGmCmUmAmGmAmAmAmUmAmGmCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmUmGmAmAmAmAmAmGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrCrGrArArCrUrGrArGrArArGrGrGrArCrGrCrGrGrUrArUrUrGrUrG*mG*mC*mA	30979
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RNACS 5050	hPKU6_R18_P10_sub1	mA*mC*mU*rUrUrGrCrUrGrCrCrArCrArArUrArCrCrUrGrUrUrUrUrArGrAmGmCmUmAmGmAmAmAmUmAmGmCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmUmGmAmAmAmAmAmGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrArArCrUrGrArGrArArGrGrGrCrCrGrCrGrArGrGrUrArUrUrGrUrG*mG*mC*mA	30981
RNACS 5051	hPKU6_R18_P10_sub4	mA*mC*mU*rUrUrGrCrUrGrCrCrArCrArArUrArCrCrUrGrUrUrUrUrArGrAmGmCmUmAmGmAmAmAmUmAmGmCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmUmGmAmAmAmAmAmGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrArArCrUrGrArGrArArGrGrArCrCrGrCrGrArGrGrUrArUrUrGrUrG*mG*mC*mA	30982
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RNACS 5053	hPKU6_R18_P10_sub6	mA*mC*mU*rUrUrGrCrUrGrCrCrArCrArArUrArCrCrUrGrUrUrUrUrArGrAmGmCmUmAmGmAmAmAmUmAmGmCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmUmGmAmAmAmAmAmGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrArArCrUrGrArGrArArGrGrArCrCrGrCrGrArGrGrUrArUrUrGrUrG*mG*mC*mA	30984
RNACS 5054	hPKU6_R18_P10_sub7	mA*mC*mU*rUrUrGrCrUrGrCrCrArCrArArUrArCrCrUrGrUrUrUrUrArGrAmGmCmUmAmGmAmAmAmUmAmGmCrArArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmUmGmAmAmAmAmAmGmUmGmGmCmAmCmCmGmAmGmUmCmGmGmUmGmCrArArCrUrGrArGrArArGrGrGrArCrCrGrCrGrArGrGrUrArUrUrGrUrG*mG*mC*mA	30985

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RNACS 5056	hPKU6_R16_P10_sub1	mA*mC*mU*rUrUrGrCrUrGrCrCrArCrArArUrArCrCrUrGrUrUrUrUrArGrAmGmCmUmAmGmAmAmAmUmAmGmCrA rArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmUmGmAmAmAmAmAmGmUmGmGmC mAmCmCmGmAmGmUmCmGmGmUmGmCrCrUrGrArGrArArGrGrGrCrCrGrArGrGrUrArUrUrGrUrG*mG*mC*mA	30987
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RNACS 5075	hPKU6_R20_P9_sub4	mA*mC*mU*rUrUrGrCrUrGrCrCrArCrArArUrArCrCrUrGrUrUrUrUrArGrAmGmCmUmAmGmAmAmAmUmAmGmCrA rArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmUmGmAmAmAmAmAmGmUmGmGmC mAmCmCmGmAmGmUmCmGmGmUmGmCrCrGrArArCrUrGrArGrArArCrGrGrCrCrGrGrGrGrUrArUrUrGrU*mG*mG *mC	31006

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RNACS 5093	hPKU6_R14_P9_sub4	mA*mC*mU*rUrUrGrCrUrGrCrCrArCrArArUrArCrCrUrGrUrUrUrUrArGrAmGmCmUmAmGmAmAmAmUmAmGmCrA rArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmUmGmAmAmAmAmAmGmUmGmGmC mAmCmCmGmAmGmUmCmGmGmUmGmCrGrArGrArArCrGrGrCrCrGrArGrGrUrArUrUrGrU*mG*mG*mC	31024
RNACS 5094	hPKU6_R14_P9_sub5	mA*mC*mU*rUrUrGrCrUrGrCrCrArCrArArUrArCrCrUrGrUrUrUrUrArGrAmGmCmUmAmGmAmAmAmUmAmGmCrA rArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmUmGmAmAmAmAmAmGmUmGmGmC mAmCmCmGmAmGmUmCmGmGmUmGmCrGrArGrArArCrGrGrArCrGrArGrGrUrArUrUrGrU*mG*mG*mC	31025
RNACS 5095	hPKU6_R14_P9_sub6	mA*mC*mU*rUrUrGrCrUrGrCrCrArCrArArUrArCrCrUrGrUrUrUrUrArGrAmGmCmUmAmGmAmAmAmUmAmGmCrA rArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmUmGmAmAmAmAmAmGmUmGmGmC mAmCmCmGmAmGmUmCmGmGmUmGmCrGrArGrArArGrGrGrCrCrGrCrGrGrUrArUrUrGrU*mG*mG*mC	31026
RNACS 5096	hPKU6_R14_P9_sub7	mA*mC*mU*rUrUrGrCrUrGrCrCrArCrArArUrArCrCrUrGrUrUrUrUrArGrAmGmCmUmAmGmAmAmAmUmAmGmCrA rArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmUmGmAmAmAmAmAmGmUmGmGmC mAmCmCmGmAmGmUmCmGmGmUmGmCrGrArGrArArGrGrGrArCrGrCrGrGrUrArUrUrGrU*mG*mG*mC	31027

RNACS 5097	hPKU6_R12_P9_sub0	mA*mC*mU*rUrUrGrCrUrGrCrCrArCrArArUrArCrCrUrGrUrUrUrUrArGrAmGmCmUmAmGmAmAmAmUmAmGmCrA rArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmUmGmAmAmAmAmAmGmUmGmGmC mAmCmCmGmAmGmUmCmGmGmUmGmCrGrArArGrGrGrCrCrGrArGrGrUrArUrUrGrU*mG*mG*mC	31028
RNACS 5098	hPKU6_R12_P9_sub1	mA*mC*mU*rUrUrGrCrUrGrCrCrArCrArArUrArCrCrUrGrUrUrUrUrArGrAmGmCmUmAmGmAmAmAmUmAmGmCrA rArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmUmGmAmAmAmAmAmGmUmGmGmC mAmCmCmGmAmGmUmCmGmGmUmGmCrGrArArGrGrGrCrCrGrArGrGrUrArUrUrGrU*mG*mG*mC	31029
RNACS 5099	hPKU6_R12_P9_sub4	mA*mC*mU*rUrUrGrCrUrGrCrCrArCrArArUrArCrCrUrGrUrUrUrUrArGrAmGmCmUmAmGmAmAmAmUmAmGmCrA rArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmUmGmAmAmAmAmAmGmUmGmGmC mAmCmCmGmAmGmUmCmGmGmUmGmCrGrArArCrGrGrCrCrGrGrGrGrUrArUrUrGrU*mG*mG*mC	31030
RNACS 5100	hPKU6_R12_P9_sub5	mA*mC*mU*rUrUrGrCrUrGrCrCrArCrArArUrArCrCrUrGrUrUrUrUrArGrAmGmCmUmAmGmAmAmAmUmAmGmCrA rArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmUmGmAmAmAmAmAmGmUmGmGmC mAmCmCmGmAmGmUmCmGmGmUmGmCrGrArArCrGrGrArCrGrGrGrGrUrArUrUrGrU*mG*mG*mC	31031
RNACS 5101	hPKU6_R12_P9_sub6	mA*mC*mU*rUrUrGrCrUrGrCrCrArCrArArUrArCrCrUrGrUrUrUrUrArGrAmGmCmUmAmGmAmAmAmUmAmGmCrA rArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmUmGmAmAmAmAmAmGmUmGmGmC mAmCmCmGmAmGmUmCmGmGmUmGmCrGrArArGrGrGrCrCrGrGrGrGrUrArUrUrGrU*mG*mG*mC	31032
RNACS 5102	hPKU6_R12_P9_sub7	mA*mC*mU*rUrUrGrCrUrGrCrCrArCrArArUrArCrCrUrGrUrUrUrUrArGrAmGmCmUmAmGmAmAmAmUmAmGmCrA rArGrUrUrArArArArUrArArGrGrCrUrArGrUrCrCrGrUrUrArUrCrAmAmCmUmUmGmAmAmAmAmAmGmUmGmGmC mAmCmCmGmAmGmUmCmGmGmUmGmCrGrArArGrGrGrArCrGrCrGrGrUrArUrUrGrU*mG*mG*mC	31033

Table E6A shows the sequences of E6 without chemical modifications. In some embodiments, the sequences of Table E6A may be used without chemical modifications, or with one or more chemical modifications.

Table E6A: Table E6 Sequences without Chemical Modifications

RNACS#	Name	IDT Notation	SEQ ID NO
RNACS4741	hPKU3_R25_P10_sub0	UGGGUCGUAGCGAACUGAGAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUG AAAAAGUGGCACCGAGUCGGUGCGCUGCCACAAUACCUCGGCCCUUCUCAGUUCGCUA	37267
RNACS4742	hPKU3_R25_P10_sub1	UGGGUCGUAGCGAACUGAGAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUG AAAAAGUGGCACCGAGUCGGUGCGCUGCCACAAUACCGCGGCCCUUCUCAGUUCGCUA	37268
RNACS4743	hPKU3_R25_P10_sub2	UGGGUCGUAGCGAACUGAGAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUG AAAAAGUGGCACCGAGUCGGUGCGCUGCCACAAUCCCUCGGCCCUUCUCAGUUCGCUA	37269

RNACS4744	hPKU3_R25_P10_sub4	UGGGUCGUAGCGAACUGAGAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCGCUGCCACAAUACCUCGCCCCUUCUCAGUUCGCUA	37270
RNACS4745	hPKU3_R25_P10_sub7	UGGGUCGUAGCGAACUGAGAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCGCUGCCACAAUACCGCGCCCCUUCUCAGUUCGCUA	37271
RNACS4746	hPKU3_R25_P10_sub8	UGGGUCGUAGCGAACUGAGAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCGCUGCCACAAUACCGCGCCCAUUCUCAGUUCGCUA	37272
RNACS4747	hPKU3_R23_P10_sub0	UGGGUCGUAGCGAACUGAGAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCUGCCACAAUACCUCGGCCCUUCUCAGUUCGCUA	37273
RNACS4748	hPKU3_R23_P10_sub1	UGGGUCGUAGCGAACUGAGAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCUGCCACAAUACCGCGGCCCUUCUCAGUUCGCUA	37274
RNACS4749	hPKU3_R23_P10_sub2	UGGGUCGUAGCGAACUGAGAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCUGCCACAAUCCCUCGGCCCUUCUCAGUUCGCUA	37275
RNACS4750	hPKU3_R23_P10_sub4	UGGGUCGUAGCGAACUGAGAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCUGCCACAAUACCUCGCCCCUUCUCAGUUCGCUA	37276
RNACS4751	hPKU3_R23_P10_sub7	UGGGUCGUAGCGAACUGAGAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCUGCCACAAUACCGCGCCCCUUCUCAGUUCGCUA	37277
RNACS4752	hPKU3_R23_P10_sub8	UGGGUCGUAGCGAACUGAGAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCUGCCACAAUACCGCGCCCAUUCUCAGUUCGCUA	37278
RNACS4753	hPKU3_R21_P10_sub0	UGGGUCGUAGCGAACUGAGAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCCCACAAUACCUCGGCCCUUCUCAGUUCGCUA	37279
RNACS4754	hPKU3_R21_P10_sub1	UGGGUCGUAGCGAACUGAGAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCCCACAAUACCGCGGCCCUUCUCAGUUCGCUA	37280
RNACS4755	hPKU3_R21_P10_sub2	UGGGUCGUAGCGAACUGAGAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCCCACAAUCCCUCGGCCCUUCUCAGUUCGCUA	37281
RNACS4756	hPKU3_R21_P10_sub4	UGGGUCGUAGCGAACUGAGAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCCCACAAUACCUCGCCCCUUCUCAGUUCGCUA	37282
RNACS4757	hPKU3_R21_P10_sub7	UGGGUCGUAGCGAACUGAGAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCCCACAAUACCGCGCCCCUUCUCAGUUCGCUA	37283
RNACS4758	hPKU3_R21_P10_sub8	UGGGUCGUAGCGAACUGAGAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCCCACAAUACCGCGCCCAUUCUCAGUUCGCUA	37284
RNACS4759	hPKU3_R19_P10_sub0	UGGGUCGUAGCGAACUGAGAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCACAAUACCUCGGCCCUUCUCAGUUCGCUA	37285

RNACS4760	hPKU3_R19_P10_sub1	UGGGUCGUAGCGAACUGAGAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCACAAUACCGCGGCCCUUCUCAGUUCGCUA	37286
RNACS4761	hPKU3_R19_P10_sub2	UGGGUCGUAGCGAACUGAGAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCACAAUCCCUCGGCCCUUCUCAGUUCGCUA	37287
RNACS4762	hPKU3_R19_P10_sub4	UGGGUCGUAGCGAACUGAGAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCACAAUACCUCGCCCCUUCUCAGUUCGCUA	37288
RNACS4763	hPKU3_R19_P10_sub7	UGGGUCGUAGCGAACUGAGAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCACAAUACCGCGCCCCUUCUCAGUUCGCUA	37289
RNACS4764	hPKU3_R19_P10_sub8	UGGGUCGUAGCGAACUGAGAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCACAAUACCGCGCCCAUUCUCAGUUCGCUA	37290
RNACS4765	hPKU3_R17_P10_sub0	UGGGUCGUAGCGAACUGAGAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCAAUACCUCGGCCCUUCUCAGUUCGCUA	37291
RNACS4766	hPKU3_R17_P10_sub1	UGGGUCGUAGCGAACUGAGAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCAAUACCGCGGCCCUUCUCAGUUCGCUA	37292
RNACS4767	hPKU3_R17_P10_sub2	UGGGUCGUAGCGAACUGAGAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCAAUCCCUCGGCCCUUCUCAGUUCGCUA	37293
RNACS4768	hPKU3_R17_P10_sub4	UGGGUCGUAGCGAACUGAGAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCAAUACCUCGCCCCUUCUCAGUUCGCUA	37294
RNACS4769	hPKU3_R17_P10_sub7	UGGGUCGUAGCGAACUGAGAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCAAUACCGCGCCCCUUCUCAGUUCGCUA	37295
RNACS4770	hPKU3_R17_P10_sub8	UGGGUCGUAGCGAACUGAGAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCAAUACCGCGCCCAUUCUCAGUUCGCUA	37296
RNACS4771	hPKU3_R25_P9_sub0	UGGGUCGUAGCGAACUGAGAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCGCUGCCACAAUACCUCGGCCCUUCUCAGUUCGCU	37297
RNACS4772	hPKU3_R25_P9_sub1	UGGGUCGUAGCGAACUGAGAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCGCUGCCACAAUACCGCGGCCCUUCUCAGUUCGCU	37298
RNACS4773	hPKU3_R25_P9_sub2	UGGGUCGUAGCGAACUGAGAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCGCUGCCACAAUCCCUCGGCCCUUCUCAGUUCGCU	37299
RNACS4774	hPKU3_R25_P9_sub4	UGGGUCGUAGCGAACUGAGAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCGCUGCCACAAUACCUCGCCCCUUCUCAGUUCGCU	37300
RNACS4775	hPKU3_R25_P9_sub7	UGGGUCGUAGCGAACUGAGAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCGCUGCCACAAUACCGCGCCCCUUCUCAGUUCGCU	37301

RNACS4776	hPKU3_R25_P9_sub8	UGGGUCGUAGCGAACUGAGAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCGCUGCCACAAUACCGCGCCCAUUCUCAGUUCGCU	37302
RNACS4777	hPKU3_R23_P9_sub0	UGGGUCGUAGCGAACUGAGAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCUGCCACAAUACCUCGGCCCUUCUCAGUUCGCU	37303
RNACS4778	hPKU3_R23_P9_sub1	UGGGUCGUAGCGAACUGAGAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCUGCCACAAUACCGCGGCCCUUCUCAGUUCGCU	37304
RNACS4779	hPKU3_R23_P9_sub2	UGGGUCGUAGCGAACUGAGAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCUGCCACAAUCCCUCGGCCCUUCUCAGUUCGCU	37305
RNACS4780	hPKU3_R23_P9_sub4	UGGGUCGUAGCGAACUGAGAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCUGCCACAAUACCUCGCCCCUUCUCAGUUCGCU	37306
RNACS4781	hPKU3_R23_P9_sub7	UGGGUCGUAGCGAACUGAGAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCUGCCACAAUACCGCGCCCCUUCUCAGUUCGCU	37307
RNACS4782	hPKU3_R23_P9_sub8	UGGGUCGUAGCGAACUGAGAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCUGCCACAAUACCGCGCCCAUUCUCAGUUCGCU	37308
RNACS4783	hPKU3_R21_P9_sub0	UGGGUCGUAGCGAACUGAGAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCCCACAAUACCUCGGCCCUUCUCAGUUCGCU	37309
RNACS4784	hPKU3_R21_P9_sub1	UGGGUCGUAGCGAACUGAGAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCCCACAAUACCGCGGCCCUUCUCAGUUCGCU	37310
RNACS4785	hPKU3_R21_P9_sub2	UGGGUCGUAGCGAACUGAGAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCCCACAAUCCCUCGGCCCUUCUCAGUUCGCU	37311
RNACS4786	hPKU3_R21_P9_sub4	UGGGUCGUAGCGAACUGAGAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCCCACAAUACCUCGCCCCUUCUCAGUUCGCU	37312
RNACS4787	hPKU3_R21_P9_sub7	UGGGUCGUAGCGAACUGAGAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCCCACAAUACCGCGCCCCUUCUCAGUUCGCU	37313
RNACS4788	hPKU3_R21_P9_sub8	UGGGUCGUAGCGAACUGAGAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCCCACAAUACCGCGCCCAUUCUCAGUUCGCU	37314
RNACS4789	hPKU3_R19_P9_sub0	UGGGUCGUAGCGAACUGAGAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCACAAUACCUCGGCCCUUCUCAGUUCGCU	37315
RNACS4790	hPKU3_R19_P9_sub1	UGGGUCGUAGCGAACUGAGAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCACAAUACCGCGGCCCUUCUCAGUUCGCU	37316
RNACS4791	hPKU3_R19_P9_sub2	UGGGUCGUAGCGAACUGAGAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCACAAUCCCUCGGCCCUUCUCAGUUCGCU	37317

RNACS4792	hPKU3_R19_P9_sub4	UGGGUCGUAGCGAACUGAGAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCACAAUACCUCGCCCCUUCUCAGUUCGCU	37318
RNACS4793	hPKU3_R19_P9_sub7	UGGGUCGUAGCGAACUGAGAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCACAAUACCGCGCCCCUUCUCAGUUCGCU	37319
RNACS4794	hPKU3_R19_P9_sub8	UGGGUCGUAGCGAACUGAGAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCACAAUACCGCGCCCAUUCUCAGUUCGCU	37320
RNACS4795	hPKU3_R17_P9_sub0	UGGGUCGUAGCGAACUGAGAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCAAUACCUCGGCCCUUCUCAGUUCGCU	37321
RNACS4796	hPKU3_R17_P9_sub1	UGGGUCGUAGCGAACUGAGAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCAAUACCGCGGCCCUUCUCAGUUCGCU	37322
RNACS4797	hPKU3_R17_P9_sub2	UGGGUCGUAGCGAACUGAGAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCAAUCCCUCGGCCCUUCUCAGUUCGCU	37323
RNACS4798	hPKU3_R17_P9_sub4	UGGGUCGUAGCGAACUGAGAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCAAUACCUCGCCCCUUCUCAGUUCGCU	37324
RNACS4799	hPKU3_R17_P9_sub7	UGGGUCGUAGCGAACUGAGAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCAAUACCGCGCCCCUUCUCAGUUCGCU	37325
RNACS4800	hPKU3_R17_P9_sub8	UGGGUCGUAGCGAACUGAGAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCAAUACCGCGCCCAUUCUCAGUUCGCU	37326
RNACS4801	hPKU3_R25_P8_sub0	UGGGUCGUAGCGAACUGAGAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCGCUGCCACAAUACCUCGGCCCUUCUCAGUUCGC	37327
RNACS4802	hPKU3_R25_P8_sub1	UGGGUCGUAGCGAACUGAGAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCGCUGCCACAAUACCGCGGCCCUUCUCAGUUCGC	37328
RNACS4803	hPKU3_R25_P8_sub2	UGGGUCGUAGCGAACUGAGAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCGCUGCCACAAUCCCUCGGCCCUUCUCAGUUCGC	37329
RNACS4804	hPKU3_R25_P8_sub4	UGGGUCGUAGCGAACUGAGAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCGCUGCCACAAUACCUCGCCCCUUCUCAGUUCGC	37330
RNACS4805	hPKU3_R25_P8_sub7	UGGGUCGUAGCGAACUGAGAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCGCUGCCACAAUACCGCGCCCCUUCUCAGUUCGC	37331
RNACS4806	hPKU3_R25_P8_sub8	UGGGUCGUAGCGAACUGAGAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCGCUGCCACAAUACCGCGCCCAUUCUCAGUUCGC	37332
RNACS4807	hPKU3_R23_P8_sub0	UGGGUCGUAGCGAACUGAGAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCUGCCACAAUACCUCGGCCCUUCUCAGUUCGC	37333

RNACS4808	hPKU3_R23_P8_sub1	UGGGUCGUAGCGAACUGAGAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCUGCCACAAUACCGCGGCCCUUCUCAGUUCGC	37334
RNACS4809	hPKU3_R23_P8_sub2	UGGGUCGUAGCGAACUGAGAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCUGCCACAAUCCCUCGGCCCUUCUCAGUUCGC	37335
RNACS4810	hPKU3_R23_P8_sub4	UGGGUCGUAGCGAACUGAGAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCUGCCACAAUACCUCGCCCCUUCUCAGUUCGC	37336
RNACS4811	hPKU3_R23_P8_sub7	UGGGUCGUAGCGAACUGAGAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCUGCCACAAUACCGCGCCCCUUCUCAGUUCGC	37337
RNACS4812	hPKU3_R23_P8_sub8	UGGGUCGUAGCGAACUGAGAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCUGCCACAAUACCGCGCCCAUUCUCAGUUCGC	37338
RNACS4813	hPKU3_R21_P8_sub0	UGGGUCGUAGCGAACUGAGAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCCCACAAUACCUCGGCCCUUCUCAGUUCGC	37339
RNACS4814	hPKU3_R21_P8_sub1	UGGGUCGUAGCGAACUGAGAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCCCACAAUACCGCGGCCCUUCUCAGUUCGC	37340
RNACS4815	hPKU3_R21_P8_sub2	UGGGUCGUAGCGAACUGAGAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCCCACAAUCCCUCGGCCCUUCUCAGUUCGC	37341
RNACS4816	hPKU3_R21_P8_sub4	UGGGUCGUAGCGAACUGAGAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCCCACAAUACCUCGCCCCUUCUCAGUUCGC	37342
RNACS4817	hPKU3_R21_P8_sub7	UGGGUCGUAGCGAACUGAGAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCCCACAAUACCGCGCCCCUUCUCAGUUCGC	37343
RNACS4818	hPKU3_R21_P8_sub8	UGGGUCGUAGCGAACUGAGAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCCCACAAUACCGCGCCCAUUCUCAGUUCGC	37344
RNACS4819	hPKU3_R19_P8_sub0	UGGGUCGUAGCGAACUGAGAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCACAAUACCUCGGCCCUUCUCAGUUCGC	37345
RNACS4820	hPKU3_R19_P8_sub1	UGGGUCGUAGCGAACUGAGAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCACAAUACCGCGGCCCUUCUCAGUUCGC	37346
RNACS4821	hPKU3_R19_P8_sub2	UGGGUCGUAGCGAACUGAGAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCACAAUCCCUCGGCCCUUCUCAGUUCGC	37347
RNACS4822	hPKU3_R19_P8_sub4	UGGGUCGUAGCGAACUGAGAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCACAAUACCUCGCCCCUUCUCAGUUCGC	37348
RNACS4823	hPKU3_R19_P8_sub7	UGGGUCGUAGCGAACUGAGAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCACAAUACCGCGCCCCUUCUCAGUUCGC	37349

RNACS4824	hPKU3_R19_P8_sub8	UGGGUCGUAGCGAACUGAGAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCACAAUACCGCGCCCAUUCUCAGUUCGC	37350
RNACS4825	hPKU3_R17_P8_sub0	UGGGUCGUAGCGAACUGAGAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCAAUACCUCGGCCCUUCUCAGUUCGC	37351
RNACS4826	hPKU3_R17_P8_sub1	UGGGUCGUAGCGAACUGAGAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCAAUACCGCGGCCCUUCUCAGUUCGC	37352
RNACS4827	hPKU3_R17_P8_sub2	UGGGUCGUAGCGAACUGAGAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCAAUCCCUCGGCCCUUCUCAGUUCGC	37353
RNACS4828	hPKU3_R17_P8_sub4	UGGGUCGUAGCGAACUGAGAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCAAUACCUCGCCCCUUCUCAGUUCGC	37354
RNACS4829	hPKU3_R17_P8_sub7	UGGGUCGUAGCGAACUGAGAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCAAUACCGCGCCCCUUCUCAGUUCGC	37355
RNACS4830	hPKU3_R17_P8_sub8	UGGGUCGUAGCGAACUGAGAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCAAUACCGCGCCCAUUCUCAGUUCGC	37356
RNACS4831	hPKU4_R24_P10_sub0	GGGUCGUAGCGAACUGAGAAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCGCUGCCACAAUACCUCGGCCCUUCUCAGUUCGCU	37357
RNACS4832	hPKU4_R24_P10_sub1	GGGUCGUAGCGAACUGAGAAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCGCUGCCACAAUACCGCGGCCCUUCUCAGUUCGCU	37358
RNACS4833	hPKU4_R24_P10_sub4	GGGUCGUAGCGAACUGAGAAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCGCUGCCACAAUACCUCGCCCCUUCUCAGUUCGCU	37359
RNACS4834	hPKU4_R24_P10_sub5	GGGUCGUAGCGAACUGAGAAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCGCUGCCACAAUACCUCGCCCAUUCUCAGUUCGCU	37360
RNACS4835	hPKU4_R24_P10_sub7	GGGUCGUAGCGAACUGAGAAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCGCUGCCACAAUACCGCGCCCCUUCUCAGUUCGCU	37361
RNACS4836	hPKU4_R24_P10_sub8	GGGUCGUAGCGAACUGAGAAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCGCUGCCACAAUACCGCGCCCAUUCUCAGUUCGCU	37362
RNACS4837	hPKU4_R22_P10_sub0	GGGUCGUAGCGAACUGAGAAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCUGCCACAAUACCUCGGCCCUUCUCAGUUCGCU	37363
RNACS4838	hPKU4_R22_P10_sub1	GGGUCGUAGCGAACUGAGAAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCUGCCACAAUACCGCGGCCCUUCUCAGUUCGCU	37364
RNACS4839	hPKU4_R22_P10_sub4	GGGUCGUAGCGAACUGAGAAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCUGCCACAAUACCUCGCCCCUUCUCAGUUCGCU	37365

RNACS4840	hPKU4_R22_P10_sub5	GGGUCGUAGCGAACUGAGAAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCUGCCACAAUACCUCGCCCAUUCUCAGUUCGCU	37366
RNACS4841	hPKU4_R22_P10_sub7	GGGUCGUAGCGAACUGAGAAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCUGCCACAAUACCGCGCCCCUUCUCAGUUCGCU	37367
RNACS4842	hPKU4_R22_P10_sub8	GGGUCGUAGCGAACUGAGAAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCUGCCACAAUACCGCGCCCAUUCUCAGUUCGCU	37368
RNACS4843	hPKU4_R20_P10_sub0	GGGUCGUAGCGAACUGAGAAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCCCACAAUACCUCGGCCCUUCUCAGUUCGCU	37369
RNACS4844	hPKU4_R20_P10_sub1	GGGUCGUAGCGAACUGAGAAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCCCACAAUACCGCGGCCCUUCUCAGUUCGCU	37370
RNACS4845	hPKU4_R20_P10_sub4	GGGUCGUAGCGAACUGAGAAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCCCACAAUACCUCGCCCCUUCUCAGUUCGCU	37371
RNACS4846	hPKU4_R20_P10_sub5	GGGUCGUAGCGAACUGAGAAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCCCACAAUACCUCGCCCAUUCUCAGUUCGCU	37372
RNACS4847	hPKU4_R20_P10_sub7	GGGUCGUAGCGAACUGAGAAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCCCACAAUACCGCGCCCCUUCUCAGUUCGCU	37373
RNACS4848	hPKU4_R20_P10_sub8	GGGUCGUAGCGAACUGAGAAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCCCACAAUACCGCGCCCAUUCUCAGUUCGCU	37374
RNACS4849	hPKU4_R18_P10_sub0	GGGUCGUAGCGAACUGAGAAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCACAAUACCUCGGCCCUUCUCAGUUCGCU	37375
RNACS4850	hPKU4_R18_P10_sub1	GGGUCGUAGCGAACUGAGAAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCACAAUACCGCGGCCCUUCUCAGUUCGCU	37376
RNACS4851	hPKU4_R18_P10_sub4	GGGUCGUAGCGAACUGAGAAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCACAAUACCUCGCCCCUUCUCAGUUCGCU	37377
RNACS4852	hPKU4_R18_P10_sub5	GGGUCGUAGCGAACUGAGAAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCACAAUACCUCGCCCAUUCUCAGUUCGCU	37378
RNACS4853	hPKU4_R18_P10_sub7	GGGUCGUAGCGAACUGAGAAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCACAAUACCGCGCCCCUUCUCAGUUCGCU	37379
RNACS4854	hPKU4_R18_P10_sub8	GGGUCGUAGCGAACUGAGAAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCACAAUACCGCGCCCAUUCUCAGUUCGCU	37380
RNACS4855	hPKU4_R16_P10_sub0	GGGUCGUAGCGAACUGAGAAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCAAUACCUCGGCCCUUCUCAGUUCGCU	37381

RNACS4856	hPKU4_R16_P10_sub1	GGGUCGUAGCGAACUGAGAAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCAAUACCGCGGCCCUUCUCAGUUCGCU	37382
RNACS4857	hPKU4_R16_P10_sub4	GGGUCGUAGCGAACUGAGAAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCAAUACCUCGCCCCUUCUCAGUUCGCU	37383
RNACS4858	hPKU4_R16_P10_sub5	GGGUCGUAGCGAACUGAGAAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCAAUACCUCGCCCAUUCUCAGUUCGCU	37384
RNACS4859	hPKU4_R16_P10_sub7	GGGUCGUAGCGAACUGAGAAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCAAUACCGCGCCCCUUCUCAGUUCGCU	37385
RNACS4860	hPKU4_R16_P10_sub8	GGGUCGUAGCGAACUGAGAAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCAAUACCGCGCCCAUUCUCAGUUCGCU	37386
RNACS4861	hPKU4_R24_P9_sub0	GGGUCGUAGCGAACUGAGAAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCGCUGCCACAAUACCUCGGCCCUUCUCAGUUCGC	37387
RNACS4862	hPKU4_R24_P9_sub1	GGGUCGUAGCGAACUGAGAAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCGCUGCCACAAUACCGCGGCCCUUCUCAGUUCGC	37388
RNACS4863	hPKU4_R24_P9_sub4	GGGUCGUAGCGAACUGAGAAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCGCUGCCACAAUACCUCGCCCCUUCUCAGUUCGC	37389
RNACS4864	hPKU4_R24_P9_sub5	GGGUCGUAGCGAACUGAGAAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCGCUGCCACAAUACCUCGCCCAUUCUCAGUUCGC	37390
RNACS4865	hPKU4_R24_P9_sub7	GGGUCGUAGCGAACUGAGAAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCGCUGCCACAAUACCGCGCCCCUUCUCAGUUCGC	37391
RNACS4866	hPKU4_R24_P9_sub8	GGGUCGUAGCGAACUGAGAAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCGCUGCCACAAUACCGCGCCCAUUCUCAGUUCGC	37392
RNACS4867	hPKU4_R22_P9_sub0	GGGUCGUAGCGAACUGAGAAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCUGCCACAAUACCUCGGCCCUUCUCAGUUCGC	37393
RNACS4868	hPKU4_R22_P9_sub1	GGGUCGUAGCGAACUGAGAAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCUGCCACAAUACCGCGGCCCUUCUCAGUUCGC	37394
RNACS4869	hPKU4_R22_P9_sub4	GGGUCGUAGCGAACUGAGAAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCUGCCACAAUACCUCGCCCCUUCUCAGUUCGC	37395
RNACS4870	hPKU4_R22_P9_sub5	GGGUCGUAGCGAACUGAGAAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCUGCCACAAUACCUCGCCCAUUCUCAGUUCGC	37396
RNACS4871	hPKU4_R22_P9_sub7	GGGUCGUAGCGAACUGAGAAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCUGCCACAAUACCGCGCCCCUUCUCAGUUCGC	37397

RNACS4872	hPKU4_R22_P9_sub8	GGGUCGUAGCGAACUGAGAAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCUGCCACAAUACCGCGCCCAUUCUCAGUUCGC	37398
RNACS4873	hPKU4_R20_P9_sub0	GGGUCGUAGCGAACUGAGAAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCCCACAAUACCUCGGCCCUUCUCAGUUCGC	37399
RNACS4874	hPKU4_R20_P9_sub1	GGGUCGUAGCGAACUGAGAAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCCCACAAUACCGCGGCCCUUCUCAGUUCGC	37400
RNACS4875	hPKU4_R20_P9_sub4	GGGUCGUAGCGAACUGAGAAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCCCACAAUACCUCGCCCCUUCUCAGUUCGC	37401
RNACS4876	hPKU4_R20_P9_sub5	GGGUCGUAGCGAACUGAGAAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCCCACAAUACCUCGCCCAUUCUCAGUUCGC	37402
RNACS4877	hPKU4_R20_P9_sub7	GGGUCGUAGCGAACUGAGAAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCCCACAAUACCGCGCCCCUUCUCAGUUCGC	37403
RNACS4878	hPKU4_R20_P9_sub8	GGGUCGUAGCGAACUGAGAAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCCCACAAUACCGCGCCCAUUCUCAGUUCGC	37404
RNACS4879	hPKU4_R18_P9_sub0	GGGUCGUAGCGAACUGAGAAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCACAAUACCUCGGCCCUUCUCAGUUCGC	37405
RNACS4880	hPKU4_R18_P9_sub1	GGGUCGUAGCGAACUGAGAAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCACAAUACCGCGGCCCUUCUCAGUUCGC	37406
RNACS4881	hPKU4_R18_P9_sub4	GGGUCGUAGCGAACUGAGAAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCACAAUACCUCGCCCCUUCUCAGUUCGC	37407
RNACS4882	hPKU4_R18_P9_sub5	GGGUCGUAGCGAACUGAGAAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCACAAUACCUCGCCCAUUCUCAGUUCGC	37408
RNACS4883	hPKU4_R18_P9_sub7	GGGUCGUAGCGAACUGAGAAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCACAAUACCGCGCCCCUUCUCAGUUCGC	37409
RNACS4884	hPKU4_R18_P9_sub8	GGGUCGUAGCGAACUGAGAAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCACAAUACCGCGCCCAUUCUCAGUUCGC	37410
RNACS4885	hPKU4_R16_P9_sub0	GGGUCGUAGCGAACUGAGAAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCAAUACCUCGGCCCUUCUCAGUUCGC	37411
RNACS4886	hPKU4_R16_P9_sub1	GGGUCGUAGCGAACUGAGAAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCAAUACCGCGGCCCUUCUCAGUUCGC	37412
RNACS4887	hPKU4_R16_P9_sub4	GGGUCGUAGCGAACUGAGAAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCAAUACCUCGCCCCUUCUCAGUUCGC	37413

RNACS4888	hPKU4_R16_P9_sub5	GGGUCGUAGCGAACUGAGAAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCAAUACCUCGCCCAUUCUCAGUUCGC	37414
RNACS4889	hPKU4_R16_P9_sub7	GGGUCGUAGCGAACUGAGAAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCAAUACCGCGCCCCUUCUCAGUUCGC	37415
RNACS4890	hPKU4_R16_P9_sub8	GGGUCGUAGCGAACUGAGAAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCAAUACCGCGCCCAUUCUCAGUUCGC	37416
RNACS4891	hPKU4_R24_P8_sub0	GGGUCGUAGCGAACUGAGAAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCGCUGCCACAAUACCUCGGCCCUUCUCAGUUCG	37417
RNACS4892	hPKU4_R24_P8_sub1	GGGUCGUAGCGAACUGAGAAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCGCUGCCACAAUACCGCGGCCCUUCUCAGUUCG	37418
RNACS4893	hPKU4_R24_P8_sub4	GGGUCGUAGCGAACUGAGAAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCGCUGCCACAAUACCUCGCCCCUUCUCAGUUCG	37419
RNACS4894	hPKU4_R24_P8_sub5	GGGUCGUAGCGAACUGAGAAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCGCUGCCACAAUACCUCGCCCAUUCUCAGUUCG	37420
RNACS4895	hPKU4_R24_P8_sub7	GGGUCGUAGCGAACUGAGAAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCGCUGCCACAAUACCGCGCCCCUUCUCAGUUCG	37421
RNACS4896	hPKU4_R24_P8_sub8	GGGUCGUAGCGAACUGAGAAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCGCUGCCACAAUACCGCGCCCAUUCUCAGUUCG	37422
RNACS4897	hPKU4_R22_P8_sub0	GGGUCGUAGCGAACUGAGAAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCUGCCACAAUACCUCGGCCCUUCUCAGUUCG	37423
RNACS4898	hPKU4_R22_P8_sub1	GGGUCGUAGCGAACUGAGAAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCUGCCACAAUACCGCGGCCCUUCUCAGUUCG	37424
RNACS4899	hPKU4_R22_P8_sub4	GGGUCGUAGCGAACUGAGAAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCUGCCACAAUACCUCGCCCCUUCUCAGUUCG	37425
RNACS4900	hPKU4_R22_P8_sub5	GGGUCGUAGCGAACUGAGAAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCUGCCACAAUACCUCGCCCAUUCUCAGUUCG	37426
RNACS4901	hPKU4_R22_P8_sub7	GGGUCGUAGCGAACUGAGAAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCUGCCACAAUACCGCGCCCCUUCUCAGUUCG	37427
RNACS4902	hPKU4_R22_P8_sub8	GGGUCGUAGCGAACUGAGAAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCUGCCACAAUACCGCGCCCAUUCUCAGUUCG	37428
RNACS4903	hPKU4_R20_P8_sub0	GGGUCGUAGCGAACUGAGAAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCCCACAAUACCUCGGCCCUUCUCAGUUCG	37429

RNACS4904	hPKU4_R20_P8_sub1	GGGUCGUAGCGAACUGAGAAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCCCACAAUACCGCGGCCCUUCUCAGUUCG	37430
RNACS4905	hPKU4_R20_P8_sub4	GGGUCGUAGCGAACUGAGAAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCCCACAAUACCUCGCCCCUUCUCAGUUCG	37431
RNACS4906	hPKU4_R20_P8_sub5	GGGUCGUAGCGAACUGAGAAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCCCACAAUACCUCGCCCAUUCUCAGUUCG	37432
RNACS4907	hPKU4_R20_P8_sub7	GGGUCGUAGCGAACUGAGAAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCCCACAAUACCGCGCCCCUUCUCAGUUCG	37433
RNACS4908	hPKU4_R20_P8_sub8	GGGUCGUAGCGAACUGAGAAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCCCACAAUACCGCGCCCAUUCUCAGUUCG	37434
RNACS4909	hPKU4_R18_P8_sub0	GGGUCGUAGCGAACUGAGAAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCACAAUACCUCGGCCCUUCUCAGUUCG	37435
RNACS4910	hPKU4_R18_P8_sub1	GGGUCGUAGCGAACUGAGAAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCACAAUACCGCGGCCCUUCUCAGUUCG	37436
RNACS4911	hPKU4_R18_P8_sub4	GGGUCGUAGCGAACUGAGAAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCACAAUACCUCGCCCCUUCUCAGUUCG	37437
RNACS4912	hPKU4_R18_P8_sub5	GGGUCGUAGCGAACUGAGAAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCACAAUACCUCGCCCAUUCUCAGUUCG	37438
RNACS4913	hPKU4_R18_P8_sub7	GGGUCGUAGCGAACUGAGAAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCACAAUACCGCGCCCCUUCUCAGUUCG	37439
RNACS4914	hPKU4_R18_P8_sub8	GGGUCGUAGCGAACUGAGAAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCACAAUACCGCGCCCAUUCUCAGUUCG	37440
RNACS4915	hPKU4_R16_P8_sub0	GGGUCGUAGCGAACUGAGAAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCAAUACCUCGGCCCUUCUCAGUUCG	37441
RNACS4916	hPKU4_R16_P8_sub1	GGGUCGUAGCGAACUGAGAAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCAAUACCGCGGCCCUUCUCAGUUCG	37442
RNACS4917	hPKU4_R16_P8_sub4	GGGUCGUAGCGAACUGAGAAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCAAUACCUCGCCCCUUCUCAGUUCG	37443
RNACS4918	hPKU4_R16_P8_sub5	GGGUCGUAGCGAACUGAGAAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCAAUACCUCGCCCAUUCUCAGUUCG	37444
RNACS4919	hPKU4_R16_P8_sub7	GGGUCGUAGCGAACUGAGAAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCAAUACCGCGCCCCUUCUCAGUUCG	37445

RNACS4920	hPKU4_R16_P8_sub8	GGGUCGUAGCGAACUGAGAAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCAAUACCGCGCCCAUUCUCAGUUCG	37446
RNACS4923	hPKU5_R20_P10_sub0	UAGCGAACUGAGAAGGGCCAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCUUGCUGCCACAAUACCUCGGCCCUUCUCAG	37447
RNACS4924	hPKU5_R20_P10_sub1	UAGCGAACUGAGAAGGGCCAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCUUGCUGCCACAAUACCGCGGCCCUUCUCAG	37448
RNACS4925	hPKU5_R20_P10_sub2	UAGCGAACUGAGAAGGGCCAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCUUGCUGCCACAAUCCCUCGGCCCUUCUCAG	37449
RNACS4926	hPKU5_R20_P10_sub3	UAGCGAACUGAGAAGGGCCAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCUUGCUGCCACAAUCCCGCGGCCCUUCUCAG	37450
RNACS4927	hPKU5_R20_P10_sub4	UAGCGAACUGAGAAGGGCCAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCUUGCUGCCACAAUACCUCGCCCCUUCUCAG	37451
RNACS4928	hPKU5_R20_P10_sub7	UAGCGAACUGAGAAGGGCCAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCUUGCUGCCACGAUACCUCGGCCCUUCUCAG	37452
RNACS4929	hPKU5_R18_P10_sub0	UAGCGAACUGAGAAGGGCCAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCGCUGCCACAAUACCUCGGCCCUUCUCAG	37453
RNACS4930	hPKU5_R18_P10_sub1	UAGCGAACUGAGAAGGGCCAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCGCUGCCACAAUACCGCGGCCCUUCUCAG	37454
RNACS4931	hPKU5_R18_P10_sub2	UAGCGAACUGAGAAGGGCCAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCGCUGCCACAAUCCCUCGGCCCUUCUCAG	37455
RNACS4932	hPKU5_R18_P10_sub3	UAGCGAACUGAGAAGGGCCAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCGCUGCCACAAUCCCGCGGCCCUUCUCAG	37456
RNACS4933	hPKU5_R18_P10_sub4	UAGCGAACUGAGAAGGGCCAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCGCUGCCACAAUACCUCGCCCCUUCUCAG	37457
RNACS4934	hPKU5_R18_P10_sub7	UAGCGAACUGAGAAGGGCCAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCGCUGCCACGAUACCUCGGCCCUUCUCAG	37458
RNACS4935	hPKU5_R16_P10_sub0	UAGCGAACUGAGAAGGGCCAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCUGCCACAAUACCUCGGCCCUUCUCAG	37459
RNACS4936	hPKU5_R16_P10_sub1	UAGCGAACUGAGAAGGGCCAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCUGCCACAAUACCGCGGCCCUUCUCAG	37460
RNACS4937	hPKU5_R16_P10_sub2	UAGCGAACUGAGAAGGGCCAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCUGCCACAAUCCCUCGGCCCUUCUCAG	37461

RNACS4938	hPKU5_R16_P10_sub3	UAGCGAACUGAGAAGGGCCAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCUGCCACAAUCCCGCGGCCCUUCUCAG	37462
RNACS4939	hPKU5_R16_P10_sub4	UAGCGAACUGAGAAGGGCCAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCUGCCACAAUACCUCGCCCCUUCUCAG	37463
RNACS4940	hPKU5_R16_P10_sub7	UAGCGAACUGAGAAGGGCCAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCUGCCACGAUACCUCGGCCCUUCUCAG	37464
RNACS4941	hPKU5_R14_P10_sub0	UAGCGAACUGAGAAGGGCCAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCCCACAAUACCUCGGCCCUUCUCAG	37465
RNACS4942	hPKU5_R14_P10_sub1	UAGCGAACUGAGAAGGGCCAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCCCACAAUACCGCGGCCCUUCUCAG	37466
RNACS4943	hPKU5_R14_P10_sub2	UAGCGAACUGAGAAGGGCCAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCCCACAAUCCCUCGGCCCUUCUCAG	37467
RNACS4944	hPKU5_R14_P10_sub3	UAGCGAACUGAGAAGGGCCAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCCCACAAUCCCGCGGCCCUUCUCAG	37468
RNACS4945	hPKU5_R14_P10_sub4	UAGCGAACUGAGAAGGGCCAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCCCACAAUACCUCGCCCCUUCUCAG	37469
RNACS4946	hPKU5_R14_P10_sub7	UAGCGAACUGAGAAGGGCCAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCCCACGAUACCUCGGCCCUUCUCAG	37470
RNACS4947	hPKU5_R12_P10_sub0	UAGCGAACUGAGAAGGGCCAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCACAAUACCUCGGCCCUUCUCAG	37471
RNACS4948	hPKU5_R12_P10_sub1	UAGCGAACUGAGAAGGGCCAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCACAAUACCGCGGCCCUUCUCAG	37472
RNACS4949	hPKU5_R12_P10_sub2	UAGCGAACUGAGAAGGGCCAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCACAAUCCCUCGGCCCUUCUCAG	37473
RNACS4950	hPKU5_R12_P10_sub3	UAGCGAACUGAGAAGGGCCAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCACAAUCCCGCGGCCCUUCUCAG	37474
RNACS4951	hPKU5_R12_P10_sub4	UAGCGAACUGAGAAGGGCCAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCACAAUACCUCGCCCCUUCUCAG	37475
RNACS4952	hPKU5_R12_P10_sub7	UAGCGAACUGAGAAGGGCCAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCACGAUACCUCGGCCCUUCUCAG	37476
RNACS4953	hPKU5_R20_P9_sub0	UAGCGAACUGAGAAGGGCCAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCUUGCUGCCACAAUACCUCGGCCCUUCUCA	37477

RNACS4954	hPKU5_R20_P9_sub1	UAGCGAACUGAGAAGGGCCAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCUUGCUGCCACAAUACCGCGGCCCUUCUCA	37478
RNACS4955	hPKU5_R20_P9_sub2	UAGCGAACUGAGAAGGGCCAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCUUGCUGCCACAAUCCCUCGGCCCUUCUCA	37479
RNACS4956	hPKU5_R20_P9_sub3	UAGCGAACUGAGAAGGGCCAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCUUGCUGCCACAAUCCCGCGGCCCUUCUCA	37480
RNACS4957	hPKU5_R20_P9_sub4	UAGCGAACUGAGAAGGGCCAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCUUGCUGCCACAAUACCUCGCCCCUUCUCA	37481
RNACS4958	hPKU5_R20_P9_sub7	UAGCGAACUGAGAAGGGCCAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCUUGCUGCCACGAUACCUCGGCCCUUCUCA	37482
RNACS4959	hPKU5_R18_P9_sub0	UAGCGAACUGAGAAGGGCCAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCGCUGCCACAAUACCUCGGCCCUUCUCA	37483
RNACS4960	hPKU5_R18_P9_sub1	UAGCGAACUGAGAAGGGCCAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCGCUGCCACAAUACCGCGGCCCUUCUCA	37484
RNACS4961	hPKU5_R18_P9_sub2	UAGCGAACUGAGAAGGGCCAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCGCUGCCACAAUCCCUCGGCCCUUCUCA	37485
RNACS4962	hPKU5_R18_P9_sub3	UAGCGAACUGAGAAGGGCCAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCGCUGCCACAAUCCCGCGGCCCUUCUCA	37486
RNACS4963	hPKU5_R18_P9_sub4	UAGCGAACUGAGAAGGGCCAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCGCUGCCACAAUACCUCGCCCCUUCUCA	37487
RNACS4964	hPKU5_R18_P9_sub7	UAGCGAACUGAGAAGGGCCAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCGCUGCCACGAUACCUCGGCCCUUCUCA	37488
RNACS4965	hPKU5_R16_P9_sub0	UAGCGAACUGAGAAGGGCCAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCUGCCACAAUACCUCGGCCCUUCUCA	37489
RNACS4966	hPKU5_R16_P9_sub1	UAGCGAACUGAGAAGGGCCAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCUGCCACAAUACCGCGGCCCUUCUCA	37490
RNACS4967	hPKU5_R16_P9_sub2	UAGCGAACUGAGAAGGGCCAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCUGCCACAAUCCCUCGGCCCUUCUCA	37491
RNACS4968	hPKU5_R16_P9_sub3	UAGCGAACUGAGAAGGGCCAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCUGCCACAAUCCCGCGGCCCUUCUCA	37492
RNACS4969	hPKU5_R16_P9_sub4	UAGCGAACUGAGAAGGGCCAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCUGCCACAAUACCUCGCCCCUUCUCA	37493

RNACS4970	hPKU5_R16_P9_sub7	UAGCGAACUGAGAAGGGCCAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCUGCCACGAUACCUCGGCCCUUCUCA	37494
RNACS4971	hPKU5_R14_P9_sub0	UAGCGAACUGAGAAGGGCCAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCCCACAAUACCUCGGCCCUUCUCA	37495
RNACS4972	hPKU5_R14_P9_sub1	UAGCGAACUGAGAAGGGCCAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCCCACAAUACCGCGGCCCUUCUCA	37496
RNACS4973	hPKU5_R14_P9_sub2	UAGCGAACUGAGAAGGGCCAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCCCACAAUCCCUCGGCCCUUCUCA	37497
RNACS4974	hPKU5_R14_P9_sub3	UAGCGAACUGAGAAGGGCCAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCCCACAAUCCCGCGGCCCUUCUCA	37498
RNACS4975	hPKU5_R14_P9_sub4	UAGCGAACUGAGAAGGGCCAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCCCACAAUACCUCGCCCCUUCUCA	37499
RNACS4976	hPKU5_R14_P9_sub7	UAGCGAACUGAGAAGGGCCAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCCCACGAUACCUCGGCCCUUCUCA	37500
RNACS4977	hPKU5_R12_P9_sub0	UAGCGAACUGAGAAGGGCCAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCACAAUACCUCGGCCCUUCUCA	37501
RNACS4978	hPKU5_R12_P9_sub1	UAGCGAACUGAGAAGGGCCAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCACAAUACCGCGGCCCUUCUCA	37502
RNACS4979	hPKU5_R12_P9_sub2	UAGCGAACUGAGAAGGGCCAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCACAAUCCCUCGGCCCUUCUCA	37503
RNACS4980	hPKU5_R12_P9_sub3	UAGCGAACUGAGAAGGGCCAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCACAAUCCCGCGGCCCUUCUCA	37504
RNACS4981	hPKU5_R12_P9_sub4	UAGCGAACUGAGAAGGGCCAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCACAAUACCUCGCCCCUUCUCA	37505
RNACS4982	hPKU5_R12_P9_sub7	UAGCGAACUGAGAAGGGCCAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCACGAUACCUCGGCCCUUCUCA	37506
RNACS4983	hPKU5_R20_P8_sub0	UAGCGAACUGAGAAGGGCCAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCUUGCUGCCACAAUACCUCGGCCCUUCUC	37507
RNACS4984	hPKU5_R20_P8_sub1	UAGCGAACUGAGAAGGGCCAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCUUGCUGCCACAAUACCGCGGCCCUUCUC	37508
RNACS4985	hPKU5_R20_P8_sub2	UAGCGAACUGAGAAGGGCCAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCUUGCUGCCACAAUCCCUCGGCCCUUCUC	37509

RNACS4986	hPKU5_R20_P8_sub3	UAGCGAACUGAGAAGGGCCAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCUUGCUGCCACAAUCCCGCGGCCCUUCUC	37510
RNACS4987	hPKU5_R20_P8_sub4	UAGCGAACUGAGAAGGGCCAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCUUGCUGCCACAAUACCUCGCCCCUUCUC	37511
RNACS4988	hPKU5_R20_P8_sub7	UAGCGAACUGAGAAGGGCCAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCUUGCUGCCACGAUACCUCGGCCCUUCUC	37512
RNACS4989	hPKU5_R18_P8_sub0	UAGCGAACUGAGAAGGGCCAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCGCUGCCACAAUACCUCGGCCCUUCUC	37513
RNACS4990	hPKU5_R18_P8_sub1	UAGCGAACUGAGAAGGGCCAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCGCUGCCACAAUACCGCGGCCCUUCUC	37514
RNACS4991	hPKU5_R18_P8_sub2	UAGCGAACUGAGAAGGGCCAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCGCUGCCACAAUCCCUCGGCCCUUCUC	37515
RNACS4992	hPKU5_R18_P8_sub3	UAGCGAACUGAGAAGGGCCAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCGCUGCCACAAUCCCGCGGCCCUUCUC	37516
RNACS4993	hPKU5_R18_P8_sub4	UAGCGAACUGAGAAGGGCCAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCGCUGCCACAAUACCUCGCCCCUUCUC	37517
RNACS4994	hPKU5_R18_P8_sub7	UAGCGAACUGAGAAGGGCCAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCGCUGCCACGAUACCUCGGCCCUUCUC	37518
RNACS4995	hPKU5_R16_P8_sub0	UAGCGAACUGAGAAGGGCCAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCUGCCACAAUACCUCGGCCCUUCUC	37519
RNACS4996	hPKU5_R16_P8_sub1	UAGCGAACUGAGAAGGGCCAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCUGCCACAAUACCGCGGCCCUUCUC	37520
RNACS4997	hPKU5_R16_P8_sub2	UAGCGAACUGAGAAGGGCCAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCUGCCACAAUCCCUCGGCCCUUCUC	37521
RNACS4998	hPKU5_R16_P8_sub3	UAGCGAACUGAGAAGGGCCAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCUGCCACAAUCCCGCGGCCCUUCUC	37522
RNACS4999	hPKU5_R16_P8_sub4	UAGCGAACUGAGAAGGGCCAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCUGCCACAAUACCUCGCCCCUUCUC	37523
RNACS5000	hPKU5_R16_P8_sub7	UAGCGAACUGAGAAGGGCCAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCUGCCACGAUACCUCGGCCCUUCUC	37524
RNACS5001	hPKU5_R14_P8_sub0	UAGCGAACUGAGAAGGGCCAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCCCACAAUACCUCGGCCCUUCUC	37525

RNACS5002	hPKU5_R14_P8_sub1	UAGCGAACUGAGAAGGGCCAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCCCACAAUACCGCGGCCCUUCUC	37526
RNACS5003	hPKU5_R14_P8_sub2	UAGCGAACUGAGAAGGGCCAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCCCACAAUCCCUCGGCCCUUCUC	37527
RNACS5004	hPKU5_R14_P8_sub3	UAGCGAACUGAGAAGGGCCAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCCCACAAUCCCGCGGCCCUUCUC	37528
RNACS5005	hPKU5_R14_P8_sub4	UAGCGAACUGAGAAGGGCCAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCCCACAAUACCUCGCCCCUUCUC	37529
RNACS5006	hPKU5_R14_P8_sub7	UAGCGAACUGAGAAGGGCCAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCCCACGAUACCUCGGCCCUUCUC	37530
RNACS5007	hPKU5_R12_P8_sub0	UAGCGAACUGAGAAGGGCCAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCACAAUACCUCGGCCCUUCUC	37531
RNACS5008	hPKU5_R12_P8_sub1	UAGCGAACUGAGAAGGGCCAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCACAAUACCGCGGCCCUUCUC	37532
RNACS5009	hPKU5_R12_P8_sub2	UAGCGAACUGAGAAGGGCCAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCACAAUCCCUCGGCCCUUCUC	37533
RNACS5010	hPKU5_R12_P8_sub3	UAGCGAACUGAGAAGGGCCAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCACAAUCCCGCGGCCCUUCUC	37534
RNACS5011	hPKU5_R12_P8_sub4	UAGCGAACUGAGAAGGGCCAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCACAAUACCUCGCCCCUUCUC	37535
RNACS5012	hPKU5_R12_P8_sub7	UAGCGAACUGAGAAGGGCCAGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCACGAUACCUCGGCCCUUCUC	37536
RNACS5013	hPKU6_R20_P11_sub0	ACUUUGCUGCCACAAUACCUGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCCGAACUGAGAAGGGCCGAGGUAUUGUGGCAG	37537
RNACS5014	hPKU6_R20_P11_sub1	ACUUUGCUGCCACAAUACCUGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCCGAACUGAGAAGGGCCGGGGUAUUGUGGCAG	37538
RNACS5015	hPKU6_R20_P11_sub4	ACUUUGCUGCCACAAUACCUGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCCGAACUGAGAACGGCCGGGGUAUUGUGGCAG	37539
RNACS5016	hPKU6_R20_P11_sub5	ACUUUGCUGCCACAAUACCUGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCCGAACUGAGAACGGACGGGGUAUUGUGGCAG	37540
RNACS5017	hPKU6_R20_P11_sub6	ACUUUGCUGCCACAAUACCUGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCCGAACUGAGAAGGGCCGCGGUAUUGUGGCAG	37541

RNACS5018	hPKU6_R20_P11_sub7	ACUUUGCUGCCACAAUACCUGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCCGAACUGAGAAGGGACGCGGUAUUGUGGCAG	37542
RNACS5019	hPKU6_R18_P11_sub0	ACUUUGCUGCCACAAUACCUGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCAACUGAGAAGGGCCGAGGUAUUGUGGCAG	37543
RNACS5020	hPKU6_R18_P11_sub1	ACUUUGCUGCCACAAUACCUGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCAACUGAGAAGGGCCGGGGUAUUGUGGCAG	37544
RNACS5021	hPKU6_R18_P11_sub4	ACUUUGCUGCCACAAUACCUGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCAACUGAGAACGGCCGGGGUAUUGUGGCAG	37545
RNACS5022	hPKU6_R18_P11_sub5	ACUUUGCUGCCACAAUACCUGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCAACUGAGAACGGACGGGGUAUUGUGGCAG	37546
RNACS5023	hPKU6_R18_P11_sub6	ACUUUGCUGCCACAAUACCUGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCAACUGAGAAGGGCCGCGGUAUUGUGGCAG	37547
RNACS5024	hPKU6_R18_P11_sub7	ACUUUGCUGCCACAAUACCUGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCAACUGAGAAGGGACGCGGUAUUGUGGCAG	37548
RNACS5025	hPKU6_R16_P11_sub0	ACUUUGCUGCCACAAUACCUGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCCUGAGAAGGGCCGAGGUAUUGUGGCAG	37549
RNACS5026	hPKU6_R16_P11_sub1	ACUUUGCUGCCACAAUACCUGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCCUGAGAAGGGCCGGGGUAUUGUGGCAG	37550
RNACS5027	hPKU6_R16_P11_sub4	ACUUUGCUGCCACAAUACCUGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCCUGAGAACGGCCGGGGUAUUGUGGCAG	37551
RNACS5028	hPKU6_R16_P11_sub5	ACUUUGCUGCCACAAUACCUGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCCUGAGAACGGACGGGGUAUUGUGGCAG	37552
RNACS5029	hPKU6_R16_P11_sub6	ACUUUGCUGCCACAAUACCUGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCCUGAGAAGGGCCGCGGUAUUGUGGCAG	37553
RNACS5030	hPKU6_R16_P11_sub7	ACUUUGCUGCCACAAUACCUGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCCUGAGAAGGGACGCGGUAUUGUGGCAG	37554
RNACS5031	hPKU6_R14_P11_sub0	ACUUUGCUGCCACAAUACCUGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCGAGAAGGGCCGAGGUAUUGUGGCAG	37555
RNACS5032	hPKU6_R14_P11_sub1	ACUUUGCUGCCACAAUACCUGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCGAGAAGGGCCGGGGUAUUGUGGCAG	37556
RNACS5033	hPKU6_R14_P11_sub4	ACUUUGCUGCCACAAUACCUGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCGAGAACGGCCGGGGUAUUGUGGCAG	37557

RNACS5034	hPKU6_R14_P11_sub5	ACUUUGCUGCCACAAUACCUGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCGAGAACGGACGGGGUAUUGUGGCAG	37558
RNACS5035	hPKU6_R14_P11_sub6	ACUUUGCUGCCACAAUACCUGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCGAGAAGGGCCGCGGUAUUGUGGCAG	37559
RNACS5036	hPKU6_R14_P11_sub7	ACUUUGCUGCCACAAUACCUGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCGAGAAGGGACGCGGUAUUGUGGCAG	37560
RNACS5037	hPKU6_R12_P11_sub0	ACUUUGCUGCCACAAUACCUGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCGAAGGGCCGAGGUAUUGUGGCAG	37561
RNACS5038	hPKU6_R12_P11_sub1	ACUUUGCUGCCACAAUACCUGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCGAAGGGCCGGGGUAUUGUGGCAG	37562
RNACS5039	hPKU6_R12_P11_sub4	ACUUUGCUGCCACAAUACCUGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCGAACGGCCGGGGUAUUGUGGCAG	37563
RNACS5040	hPKU6_R12_P11_sub5	ACUUUGCUGCCACAAUACCUGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCGAACGGACGGGGUAUUGUGGCAG	37564
RNACS5041	hPKU6_R12_P11_sub6	ACUUUGCUGCCACAAUACCUGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCGAAGGGCCGCGGUAUUGUGGCAG	37565
RNACS5042	hPKU6_R12_P11_sub7	ACUUUGCUGCCACAAUACCUGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCGAAGGGACGCGGUAUUGUGGCAG	37566
RNACS5043	hPKU6_R20_P10_sub0	ACUUUGCUGCCACAAUACCUGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCCGAACUGAGAAGGGCCGAGGUAUUGUGGCA	37567
RNACS5044	hPKU6_R20_P10_sub1	ACUUUGCUGCCACAAUACCUGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCCGAACUGAGAAGGGCCGGGGUAUUGUGGCA	37568
RNACS5045	hPKU6_R20_P10_sub4	ACUUUGCUGCCACAAUACCUGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCCGAACUGAGAACGGCCGGGGUAUUGUGGCA	37569
RNACS5046	hPKU6_R20_P10_sub5	ACUUUGCUGCCACAAUACCUGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCCGAACUGAGAACGGACGGGGUAUUGUGGCA	37570
RNACS5047	hPKU6_R20_P10_sub6	ACUUUGCUGCCACAAUACCUGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCCGAACUGAGAAGGGCCGCGGUAUUGUGGCA	37571
RNACS5048	hPKU6_R20_P10_sub7	ACUUUGCUGCCACAAUACCUGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCCGAACUGAGAAGGGACGCGGUAUUGUGGCA	37572
RNACS5049	hPKU6_R18_P10_sub0	ACUUUGCUGCCACAAUACCUGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCAACUGAGAAGGGCCGAGGUAUUGUGGCA	37573

RNACS5050	hPKU6_R18_P10_sub1	ACUUUGCUGCCACAAUACCUGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCAACUGAGAAGGGCCGGGGUAUUGUGGCA	37574
RNACS5051	hPKU6_R18_P10_sub4	ACUUUGCUGCCACAAUACCUGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCAACUGAGAACGGCCGGGGUAUUGUGGCA	37575
RNACS5052	hPKU6_R18_P10_sub5	ACUUUGCUGCCACAAUACCUGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCAACUGAGAACGGACGGGGUAUUGUGGCA	37576
RNACS5053	hPKU6_R18_P10_sub6	ACUUUGCUGCCACAAUACCUGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCAACUGAGAAGGGCCGCGGUAUUGUGGCA	37577
RNACS5054	hPKU6_R18_P10_sub7	ACUUUGCUGCCACAAUACCUGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCAACUGAGAAGGGACGCGGUAUUGUGGCA	37578
RNACS5055	hPKU6_R16_P10_sub0	ACUUUGCUGCCACAAUACCUGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCCUGAGAAGGGCCGAGGUAUUGUGGCA	37579
RNACS5056	hPKU6_R16_P10_sub1	ACUUUGCUGCCACAAUACCUGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCCUGAGAAGGGCCGGGGUAUUGUGGCA	37580
RNACS5057	hPKU6_R16_P10_sub4	ACUUUGCUGCCACAAUACCUGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCCUGAGAACGGCCGGGGUAUUGUGGCA	37581
RNACS5058	hPKU6_R16_P10_sub5	ACUUUGCUGCCACAAUACCUGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCCUGAGAACGGACGGGGUAUUGUGGCA	37582
RNACS5059	hPKU6_R16_P10_sub6	ACUUUGCUGCCACAAUACCUGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCCUGAGAAGGGCCGCGGUAUUGUGGCA	37583
RNACS5060	hPKU6_R16_P10_sub7	ACUUUGCUGCCACAAUACCUGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCCUGAGAAGGGACGCGGUAUUGUGGCA	37584
RNACS5061	hPKU6_R14_P10_sub0	ACUUUGCUGCCACAAUACCUGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCGAGAAGGGCCGAGGUAUUGUGGCA	37585
RNACS5062	hPKU6_R14_P10_sub1	ACUUUGCUGCCACAAUACCUGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCGAGAAGGGCCGGGGUAUUGUGGCA	37586
RNACS5063	hPKU6_R14_P10_sub4	ACUUUGCUGCCACAAUACCUGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCGAGAACGGCCGGGGUAUUGUGGCA	37587
RNACS5064	hPKU6_R14_P10_sub5	ACUUUGCUGCCACAAUACCUGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCGAGAACGGACGGGGUAUUGUGGCA	37588
RNACS5065	hPKU6_R14_P10_sub6	ACUUUGCUGCCACAAUACCUGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCGAGAAGGGCCGCGGUAUUGUGGCA	37589

RNACS5066	hPKU6_R14_P10_sub7	ACUUUGCUGCCACAAUACCUGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCGAGAAGGGACGCGGUAUUGUGGCA	37590
RNACS5067	hPKU6_R12_P10_sub0	ACUUUGCUGCCACAAUACCUGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCGAAGGGCCGAGGUAUUGUGGCA	37591
RNACS5068	hPKU6_R12_P10_sub1	ACUUUGCUGCCACAAUACCUGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCGAAGGGCCGGGGUAUUGUGGCA	37592
RNACS5069	hPKU6_R12_P10_sub4	ACUUUGCUGCCACAAUACCUGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCGAACGGCCGGGGUAUUGUGGCA	37593
RNACS5070	hPKU6_R12_P10_sub5	ACUUUGCUGCCACAAUACCUGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCGAACGGACGGGGUAUUGUGGCA	37594
RNACS5071	hPKU6_R12_P10_sub6	ACUUUGCUGCCACAAUACCUGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCGAAGGGCCGCGGUAUUGUGGCA	37595
RNACS5072	hPKU6_R12_P10_sub7	ACUUUGCUGCCACAAUACCUGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCGAAGGGACGCGGUAUUGUGGCA	37596
RNACS5073	hPKU6_R20_P9_sub0	ACUUUGCUGCCACAAUACCUGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCCGAACUGAGAAGGGCCGAGGUAUUGUGGC	37597
RNACS5074	hPKU6_R20_P9_sub1	ACUUUGCUGCCACAAUACCUGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCCGAACUGAGAAGGGCCGGGGUAUUGUGGC	37598
RNACS5075	hPKU6_R20_P9_sub4	ACUUUGCUGCCACAAUACCUGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCCGAACUGAGAACGGCCGGGGUAUUGUGGC	37599
RNACS5076	hPKU6_R20_P9_sub5	ACUUUGCUGCCACAAUACCUGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCCGAACUGAGAACGGACGGGGUAUUGUGGC	37600
RNACS5077	hPKU6_R20_P9_sub6	ACUUUGCUGCCACAAUACCUGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCCGAACUGAGAAGGGCCGCGGUAUUGUGGC	37601
RNACS5078	hPKU6_R20_P9_sub7	ACUUUGCUGCCACAAUACCUGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCCGAACUGAGAAGGGACGCGGUAUUGUGGC	37602
RNACS5079	hPKU6_R18_P9_sub0	ACUUUGCUGCCACAAUACCUGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCAACUGAGAAGGGCCGAGGUAUUGUGGC	37603
RNACS5080	hPKU6_R18_P9_sub1	ACUUUGCUGCCACAAUACCUGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCAACUGAGAAGGGCCGGGGUAUUGUGGC	37604
RNACS5081	hPKU6_R18_P9_sub4	ACUUUGCUGCCACAAUACCUGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCAACUGAGAACGGCCGGGGUAUUGUGGC	37605

RNACS5082	hPKU6_R18_P9_sub5	ACUUUGCUGCCACAAUACCUGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCAACUGAGAACGGACGGGGUAUUGUGGC	37606
RNACS5083	hPKU6_R18_P9_sub6	ACUUUGCUGCCACAAUACCUGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCAACUGAGAAGGGCCGCGGUAUUGUGGC	37607
RNACS5084	hPKU6_R18_P9_sub7	ACUUUGCUGCCACAAUACCUGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCAACUGAGAAGGGACGCGGUAUUGUGGC	37608
RNACS5085	hPKU6_R16_P9_sub0	ACUUUGCUGCCACAAUACCUGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCCUGAGAAGGGCCGAGGUAUUGUGGC	37609
RNACS5086	hPKU6_R16_P9_sub1	ACUUUGCUGCCACAAUACCUGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCCUGAGAAGGGCCGGGGUAUUGUGGC	37610
RNACS5087	hPKU6_R16_P9_sub4	ACUUUGCUGCCACAAUACCUGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCCUGAGAACGGCCGGGGUAUUGUGGC	37611
RNACS5088	hPKU6_R16_P9_sub5	ACUUUGCUGCCACAAUACCUGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCCUGAGAACGGACGGGGUAUUGUGGC	37612
RNACS5089	hPKU6_R16_P9_sub6	ACUUUGCUGCCACAAUACCUGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCCUGAGAAGGGCCGCGGUAUUGUGGC	37613
RNACS5090	hPKU6_R16_P9_sub7	ACUUUGCUGCCACAAUACCUGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCCUGAGAAGGGACGCGGUAUUGUGGC	37614
RNACS5091	hPKU6_R14_P9_sub0	ACUUUGCUGCCACAAUACCUGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCGAGAAGGGCCGAGGUAUUGUGGC	37615
RNACS5092	hPKU6_R14_P9_sub1	ACUUUGCUGCCACAAUACCUGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCGAGAAGGGCCGGGGUAUUGUGGC	37616
RNACS5093	hPKU6_R14_P9_sub4	ACUUUGCUGCCACAAUACCUGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCGAGAACGGCCGGGGUAUUGUGGC	37617
RNACS5094	hPKU6_R14_P9_sub5	ACUUUGCUGCCACAAUACCUGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCGAGAACGGACGGGGUAUUGUGGC	37618
RNACS5095	hPKU6_R14_P9_sub6	ACUUUGCUGCCACAAUACCUGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCGAGAAGGGCCGCGGUAUUGUGGC	37619
RNACS5096	hPKU6_R14_P9_sub7	ACUUUGCUGCCACAAUACCUGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCGAGAAGGGACGCGGUAUUGUGGC	37620
RNACS5097	hPKU6_R12_P9_sub0	ACUUUGCUGCCACAAUACCUGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCGAAGGGCCGAGGUAUUGUGGC	37621

RNACS5098	hPKU6_R12_P9_sub1	ACUUUGCUGCCACAAUACCUGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCGAAGGGCCGGGGUAUUGUGGC	37622
RNACS5099	hPKU6_R12_P9_sub4	ACUUUGCUGCCACAAUACCUGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCGAACGGCCGGGGUAUUGUGGC	37623
RNACS5100	hPKU6_R12_P9_sub5	ACUUUGCUGCCACAAUACCUGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCGAACGGACGGGGUAUUGUGGC	37624
RNACS5101	hPKU6_R12_P9_sub6	ACUUUGCUGCCACAAUACCUGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCGAAGGGCCGCGGUAUUGUGGC	37625
RNACS5102	hPKU6_R12_P9_sub7	ACUUUGCUGCCACAAUACCUGUUUUAGAGCUAGAAAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUCGGUGCGAAGGGACGCGGUAUUGUGGC	37626

The gene modifying system comprising mRNA encoding the gene modifying polypeptide listed above and a template RNA listed above were transfected into human hepatoblasts differentiated from CRISPR-edited iPSCs containing the R408W mutation in the human PAH gene. Briefly PAH iPSCs are dissociated into single cells and then replated onto Geltex-coated plates. The iPSCs were then differentiated into definitive endoderm cells by treatment with Activin A, FGF2, and ChIR for 7 days. Definitive endoderm cells are then further patterned into foregut endoderm cells by activation of the BMP4 and FGF2 signaling pathway for an additional 6 days. Lastly, foregut endoderm cells were patterned into hepatoblast cells by treatment with oncostamin M, dexamethasone, hepatocyte growth factors, and ChIR for 12 days. Hepatoblasts were then sub-cultured onto collagen1-coated plates and expanded in media containing FGF19, Dexamethazone, ChIR, and SB431542 prior to transfection. The gene modifying polypeptide and template RNA were delivered by nucleofection in the RNA format. Specifically, 4 µg of gene modifying polypeptide mRNA were combined with 10 µg of chemically synthesized template RNA, in 5 µL of water. The transfection mix was added to 100,000 iPSCs in Buffer P3 [Lonza], and cells were nucleofected using program DG-138. After nucleofection, cells were grown at 37˚C, 5% CO_2 for 3 days prior to cell lysis and genomic DNA extraction. To analyze gene editing activity, primers flanking the target insertion site locus were used to amplify across the locus. Amplicons were analyzed via short read sequencing using an Illumina MiSeq. Conversion of T>C indicates successful editing.

As shown by FIG. 31A, treating hepatoblasts with gene modifying systems comprising exemplary hPKU3 template RNAs comprising a variety of silent substitutions (FIG. 31B) resulted in editing at the target locus. The results show that silent substitution 4 (sub4) resulted in comparable rewriting % as the template RNA without silent substitutions, whereas other silent substitutions resulted in lower rewriting %.

As shown by FIG. 32A, treating hepatoblasts with gene modifying systems comprising exemplary hPKU4 template RNAs comprising a variety of silent substitutions (FIG. 32B) resulted in editing at the target locus. The results show that silent substitution 4 (sub4) resulted in comparable or higher rewriting % as the template RNA without silent substitutions, whereas other silent substitutions resulted in lower rewriting %.

As shown by FIG. 33A, treating hepatoblasts with gene modifying systems comprising exemplary hPKU5 template RNAs comprising a variety of silent substitutions (FIG. 33B)

resulted in editing at the target locus. The results show that silent substitution 4 (sub4) resulted in comparable or higher rewriting % as the template RNA without silent substitutions, whereas other silent substitutions resulted in lower rewriting %.

As shown by FIG. 34A, treating hepatoblasts with gene modifying systems comprising exemplary hPKU6 template RNAs comprising a variety of silent substitutions (FIG. 34B) resulted in editing at the target locus. The results show that silent substitutions 5, 6, and 7 (sub5, sub6, and sub7, respectively) resulted in much higher rewriting % as the template RNA without silent substitutions, which had a very low rewriting %. These results demonstrate that silent substitutions can rescue the low rewriting activity of exemplary hPKU6 template RNAs.

Taken together, these results demonstrate that silent substitutions can increase the rewriting activity of exemplary template RNAs that target a therapeutically relevant human locus, and in some cases rescue otherwise low rewriting activity.

It should be understood that for all numerical bounds describing some parameter in this application, such as “about,” “at least,” “less than,” and “more than,” the description also necessarily encompasses any range bounded by the recited values. Accordingly, for example, the description “at least 1, 2, 3, 4, or 5” also describes, inter alia, the ranges 1-2, 1-3, 1-4, 1-5, 2-3, 2-4, 2-5, 3-4, 3-5, and 4-5, et cetera.

For all patents, applications, or other reference cited herein, such as non-patent literature and reference sequence information, it should be understood that they are incorporated by reference in their entirety for all purposes as well as for the proposition that is recited. Where any conflict exists between a document incorporated by reference and the present application, this application will control. All information associated with reference gene sequences disclosed in this application, such as GeneIDs or accession numbers (typically referencing NCBI accession numbers), including, for example, genomic loci, genomic sequences, functional annotations, allelic variants, and reference mRNA (including, e.g., exon boundaries or response elements) and protein sequences (such as conserved domain structures), as well as chemical references (e.g., PubChem compound, PubChem substance, or PubChem Bioassay entries, including the annotations therein, such as structures and assays, et cetera), are hereby incorporated by reference in their entirety.

Headings used in this application are for convenience only and do not affect the interpretation of this application.